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(NL); WEZEL GILLES PHILIPPUS
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AX007216 Sequence
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AL096823 Streptomy
AL07224 Sequence
AL096771 Streptomy
AX007220 Sequence
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AL137778 Streptomy
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AX0721705 Streptomy
AX211705 Streptomy
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AX07564 Saccharop
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AR103045 Sequence
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms abstant: wo 0000613-A 1 06-3NN-2000;
UNIV LEIDEN (NL); RRALB BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARI (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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D87846 Streptomyce
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Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/db_xref="G1:2281004"
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nutrient rich media
Actinomycetol. 9, 124-135 (1995)
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385, 389
392, 802
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/codon_start=1
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GDAPVTWAFTDKIPLDGLNSPSGDGDVHIGPTEPEGGLGDVHIRLQVGADRALFRAGTA
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Kawamoto, S. and Ensign, J. C.
Cloning and characterization of a gene involved in regulation of sporulation and cell division of Streptomyces griseus
Actinomycetol. 9, 136-151 (1995)
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Isolation of mutants of Streptomyces griseus that sporulate
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                of Streptomyces griseus"
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/translation="MMSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAF GRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRT DKLVPLGGEHTLGDFDGNLEDALGRILAEEQNAG" ö 4 (bases 1 to 1513)
Shinichi, K. and Ensign, J.
Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus
Unpublished (1995)
5 (bases 1 to 1513) Direct Submission Submitted"(06-APR-1995) Kawamoto Shinichi, National Food Research Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2, Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996) Location/Qualiflers 121 ttccacettcccggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggac 180 240 300 360 724 61 ttccgtattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacg 120 604 664 784 484 Gaps Kawamoto, S., Watanabe, H., Hesketh, A., Ensign, J.C. and Ochi, K. Expression analysis of the ssgA gene product, associated with sporulation and cell division in Streptomyces griseus Microbiology (Reading, England) 143 (Pt 4), 1077-1086 (1997) 97286526 ö Length 1513; Indels

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Streptomyces netropsis SsgA (ssgA) gene, complete cds.
AF195772
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GDAPVTWAFCRELLLDGINRPSGDGDYHIAPTDPEGLSDVSIRLQVGADRALFRAGAP
PLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGKILABEQNAG"
158 c 168 t 162 g 68 t
                                                                                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 438)

1 (bases 1 to 438)

2 (cloning and sequencing of the Streptomyces netropsis ssgA gene Unpublished

2 (bases 1 to 438)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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 437
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               361 GAGGACGCACTGGCCGCATCCTCGCCGAGCAGCAGCAGCAGCCGCTG 407
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  gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg
                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (18-OCT-1999) Biochemistry, Unive
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
1. 438
//Organism="Streptomyces netropsis"
/db_xref="taxon:55404"
1. 438
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Pred. No. 2.9e-33;
0; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAG28483.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to S
division protein"
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/transl_table=11
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                                                                                                                                     AF195772.1 GI:11066162
                                                                                                                                                               Streptomyces netropsis.
Streptomyces netropsis
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84.2%;
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Patent: WO 0000613-A 3 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
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Pred. No. 2.2e-43;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                          AX007218 407 bp
Sequence 3 from Patent WO0000613.
AX007218
                                                                                                                                                                                                                                                                                                                                                     /organism="Streptomyces/db_xref="taxon:1911"
                                                                                                                                                                                                                                                                                                                                                                                                          1. .>405
/gene="ssgA"
/note="strain ATTC of
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/gene="ssgA"

/note="strain ATCC of Streptomyces netropsis"

/codon_start=1

/transl_table=11

/product="ssgA"

/product="ssgA"

/protein_id="cACO7388.1"

/db_xref="d1:9995091"

/translation="MSFLVSEELSFKIPVELRYETRDPYAVRWTFHLPGDAPVTWAFG
                                                                                                                                                                                                                                                                                                                                                              filamentous microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
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361 CAGACTCTGGGTGACTTCGAGGACAGCCTGGAGGCCGCGCTCGGCAAGATCCTCGCCGAG 420
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                                            cacacgetgggtgaettegaeggeaacetggaggaegeaetgggeegeateetegeegag
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151 c 131 g 62 t
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83.38;
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., using a specially developed Hidden Markov Model (Krogh et al., program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abab; bldA regulation; cysA; cystathionine/methionine gamma-synthase/lyse; gntR-family; integrated element; korSA; lysR-family; membrane protein; phosphotyrosine protein phosphatase; pra; psAM2; ptpA; ssgA; thiamine biosynthesis; thlC; transcriptional regulator; trasA.

Streptomyces coelicolor A3(2)
Bacteria; Flrmincutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetales; Streptomycineae; Streptomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

I (bases 1 to 15441)
Klaser, M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 08-JUL-1999
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James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (08-UUL-1999) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrelldsanger.ac.uk Cosmids supplied by Prof. David AA. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                 241 GGGGGGACCGCGCCTCTTCCGTGCAGGCGCCCGCCGCGGGTGGTCGCTTCCTCGACCGC 300
                                                                                                                                    acgacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor cosmid Q11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seeger, K. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 15441)
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transcriptional regulator, len: 301 aa; previously sequenced as TR:053869 (EMBL:037580) S.coelicolor lysR-like protein (301 aa). Highly similar to SW:ARAB_STRAT (EMBL:037580), arab, Streptomyces antibioticus transcriptional regulatory protein (301 aa), fasta soores; opt: 1581 z-score: 1813.2 E(): 0, 80.3% identity in 300 aa overlap. Similar to many other transcriptional regulators. Contains probable helix-turn-helix motif at aa 17-38 (Score 1659, +4.84 SD). Contains Pfam match to PF00126 HTHL! Bacterial regulatory helix-turn-helix protein, lysR family and PS00044 Bacterial regulatory proteins, lysR family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SCQ11.01c, hypothetical protein, partial CDS, len: 995 as: unknown function, previously sequenced as TR:0380 (EMBL:03780), S.coelicolor hypothetical protein ORF5 downstream of phosphotyrosine protein phosphatase (159 aa). Weak similarity to the N-terminus of TR:069888 (EMBL:AL02797) Streptomyces coelicolor hypothetical protein (172 aa). fasta scores; opt: 158 z-score: 206.4 E(): 0.00036, 46.2% identity in 65 aa overlap. Continues as SCH24.40c in cosmid H24 (EMBL:AL049826)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTVRPVVKRTARAVLLDGDHLILIKRTKPGVDPYWVTPGGGVEPDDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDEVHVLVATPHWAERAGVEDVRDTDASALKHVPVVEVHESLPFVGRYWASVFDARPA
SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
RTGTLAMPHIARAHEWLLRAAADWN"
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RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAETGLEDDSTLRTLHLAGPPEFTA
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/protein_id="CAB46957.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="sequence corresponding to EMBL:U37580 from 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="overlap with Streptomyces coelicolor cosmid H24 (EMBL:AL049826) from 41528 to 41625" complement(360, 1265) /gene="SCQ11.02c"
                                        ø
                              overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.
Cosmid Q11 Lies between H24 and D78 on the Asel-O
   It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCQ11.02c"
/note="Match to PF00126 HTH_1, Bacterial regulatory
holix-turn-helix protein, lysR family Score 145.96"
complement(1125. .1217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(360. .1265)
/gene="SCQ11.02c"
/note="SCQ11.02c, abaB, probable lysR-family
                                                                                                                                                                                                                            /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=SCQ11.01c
/product="hypothetical protein"
/protein.id="CAB46956.1"
/db_xref="G1:5457268"
                                                                                                                                                                                                                                                                                         /db_xref="taxon:100226"
/clone="cosmid 011"
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                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCQ11.01c"
complement(<1.289)
/gene="SCQ11.01c"
                                                                                                                             genomic restriction fragment.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1. .4279)
                                                                                                                                                                                                                                                                                                                                                                 complement(1. .289)
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/label=abaB
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                                                                                                                                                                                                                                                              /strain="A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="abaB
sequenced clone.
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                                                                                                                                                            FEATURES
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gamma-synthase/lyse, len: 392 as; previously sequenced as SW.CYSA_STRCO (EMBL.U37580), cysA, S.coelicolor putative cystathionine gamma-lyses (392 as), previously sequenced as SW.CYSA_STRCO (EMBL.U37580), cysA, S.coelicolor putative cystathionine gamma-lyses (392 as), Enfiniar to many e.g. SW.MEGL_PSEPU (EMBL.D88554), mdcA, Pseudomonas putida methionine gamma-lyses (398 as), fasta scores; opt: 608 z-score: 653.6 E(): 4.5e-29, 36.9% identity in 404 as overlap. Highly similar to TR:053668 (EMBL.X91393) Streptomyces antibioticus hypothetical protein found upstream of the abaB gene (232 as) (87.1% identity in 232 as overlap). Contains Pfam match to PF01053 Cys_Met_Meta_PP, Cys/Met metabolism PLP-dependent enzyme and PS008688 Cys/Met metabolism enzymes pyridoxal-phosphate attachment site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine-phosphatase (164 aa). Contains Pfam match
to PF01451 LMWPc, Low molecular weight phosphotyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVFAAHFHLPGDPTGPYTYGRDENPTWTRLESAIGELEAPGEAGVETLVFASGMAAIS
SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IETPSNPGLDVCDVRRLVEAÄHAGGALVÄVDNTLATPLGQRPLELGÄDFSVASGTKÖL
TRGDVLLGYVAGRDAGAMAÄVRRMKTVAA. IPGOPBAMLAHRSTATLÖLKVDRODST
ALKVAGALRTRPETTGLRY PGLPDDPSHKVASQOMLRYGCVVSFTLESRARADBRELDA
LRLVEGATSFGGVRSTAERRGKWGGDAVPEGFTRLSVGAEDPDDLUADLLRALDETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWHEGEGADPRTEAVLADHGYGLDHAARQFQQSWFSRLDLVVALDAGHLRALRRLAPT
ERDAAKVRLLRSYDPAVAGGDLDVPDPYYGGRDGFEECLEMVEAASTGLLAAVREQVE
GRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MTYRVCFVCTGNICRSPMAEAVFRARVEDAGLGHLVEADSAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                   complement(1518. .2696)
/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
/note="PS00044 Bacterial regulatory proteins, lysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-tyrosine-phosphatase, len: 164 aa; previously sequenced as SW:PTPA_STRCO (EMBL:U37580), ptpA, S.coelicolor low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15441;
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/gene="SCQ11.04c"
/note="SCQ11.04c, ptpA, low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=cysA
/product="putative cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PS00868 Cys/Met metabolism enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
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77.6%; Pred. No. 9.9e-28;
ive 0; Mismatches 98
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/product="low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein-tyrosine-phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma-synthase/lyase"
/protein_id="CAB46958.1"
/db_xref="G1:5457270"
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                                                            .2696)
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/gene="SCQ11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB46959"
/db_xref="G1:5457271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein phosphatase"
                                                                                         /gene="SCQ11.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2031.
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/transl_table=11
                                                            complement (1518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ptpA"
                                                                                                                      /note="cysA"
                                signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 64.2
Best Local Similarity 77.6
Matches 340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                gene
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/note="similar to Streptomyces griseus SsgA; possible cell
division protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 408) van Wezel,G.P., Rousseau,C. and Kraal,B. Cloning and sequencing of the Streptomyces goldeniensis ssgA gene Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                 306 accgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacac 365
                                                                              Gaps
                                                                                                       65
                                                                                                                                9
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van Wazel,G.P.
Direct Submission
Submitted (18-OCT-1999) Biochemistry, University of Leiden, 9502, Lidden 2300 RA, Netherlands
Location/Qualifiers
                                                                                                                                                          ccttcccggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggtggacgggct
                                                                                                                                                                                                                                                                  6 cgagtcggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcgttccg
                                                                                                                                                                                                                                        121 CCTCCCCGGAGACGCCCCGGTCACCTGGGTCTTCGGGCGTGAACTGCTGGTCGAGGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                             366 gctgggtgacttcgacggcaacctggaggacgcactggggccgcatcctcgccgaggagca
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Streptomyces goldeniensis SsgA (ssgA) gene, complete cds.
AF195770
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                                                    Length 566;
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    408
/organism="Streptomyces goldeniensis"
/db_xref="ATCC:21386"

                                                    Score 265; DB 1; L
Pred. No. 2.7e-25;
0; Mismatches 105;
 80
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 192
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                                                    60.5%;
75.8%;
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                                                                              Matches 328; Conservative
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//note="similar to Streptomyces griseus SsgA; possible cell division protein"
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPCDAPVTWVFG
RELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTD
QGLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
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Streptomyces albus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 566)
van Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and semencing of the Streptomyces albus ssgA gene
                                                                                                                                                                                     5684
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Submitted (18-OCT-1999) Biochemistry, University of Leiden,
9502, Leiden 2300 RA, Netherlands
                                                                                                                                                                                                                                                                 ttccgtattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacg
                                                                  ttccaccttcccggcgatgccctgtgacctgggcgttcggccgcgagctgctggtggac
                                                                                                                        atgcgcgagtcggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcg
                                                                                                                                                                                                                                        CTGGCCGAGGTGCTGATCCGACTTCAGGTCGGCAGCGACCAGGCGCTGTTCCGTTCCTCC
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/db_xref="GI:11066161"
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26. 433
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van Wezel, G.P.
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Box

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RELLIDGGRERCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPLGGERSLADFDALLDEALDRILAEEGNAG"
135 c 145 g 77 t
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Patent: WO 0000613-A 5 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
                                                                                                                                                                                                                                                                                                                                                            61.ACCTGTGATCCCCTACGCGGTGACCTTTCATCTGCCCGGAGATGCCCCGGTGACC 120
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        271
        ggcgcgggaccgtgcgctgttccgggcggggacggcaccgctggtggcgttcctcgaccgg
        330

        241
        GGGAGCGACCAGGCGATGTTCCGGGTCGGCACGGCGCCGCTGGTGGCCTTCCTGGACCGC
        300

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Streptomyces albus G
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/note="strain ATCC of Streptomyces albus
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                                                                                                                                                                                               Score 259.8; DB 6;
Pred. No. 1.3e-24;
0; Mismatches 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                     /product="SsgA"
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       /transl_table=11
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                                                                                                                                                                                               Query Match 59.3%;
Best Local Similarity 77.4%;
Matches 315; Conservative
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RELLIDGGRRPCGDGDVHTAAADPEFRGEVITRLQVGSDQAMFRVGTAPLVAFLDRTD
RYPVELGGRRSLADFALLDBALLDRALLDRALLDFT.
135 c 145 g 71 t
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
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/gene="ssgA"
/note="strain ATCC of Streptomyces goldeniensis"
/codon_start=1
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/db_xref="taxon:121022"
                                                                                                                                                                                             Score 260.8; DB 1;
Pred. No. 1e-24;
0; Mismatches 92;
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Patent: WO 0000613-A 7 06-JAN-2000;
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77.5%;
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                                                                                                                                                                                            Query Match
Best Local Similarity 77.5
Matches 316; Conservative
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TITLE
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KEYWORDS
SOURCE
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The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/Cgl.bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream initiation codon. Thosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between and overlaps cosmids E6 and E56 on the AseI-E genomic restriction fragment.

Some and a standard overlaps cosmids E6 and E56 on the contrapt of the contrap
Submitted (16-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinkton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SCE19A.01, hypothetical protein, partial CDS, len: >31 aa; unknown function, similar to members of the alkyl hydroperoxide reductase C/thiol-specific antioxidant family e.g. TR:053226 (EMBL:AL021185), bcp, Mycobacterium tuberculosis bacterioferritin comigratory protein (157 aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06, 63.3% identity in 30 aa overlap"
                                                                                                                                                                                                               Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
                                                                                                                                                                                                                                                                                                                                                         (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement(231. .845)
/gene="SCE19A.02c"
/note="SCE19A.02c, conserved hypothetical protein, len:
200 aa; unknown function, similar to many e.g.
SW:X03Q_MYCTU (EMBL:277902) Mycobacterium tuberculosis
hypothetical protein (204 aa), fasta scores; opt: 633
                                                                                                                                                                                                                                                                                          Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"hypothetical protein"
/protein_id="CASS50882.1"
/baxef="G1:5531350"
/tanslation="IVVDEGGKVERALYNVRATGHVAKIIKDLGI"

    .35284
    /organism="Streptomyces coelicolor A3(2)"

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/db_xref="taxon:100226"
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/label=SCE19A.01
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                      /troduct-"SsgA"
/protein_id="CAC07386.1"
/db_xref="GI:9995087"
/db_xref="GI:9995087"
/translation="MSFLVSELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
/translation="MSFLVSELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
/ranslation="MSFLVSERLAFFIPVELRYETVGVGSEQALFRVGKAPLLAFLDRTD
QGISLGSERAHADFDSHLDDALNRSLAEEQSAG"
150 c 139 g 61 t
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Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 35284)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ACGTCGATCCGTACGGGTGCGGTGCGTCCACCTCCCCGGAGACGCCCCGGTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgat 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 gtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgacc 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TGGGTCTTCGGGCGTGAACTGCTGGTCGAGGGAGTCCTGGACGCCGCGGGCGACGCGAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 atgagettectegtetecgaggagetetegtteegtatteeggtggageteegataegag 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAGCTTCCTCGTCTCCGAGGAGCTCGCCTTCCGCATCCCGGTGGAGCTGCGGTACGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcgcggaccgtgcgctgttccgggggggggggcggcaccgctggtggcgttcctcgaccgg
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James,K.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 239; DB 6; Length 40
Pred. No. 6e-22;
0; Mismatches 105; Indels
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Streptomyces coelicolor cosmid E19A.
           /transl_table=11
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Best Local Similarity 74.2%;
Matches 302; Conservative
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AUTHORS
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/labelsCE19A.05c
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/product="hypothetical protein"
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/oonplement(2385. 2489)
/gene="SCE19A.05c"
/note="Pfam match to entry PF00367 PTS_EIIB,
phosphotransferase system, EIIB, score 43.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetyltransferase; acyltransferase; adenine
phosphoribosiltransferase; DNA helicase; DNA polymerase III;
elongation factor; endodeoxyribonuclease; GTP pyrophosphokinase;
membrane protein; membrane transferase; protein-export membrane
protein; requiator; secreted protein; sugar transferase;
threonine-tRNA synthetase; transport system inner membrane protein.
unknown function, similar to parts of many sugar permeases e.g. TR:P96159 (EMBL:U65013), malx, Vibrio furnissii PTS (phosphocenol.pyruvate-dependent sugar phosphotransferase system) permease for glucose (523 aa), fasta scores; opt: 217 z-score: 287.9 E(): 1.1e-08, 48.1% identity in 77 aa overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20183 GCCGGGCTACCACACGCACGATCCCTACGCGTGCACATCACTTCCACATCGAC 20242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SCE19A.06"
/note="SCE19A.06, possible PTS transmembrane component,
len: 431 aa; similar to many PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20123 GTGGAACGCGAGCTGGAGCTCAGGCTCGTCGTCGCCCGAGAGCGGCATTCCGGTGCCG 20182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20303 CCGTCCGGGCACGGGACGTGCGGGTGTGGCCGTCGAAGACGGAGGGCCCGCAGCGTCGTA 20362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20363 CTCGTCGCCCTGAGCAGCCCGGACGCCGCCCTCCTGGAGGCGCCCCACGCCCCAGGTG 20422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            giggagetecgatacgaggteggegatecgtatgeeateeggatgaegtteeacetteee 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 ggcgatgcccctgtgacctgggcgttcggccgcgagctgctggacgggctcaacagc 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gitcaagcagaggicaigaigagcitccicgiciccgaggagcicicgitccgiaitccg 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccgagccgacgacgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtggcgttcctcgaccggacggacagctcgtgccgctcggccaggagcacacgctgggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cacatocggotocaggtcggcgcggtgccgtgctccgggcgggggggggcggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 113.4; DB 1;
Pred. No. 2.1e-06;
0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20483 GGGATCGACGACGGCTGGCCGAGCTGCTCGCCAG 20517
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Streptomyces coelicolor cosmid L2.
AL137778 1 GI:6822206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2660. .3955
/gene="SCE19A.06"
2660. .3955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 55.4%;
Conservative
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219; Conserv
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Best Local S
Matches 219
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VERSION
KEYWORDS
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ADAIADSVTELQQAVENADDPTQWEESLNSIDKNLDRIGDGTDNTDVNKAVDDLGKAV
BNVRRSVBKNDEPTPLESPYTDAAGELTKVCTP"
complement(1201. .1233)
/gene="SCG19A.03c"
/note="SCG19A.03c"
/note="SGG0013 Prokaryotic membrane lipoprotein lipid
attachment site"
complement(1454. .2191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1454. .2191)
/gene="SCE19A.04c"
/note="SCE19A.04c, rph, probable ribonuclease PH, len: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative ribonuclease PH"

/protein_id="cAB50985.1"

/db_xref="GI:531353"

/translation="MSRIDGRTPQQLRPVTIERGWSKHAEGSVLVSFGDTKVLCNASV

TEATSTARMAGGSGRWTAETAMLPRATHRGDRSSVGRIGGRTHEETSRLIGRSLRAV

IDYKALGERIVVLDCDVLQADGGTFRAATTGAVALADAVAWAGGSKLIKANKPLTG

TVSAVSVGIVDGTPLLDLRYEEDVRADTDMNVVCTGDGRFVVGTAEAEPFRADELN
                                                                                                                                                                                                                                                                                                           TGVTFAENALLKAHALAEATGLPAVADDSGLCVDVLNGAPGIFSARWAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGQLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTAEEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jotes "SCE19A.03c, possible secreted protein, len: 134 aa; unknown function, probable CDS suggested by GC frameplot, positional base preference and amino acid composition. Contains probable N-terminal signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                 /translation="MTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as; highly similar to many e.g. SW:RNPH_ECOLI (EMBL:X00781), rph, Escherichia coli ribonuclease PH (238 ab., fasta scores; opt: 916 z-score: 1116.8 E(): 0, 60.8% identity in 240 aa overlap. Contains Pfam match to entry PF01138 RNBASE_PH, 3' excribonuclease family and PS01277 Ribonuclease PH signature"
     z-score: 743.6 E(): 0, 52.0% identity in 200 aa overlap. Similar to SW:YGGV_ECOLI (EMBL:U28377), yggV, Escherichia coli hypothetical protein (197 aa) (49.5% identity in 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfarm match to entry PF01138 RNase_PH, 3' exoribonuclease family, score 266.70, E-value 3.1e-76" complement(1805. .1843) /gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2268. .2501)
/gene="SCE19A.05c"
/note="SCE19A.05c, hypothetical protein, len: 77 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS01277 Ribonuclease PH signature"
                                                                                                                                                                                                /product="hypothetical protein"
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/db_xref="G1:5531351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLLDLATAGCTELAELQRKALDATLER"
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/note="bf--
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/gene="SCE19A.05c"
                                                                                                                                                                                                                                                                                                                                                                                        complement(892. 1296)
/gene="SCE19A.03c"
complement(892. 1296)
/gene="SCE19A.03c"
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/label=SCE19A.03c
                                                                                                                                                                         /label=SCE19A.02c
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                                                                                                                   /codon_start=1
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                                                                                            overlap)"
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Gaps

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BCT 29-JAN-2000

us-09-749-185-1.rge

SOURCE

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identical to previously sequenced SW.RELA_STRCO (EMBL.X87267) Streptomyces coellcolor GTP pyrophosphokinase (EC 2.7.6.5) RelA, 847 aa and highly similar to SW.RELA_STRAT (EMBL.AF072829) Streptomyces antibioticus RelA protein, 841 aa; fasta scores: opt: 4965 z-score: 4906.2 E(): 0; 90.3% identity in 848 aa overlap and to SW.RELA_CORGL (EMBL.AF038651) Corynebacterium glutamicum GTP pyrophosphokinase (EC 2.7.6.5) RelA, 760 aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.7% identity in 774 aa overlap. Contains Pfam match to entry PF01842 ACT, ACT domain and match to Prosite entry PS00017 ATP/GTP-binding site motif A (P-loop) "//trasis_Lable=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="GTP_Prophosphokinase"
/product="GTP_Prophosphokinase"
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PVLEPLLRIVRGNDFXILTSTRQIEBARYOREMHHGQKRRESDPYTTHDLAYTIL
AELGMDPATLMAGLLHDTVEDTEYGLEDLRRDEVANTLUNGOVTKLDKVKFGBAQA
ETVRKMYVAMARDPPRVIX TKAADREHNMRTHRYLKREKGEKRARFILETAPLAHRLG
MNTIKWELEDLAFAILYPKMYDEIVRLANGTROPAETAVTDPWCTARARIKAT
VTGRRKHYSGYGKAYPENGROFAETEDPWGKFTEDPWGGTYHARNPVGGR
FKDYTAMPRENMYQSLHTTVIGPGGKFVPELQINTFDMHRRAFGILDMGDKATGROPATA
TPKGOVIALPAGAGTPVDFRAYANTTPVGHRTGARVGRUPTSTR
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/note="previously sequenced region Sw:SCSECAPT EMBL:X85969
S.coelicolor sect & apt genes"
complement(3708. .3781)
complement(3708. .4568)
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TGDSLYTLAHEMRYSDISALYAAIGEGHVSARNIVOKLVQALGGEBAATEELIDESVPP
SERGREKREMAANDPGRYVKGVSDVWYKLARCCTPVPGDPIIGFVTRGSGVSVHRSDCV
NVDSLSREPERILEVEWAPYOSSYELVAIOVEALDRSRLSDYTRVLSDQHVNILSAA
VQTSRDRVATSRFTFEMGDDFKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
                                                                                                                               AVDHLIREQVDAHHAVGDLEALRARIDOLVALVETRREEKAORAKOSDEARGAKEALV
AEAEELARSDQWRAAGERLASLVDPWKGLPRLDRKSDDELHHRESHARSAFSKRRÖH
FRACDAQAGREBRRITKBRLVSPRAEALSUSTDMGPTAARYBLMSEWKAAGRAQREHEDD
LWMRFRGAQDVFFARKSSVFARDAGOSENIKLKEELVTEARKLVPYTDLKSRRAAFR
SVNERWEAIGHVPRDARPKSRGGCTRSGGPSRRPRRPSGAGFPFRHARVPRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDKLRSQVEQARAQGNDAKADKLARELEGRQALLDQALKGLHEF
GG"
                                                                                                         /translation="SWQAGSPEEALAYFERKYEGLVVEIGLLEKRVKTTDLSAKDAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         len: 847 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anote Pfam match to entry PF01842 ACT, ACT domain, score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /noice-"previously sequenced region SW:SCAPTRELA EMBL:X87267 S.coelicolor apt & relA genes" complement(1229. .3772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="relA"
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/db_xref="G1:6822207"
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                                                                                                                                                                                                                                                                                                                                                      /gene="SCL2.02"
1010: 1150
/gone: SCL2.02
/note="SCL2.02, unknown, len: 46 aa"
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/gene="relA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="relA"
complement(1229. .3772)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The more also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Rucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp. CAUTION: We may not have predicted the jun/cg1-bin/framePlot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
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similar to TR:032356 (EMBL:29820) Mycobacterium
tuberculosis hypothetical 49.8 kD protein MTCY174.11, len:
450 aa; fasta scores: opt: 843 z-score: 874.7 E(): 0;
65.9$ identity in 296 aa overlap. Contains possible
coiled-coils region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (28-JAN-2000) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 38640)
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                       set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                                  Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                           for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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/strain="A3(2)"
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          Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2)
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Seeger, K.J. and Harris, D.
Unpublished
3 (bases 1 to 38640)
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COMMENT

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/translation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
SVSDAERRLAGLERASGARLGVXAYDTGSGRTVAYRADELFPMCSVFKTLSSAAVLRD
LDRNGFELSRTLYTQDDVEQADGAGFETGKPONLANAQLTVBELCEVSITASDNCAA
NLMLRELGGPAAVTRVRSLGDRVTRLDRWEPELNSAEPGRYTDTTSPRAITRTYGRL
VLGDALNPRDRRLLYSWLLANTTSGDRRRAGLPDDWTLGGRYGTNNDAGVTWP
PGRAPIVLTVLTAKTEQDAARDDGLVADAARVLAETLG"
                                                                                                                                                                                                                                                                                                                            BCT 26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
I (bases I to 1410)
Dehottay, P., Dusart, J., De Meester, F., Joris, B., Van Beeumen, J.,
Erpicum, T., Frere, J.-M. and Ghuysen, J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G
                                                                 35359 CACCGGCACTTCGATCTCGATCAGGAGCTCTCGCACATCCTGGCGGAAAGCTAGGGCGGG 35418
        cacacgetgggtgacttcgacggcaacctggaggacgcactgggccgcatcetcgccgag 420
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Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
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S.albus beta-lactamase gene, complete cds.
M28303
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Eur. J. Biochem. 166, 345-350 (1987)
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/protein_id="AAA26775.1"
/db_xref="G1:153339"
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/gene="beta-lactamase"
/note="inverted repeat"
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/transl_table=11
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/note="Pfam match to entry PF00156 Pribosyltran,
Phosphoribosyl transferase domain, score 150.30, E-value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34999 ATGAACACCACGGTCAGCTGCGAGCTGCACCTGCGCCTCGTTGTGTGGGGGAGTCCTCC 35058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGGCGTCGTGTGCATCGCTCTCAGCTCCCCGGAGGCCGAGGCACTGCTCGAGGCCCCCG 35298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 acggcaccgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggag 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 atgogogagtcggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcg 60
EMBL:X87267 S.coelicolor apt & relA genes" complement(3956. .4453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00103 Purine/pyrimidine phosphoribosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 38640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="adenine phosphoribosiltransferase"
/protein_id="CaB70916.1"
/db_xref="G1:6822210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107.4; DB 1;
Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transferases signature
complement(4468, 4503)
complement(4501, .5622)
/gene="secf"
                                                                                                                            complement(3956. .4453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3980. .4429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4103. .4141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4501. .5622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="secF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="apt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local (
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GIALAEETGEWIVWLGLKATSALTAVLRGEREAAARSVRELRAHSLFPVWPFASVWAQ
OVEGLLALFDSRAVEAYDALARAFDKTDPHYHSTSRWLLVPDLVDAAAAAGRNEQARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2787. .3257
/gene="SC8A11.03"
/gene="SC8A11.03, possible regulator, len: 156 aa; similar to TR:09S2F7 (EMBL-AL096852) Streptomyces coelicolor putative regulator SCE19A.24, 142 aa; fasta scores: opt: 272 z-score: 353.0 E(): 3.4e-12; 36.9% identity in 130 aa
                                                                                                                                                                                                                                                                          'note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="TGAARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
VRARILQRAAGNPLALVELPRAAQGISPPLDDLPLTQRLETAFASRTDSLTRECRTFL
LVLAAEPTAPLNQLLDVASRLAGSEVTVYALQBAVDAGLVVLTGRTPEFRHPLMRSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTRATVADRLSTHRALAETLEGSPGRRLVHLAAATLGPDDELAGGLERFADDAGKRGG
TAAAVPALROAGELVHDPRRGYGLLVARAELASEI NBKVGAOTLLINRADLAEPGFPTER
ARLALVSDKAAFEDPEGRRTODMIDAAAGAFDVGSTSVAENLLWAARCFFODGDA
RVRAQAAAELDRWKPDPDAPHVLTVRAYTEPYRGTDLIARLEKLRPDREDGRLLHYL
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QHGRRLRRQRRNVDARKPLRLARDEFDRVGAQPWADMAREQLRAAGESDGRRRPSKGE
SLTVQERQIAELASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
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YTVTVDQVRaEVAQLMGATEEEFTRPRSAGRLRARPAPRRACRGW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (fragment), len: >750 aa, similar to TR:09S124 (EMBL.AL109747) Streptomyces coelicolor probable transcriptional regulator SCJ21.13, 919 aa; fasta scores: opt: 818 z score: 913.7 E(): 0; 3z.6% identity in 775 aa overlap. Contains Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family and match to Prosite entry PS00622 Bacterial regulatory proteins, luxR family signature. Also contains a possible helix turn helix motif at residues 699. 720 (+3.25 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2093. [2176]
/gene="SCBAll.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative transcriptional regulator (fragment)"
/protein_id="CAC01573.1"
/db_xref="GI:9716212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Journal 2042. 2239

Jone-"SCBA11.01"

/note-"Pfam match to entry PF00196 GerE, Bacterial

/note-"Pfam match in entry PF00196 GerE, Bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SC8All.01"
/note="SC8All.01, possible transcriptional regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
/product="hypothetical protein SCBAll.02c"
/protein_id="CAC01574.1"
/db_xref="G1:9716213"
                                                                      /organism="Streptomyces coelicolor A3(2)"
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/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
                                                                                                                                     /db_xref-"taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2184. .2453)
/gene="SC8A11.02c"
                                                                                                                                                                           /clone="cosmid 8A11'
       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2/87. .3257
/gene="SC8A11.03"
2787. 3257
                                                                                                                                                                                                                                           /gene="SC8A11.01"
                                                                                                                                                                                                                                                                                                                                                                                    /qene="SC8A11.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                         /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signature"
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                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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       FEATURES
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The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        correct initiation codon. Where possible we choose an initiation codon (aty, qty, ttg or (att)) which is preceded by an upstream cribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the cannot be the entire insert of the sequenced clone. If may be shorter because we only sequence coverlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                         amino acid transport integral membran protein; branched amino acid
binding secreted protein; branched amino acid transport system
ATP-binding protein; branched amino acid transport system permease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           integral membrane protein; ion transport integral membrane protein; bobysaccharide blosynthesis protein; regulator; regulatory protein; secreted amidase; secreted protein; sigma factor; transcriptional regulator; transcriptional regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission

Direct Submission
Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA E-mail: Barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                           BCT 04-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 \ (\text{bases 1 to } 32704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSKs and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A. A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                           linear
232 cccgagggcctcggagatgtccacatccggctcc 265
                                                                                                                                                                                                                                                                   Streptomyces coelicolor cosmid 8A11. AL391041
                                                                  181 rccrcggrcagggggrccrgracggggrcccc 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 32704)
Saunders, D.C. and Harris, D.
                                                                                                                                                                                                                                                                                                                                             AL391041.1 GI:9716211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
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ACCESSION
                                                                                                                                                                 RESULT 14
SC8A11
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JOURNAL
REFERENCE
AUTHORS
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/gene="SC8A11.04c; probable secreted peptidase, len: 1253
a2, similar to TR:09RL54 (EMBL.A121256) Streptomyces
a2, similar to TR:09RL54 (EMBL.A121256) Streptomyces
colicolor probable secreted peptidase SCF51A.10, 1245 az;
fasta scores: opt: 1827 z-score: 1848:3 E(): 0; 37.24
identity in 1300 aa overlap, to TR:095684 (EMBL.D83672)
Streptomyces albogriseolus subtilisin-like protease, 1102
a3, fasta scores: opt: 1365 z-score: 1380.6 E(): 0; 33.48
identity in 1268 aa overlap and to Streptomyces coelicolor
probable secreted peptidase Scandilisto, 1239 az; fasta
scores: opt: 1835 z-score: 1467.4 E(): 0; 46.99 identity
in 1279 aa overlap. Contains Pfam matches to entries
PF00082 Peptidase_S8, Subtilase family and PF02225 PA, PA
domain and matches to Prosite entries PS00136 Serine
proteases, subtilase family, aspartic acid active site,
PS00137 Serine active site, Also contains possible
family, serine active site. Also contains possible
family, serine active site. Also contains possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSGDHHGVOAQHSAAQALLPLSLCLSQMTGALEWEDVPAEFRYD
PDHPLLVTTRFAPEGAPPVTWHVGRDLLHEGIRTTSGLGDVQVWADTPTDRETAWLQV
NAHGDIAIFSLPVPELEMIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
complement (3297...7058)
/gene="SCBA11.04c"
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HPVPRXAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSGGRAVEYRQDISLLGQ
PLGIVPTQVRAQGELTSWYTADDDVRWVSFASRPDLGQRGVARSYEPRSTTRETWFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQHPRLLSDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGE
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TPLPLVQLDYAVAVDLSGRAHRRTELTVTASHLEGAAGAGAIRTATVEVSYDDGATWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry PF02225 PA, PA domain, score 19.00, E-value 0.058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2896 TICCGCCGGAGTICCGTTACGATCCCGACCACCCCCTCCTCGTCACGATCCGCTTCGCCC 2955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2956 ccgaggggccccaccgccfcaccrggcargrcggccgrgaccrgcrgcacgagggccrgc 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 ttccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttccacc 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 ttcccggcgatgcccctgtgacctgggcgttcggccgcgagctgctggtggacgggctca 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTALRKSADGWTARLDAPGRARYASLRTTAKDTEGNGVGQTLIRAFGLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 32704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 85.2; DB 1; Length 32
Pred. No. 0.0087;
0; Mismatches 148; Indels
/product="putative regulator"
/protein_id="CAC01575.1"
/db_xref="GI:9716214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4374. .4613)
/gene="SC8A11.04c"
                                                                                                                                                                                                         .7058)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                            complement (3297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.5%;
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Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                           gene
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BCT 05-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submitssion
Submitted (07-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK On May 10, 2000 this sequence version replaced gi:4584464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
1 (bases 1 to 37245)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
Kinashi, H. and Hopwood, D.A.
As tof ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
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CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The more significant matches with motifs in the PROSITE database
                                                               3016 GCACCACGAGCGGCCTGGGGGACGTCCAGGTGTGGGCCGACACCCCCACCGGAGGA 3075
                                                                                                                                                                                                3076 CCGCGTGGCTCCAGGTCAACGCACACGGTGACATAGCCATCTTCAGCCTGCCCGTCCCGG 3135
                                                                                                                                                                                                                                                                                                                              188 acagecegageggegaeggegatgtgeacateggeeegaeegageeegaggeeteggag 247
                                                                                                                                                                                                                                                                   367
                                                                                                                                 248 atgtecacatecggetecaggteggegeggacegtgegetgtteegggeggggaeggeac
                                                                                                                                                                                                                                                                   308 cgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3196 GGCTCGGAACCGACGCCTTCCT 3217
                                                                                                                                                                                                                                                                                                                                                                                                        368 tgggtgacttcgacggcaacct 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 37245)
Oliver, K. and Harris, D.
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL049587
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VERSION
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AUTHORS
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JOURNAL
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MEDLINE
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jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13pb before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most imporrant: This sequence MX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches to entry PF00005 ABC_tran, ABC transporter and two Prosite matches to PS00017 ATP/GTP-binding site motif A (P-loop). Also contains possible membrane spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAHGWETLEVDPADDCPDSVFVEDAVVVFRNVALITRPGAESRRAETAGVEEAVARLG
SCNWWWEGFTLDGGDVLKIGDTITVGRGGRTWAAGVQQLRAAFEPLGARVVAVPVSK
VLHIKSAVTALPDGTYJGHTPLTDVPSLFPPRLDVPEESGAHVVLLGGSRLLMAASAP
KTAELLADLGHEPYLVDIGEFEKLEGCVTCLSVRLRELYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MSEFISITGARENNLQDVTLRIPKGRLTVFTGVSGSGKSSVVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIAVESRRQLNETFTWFVRNRLPKYERPHADALEGLTPAIVVDQRPVGGHSRSTVGTM
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RIDGHSIADCSRMQITDLIAVLRGIDDPVALPVAGAAVAALERVEAIGLGYLSLDRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MPSKKALVRRPSPRLAEGLVTHVEREKVDHGLALEQWDAYVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Gene="SC5F2A.02c" // Anote="SC5F2A.02c" //
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADGAVRFPPFAAGTWQGQTYTNTEELDTGKPVGDFTAAERAFLMRGRPGSKVTVSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCSF2A.01c, ddah, dimethylarginine dimethylaminohydrolase, len: 258 as; hydrolyses dimethylaminohydrolase, len: 258 as; hydrolyses asymmetrically methylated arginine with preference for dimethylated arginine over monomethylated arginine (experimental). Similar to TR:D1038106 (EMBL:AB001915) NG,NG-dimethylarginine dimethylathaninohydrolase from Homo sapiens (286 as) fasta scores; opt: 323, z-score: 384.7, E(): 4.1e-14, (35.7% identity in 272 as overlap)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
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/protein_id="CAB40668.1"
/db_xref="GI:4584465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .37245
/organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Nominal overlap with cosmid 4C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="UvrA-like ABC transporter"
/protein_id="CAB40669.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3234)
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/codon_start=1
/trans1_table=11
/labe1=SC5F2A.02c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(83. .859)
/gene="SC5F2A.01c"
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FEATURES

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/db_yref="guideling"
/db_yr
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DOSATGISARSTPATYLGIMDYVRKYPARETGAEPGFFSFRANSGACGTCEGRGIHTD
LAFMDPVTTTCHDCGGRREVLRLYPGRSVADVLAMTAGQALGFFSDFGYRRLR
ALRDVGLTYLLGPPLSTLSGGERQRIKLATRHRTGAVYVLDEPTTGLHMSDVEGLL
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ATLSGGEGQRLKTVRHLGSSLTGMTYIFDEPSVGLHPRDVGRLGDLLLRLRDKGNTVL
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Query Match 18.4%; Score 80.8; DB 1; Length 37245; Best Local Similarity 54.5%; Pred. No. 0.031; Matches 216; Conservative 0; Mismatches 162; Indels 18; Gaps
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Search completed: July 18, 2002, 11:21:23 Job time: 13693 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			Description						AAZ49729 Streptomyces albus				
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AC XX XX XX KW	AAZ49727; 18-APR-2000 Streptomyces ssqA; liquid	27; :-2000 .omyces liquid	(fir grie cult	(first entry) griseus ssgA culture; fila	Y) A gel lamel	Ω	secondary metabolit	lite,
X X X X X X X X X X X X X X X X X X X	segon tradition mycelium; an hypocholeste herbicide; a bioinsectici Streptomyces Key CDS	ssya, inquire curture; mycelium; antibiotic. hypocholesterolaemic herbicide; antiparasi bioinsecticide; recep Streptomyces griseus. Key CDS 314 /*tag	curi ibic olae tipa e; r gris	culture; intemented bar ibiditic, antitumour age olaemic agent; enzyme i tiparasitic agent; rumi e; receptor agonist; an griseus. Location/Qualifiers 31438 /*tag= a /*tag= a /*tag= a	titum nt; a agei agoi AQua	un culture; linamentous bacteria; secon antiblotic, antitumour agent; immunosu terolaemic agent; enzyme inhibitor; an antiparasitic agent; ruminant growth cide; receptor agonist; antagonist; bies griseus. Location/Qualifiers 31438 /*tag= a /product= "SsgA protein"	puraly merc pprassive timigraino promoter; omass; ds	agent; agent; agent; ATCC 23345;
X X X X X X X X X X X X X X X X X X X	WO20000061 06-JAN-200 25-JUN-199 26-JUN-199 (UYLE-) RI	WO20000613-A1 06-JAN-2000. 25-JUN-1999; 26-JUN-1998; (WLE-) RIJKSU	· z	MO200000613-A1. 06-JAN-2000. 25-JUN-1999; 99WO-NL00395 26-JUN-1998; 98EP-0202148 (UYLE-) RIJKSUNIV LEIDEN.	395. 148.			

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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, runniant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
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mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agonist; antagonist; biomass; ds.

    271 ggcgcggaccgtgcgctgttccgggcggggacggcaccgctggtggcgttcctcgaccgg
    241 ggcgcggaccgtgcgctgttccgggcggggacggcaccgctggtggggttcctcgaccgg

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Matches 407; Conservative
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                                                                                            Streptomyces griseus
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                                                                                                                                                                                                                   The present sequence is a DNA (ATCC 23345) encoding S. griseus Ssgh protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, hebbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ttccgtattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atgogogagtcggttcaagcagaggtcatgatgagcttcctcgtcccgaggagctctcg
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                                                                                                                                enhancing fragmentation in filamentous improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 438;
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 438 BP; 68 A; 145 C; 153 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 438; DB 21;
Pred. No. 1.8e-75;
0; Mismatches 0;
       (NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO
                                         Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces griseus ssgA gene-2.
                                                                                                                                                                                     Claim 1; Page 27; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 438; Conservative
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                                                                                                                                Reducing branching and
                                                                                                                                                   microorganisms used to
                                                                           WPI; 2000-147269/13.
P-PSDB; AAY44649.
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                                         Van Wezel GP,
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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive
                                                                                                                                                                                                                                                                                                 241 ggcgcggaccgcgccctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc 300
accegggatecetacgeggtgeggatgacettecaceteceeggagaegeetgtgaee 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myčelium; antibiotic, antitumour agent; immunosupprešsive agent;
hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent;
herbicide; antiparasitic agent; ruminant growth promoter; ATCC 21386;
bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                         tgggcgttcggccgcgagctgctgctgctggacgggctcaacagcccgagcggcgacggcgat
                                                         gtgcacatcggcccgaccgagcccgagggctcggagatgtccacatccggctccaggtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                        gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 437
                                                                                                                                                                                                                                                                                                                                                                                           gaggccgcctcggcaagatcctcgccgaggagcagaacgccggctg 407
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/label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces goldeniensis ssgA gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98EP-0202148.
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DB; AAY44651.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-1998;
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                                                                                                                                                                                                                                                                                                           ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agonist; antagonist; biomass; ds.
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Pred. No. 1e-48;
0; Mismatches 68; Indels 0;
                    gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 437
                                         63 A; 151 C; 131 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONDERZO.
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NEDERLANDSE ORG WETENSCHAPPELIJK
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SsgA_protein
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1..405
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                                                                                                                                                         BP,
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83.3%;
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Best Local Similarity 83.3
Matches 339; Conservative
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/label= /
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Luiten

Kraal B,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bloinsecticides, receptor agonists and antagonists and blomass.
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                                                                                                                                                    DB 21; Length 407;
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                                                                                                                                                  59.3%; Score 259.8; DB 21;
.larity 77.4%; Pred. No. 2.3e-41;
Conservative 0; Mismatches 92;
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NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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1..405
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                                                                                                                                                                        Local Similarity
es 315; Conserv
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The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances tragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entreme inhibitors, antimigraine agents, herbicides, antiparaslic agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 accgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgcccggtcacc 120
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transgenic plant; insect resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc
                                                                          Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 239; DB 21;
Pred. No. 2.2e-37;
0; Mismatches 105;
                                                                                                                                                       Disclosure; Fig 5; 60pp; English.
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74.28;
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2000-147269/13
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                           P-PSDB; AAY44650
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AAF88315/c
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DE19957268-A1

us-09-749-185-1.rng

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II): (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide apyrone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression clones in a gene bank. Cells transformed with (1) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in forosamine and trimethylrhamnose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
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                                                                                                                                                                                                                                                                                                                                                                       Salas JA;
                                                                                                                                                                                                                                                                                                                                                                       Velten R,
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                                                                                                                                                                                                                                                                                                                                                                       Froede R,
                                                                                      99DE-1057268
                                                                                                                                                                            99DE-1040596
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                                                                                                                                                                                 27-AUG-1999;
                                                                                      29-NOV-1999;
08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                       Eberz G,
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Forosamine; trimethylrhamnose; polyketide synthase; biosynthesis; spinosyn; polyketide aglycone; transgenic plant; insect resistance;

spinosyn; polyketide aglycone; macrolide; insecticidal; ds.

Saccharopolyspora spinosa.

DE19957268-A1.

08-MAR-2001

spinosa DNA fragment SEQ ID 1.

(first entry)

28-AUG-2001

AAF88312;

AAF88312 standard; DNA; 50000 BP

AAF88312

RESULT

Salas JA;

Velten R,

Froede R,

Moehrle V,

Eberz G,

(FARB) BAYER AG

27-AUG-1999; 29-NOV-1999;

99DE-1057268. 99DE-1040596

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                                                                                                                                                 64 cgtattccggtggagctccgatacgaggtcggcgatccgtatgccatccggatgacgttc 123
                                                                                                                                                                                                                           cacetteeceggegatgeecetgtgacetgggegtteggeegegagetgetgetggaeggg 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcaccgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcac 363
                                        Gaps
                                                                       4 cgcgagtcggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcgttc 63
                                                                                                                                                                       21040 CCAGTCGGCGTGGAGCTGCGGTACGGTACGAATCCGTACGAGTCTCATGAAGCTC
                                                                                                                                                                                                                                                                                                                      10920 CTGATCGCCGAGGCAGGCGAAGGCGATGTGCGGATCGGCC---CTCGACGGGGTTTTCCG
 DB 22; Length 45624;
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                                  Indels
                                    198;
                   1.8e-06;
                                    Mismatches
Score 77.2;
Pred. No. 1.8
                                    ö
17.6%;
                                    Conservative
                 Similarity
                                  209;
 Query Match
                   Best Local
Matches 2(
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20743 CGGTGGATGAACGTCGACGAGGTGCTGAGCCAGCTGCTCTCGCACAACCT 20694

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           markers for sequencing of the Saccharopolyspora spinosa genome. (II) are marcholdes with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce expression against a gene bank of the standard with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacggcacggtgctcgccaccatgatcttcaacctggtagccccggcgggtgtgatcgcg 24584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgcgagtcggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcgttc 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               forosamine, trimethylrhamnose and polyketide synthase biosynthesis
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51.0%; Pred. No. 1.8e-06;
ive 0; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 14-31; 354pp; German.
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Best Local Similarity
Matches 209; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-267102/28.
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Streptomyces
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                                                                       Matches 178;
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                                               Query Match
Best Local S
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           24645 aacgtaggcacggacggtcaggtggactgggtgatcgccgcgcgacctgctggccgacggg 24704
                                                                                                         999ttggtcgtgatcgagatgagctcgccgtcgggggcaggcctccttcgaggtgaatgct 24821
                                                                                                                                                        gaccagcttgcggacttcttgaacgacacctacgacgtggtcgaacctggtgatgaacac 24881
                                                                                                                                                                                                                                                                                                                                                           ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigratine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agent; antagonist; blomass; ds.
                                   ctgatcgccgaggcaggcgaaggcgatgtgcggatcggcc---ctcgacggggttttccg
                                                                                  ggagatgtccacatccggctccaggtcggcgcggaccgtgcgctgttccggggcgggacg
                                                                                                                                 gcaccgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                      24882 cggtggatgaacgtcgacgaggtgctgagccagctgctctcgcacaacct 24931
                                                                                                                                                                             364 acgctgggtgacttcgacggcaacctggaggacgcactgggccgcatcct 413
(UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "SsgA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 31..438
                                                                                                                                                                                                                                                                                                                                       Streptomyces griseus ssgA gene-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 27; 60pp; English.
                                                                                                                                                                                                                                                               AAZ49727 standard; DNA; 438 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces griseus.
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                                                                                                                                                                                                                                                                                        AAZ49727;
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                                                                                                                                                                                                                                                                                                                                        192 cccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgt 251
                                                                                                                                                                                                                                                                                                                                                                       208 ceccercececrceecrererreaeccerceaecaecaecreeceeccaaceccaae 149
                                                                                                                                                                                                                                                                                                                                                                                                            311
                                                                                                                                                           371
                                                                                        Gaps
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                                                                                                                       12 ggttcaagcagaggtcatgatgagcttcctcgtctccgaggagctctcgttccgtattcc 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                             148 TCACAGGGGCATCGCCGGGAAGGTGGAACGTCATCCGGATGGCATACGGATCGCCGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthase; PKS; macrolide; nystatin; PKS gene cluster;
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                                                 Length 438;
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                                                                                      0; Mismatches 199; Indels
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/note= "CDS does not include stop codon"
complement (1056..2576)
Sequence 438 BP; 68 A; 145 C; 153 G; 72 T; 0 other;
                                                   DB 21;
                                                 Score 58.6; DB 2 Pred. No. 0.0075;
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50260..51015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "NysB protein"
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51405..54305
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                                               13.4%;
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6952..16530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 TGACCTCTGCTTGAACC 12
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                                                                                      Conservative
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                                                                    Similarity
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51083 catgccacccggcgacgcgcgttgcgtgcgctgtggagcacccgtcggtgcgtacgc 51142
50786 aggocatogagacctaccgctgcccgacgtcaccgtccgggcgccgctgaccgtcc 50845
                                                                                                                                                                              50963 aggeceeggegateategatetgeteegggegeacetegeeggeaaeggetagegggege 51022
                                                                                                                                                 acggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggc 262
                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                      323 tcgaccggaccgaccactcgtgccgctcggc-caggagcacacgctgggtgacttcgac 381
                                                                                                                                                                                                            gatacgaggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccc
                                                           50846 teaceggegacegegaceegaagaceteeetggaeggaega---ggegtggegegee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;
                                                                                                                                                                                                                                                                                                                                                   /note= "CDS does not include start codon"
complement (59045..60241)
                                                                                                                                                                                                                                                                                                                                 382 ggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaac 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "CDS does not include start codon" complement (60238..61296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces noursei nystatin PKS gene cluster DNA.
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/product= "NysD2 complete protein"
120628..121308
/*tag= h
/product= "NysR4 (long) protein"
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34792..51099
/*tag= b
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complement (58786..58980)
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51155..57355
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6337..34771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces noursei.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130,
AAE10131, AAE10132, AAE10133, AAE10134, AAE10135, AAE10136, AAE10137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nystatin polyketide synthase polynucleotides and polypeptides useful as antibiotics and antifungals
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61736..62497
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                                                                                                                                                                                                                                                                                                       start codon"
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letta H, Gulliksen O;
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SINTEF STIFTELSEN IND TEK FORSK.
ALPHARMA AS.
                                                                                                                                                                                                                          /product= "NysR5 protein"
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complement (62551..63615)
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60415..61047
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                                                                         /note= "CDS a
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2000GB-0009387.
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DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
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14-APR-2000;
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(FJAE/)
(BRAU/)
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(DZIE/)
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Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode; insect; polyketide; polyketide synthase; PKS; extender module; initiator module; acyl transferase domain; AT; acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; dehydratase domain; DH; enoyl reductase domain; ER; beta-ketoreductase;
                                                                                                        DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes
                                                                                                                                                                                                                                                                                                                                          /hote= "Protein involved in transcription control"
2024..2791
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/note= "Spinosyn biosynthesis protein I"
complement (17749..18501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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complement (5363..6751)
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1967..10427
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16556..17743
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complement (3416..4165)
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/product= ORFL16
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              AAZ21501 standard; DNA; 80161
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AAZ21501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111164 acaccaccggggacttcgacctcaaggtgcttcccggtgggcacttcttcgtcagctccg 111223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antitiungal antibiotics. The present sequence is a Streptomyces noursel nystatin PKS gene cluster DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 gatacgaggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccc 142
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P-PSDB; AAE10143, AAE10144, AAE10145, AAE10146, AAE10147, AAE10148.
AAE10149, AAE10150.
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                                                                                                                                                                                                                                                                                                                                                                                      New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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Best Local Similarity 49.3%; Pred. No. 0.029;
Matches 201; Conservative 0; Mismatches 203;
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letta H, Gulliksen O;
                                                                                                        NORGES TEKNISK NATURVITENSKAPELIGE
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            08-FEB-2001; 2001WO-GB00509.
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2000GB-0008786.
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DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
                                                                                                                                       ALPHARMA AS.
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                                                                        14-APR-2000;
                                           08-FEB-2000;
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(BRAU/) I
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/note= "Acyl carrier protein domain (ACP3): part of
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extender module 4"
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/note= "Dehydratase domain (DH5): part of extender
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/product= spnD
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/*tag= ap
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/note= "Beta-ketoreductase domain (KR3): part
extender module 3"
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/note= "Acyl carrier protein domain (ACPi): part of the
initiator module"
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initiator module"
22692..23669
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/note= "Acyl carrier protein domain (ACP1): part of
extender module 1"
38916..35374
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/note= "Beta-Ketoreductase domain (KR2): part of
extender module 2"
34886..30295
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/note= "Beta-ketoreductase domain (KR1): part of
extender module 1"
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/note= "Beta-ketosynthase domain (KS2): part of
extender module 2"
30629..31621
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/note= "Acyl transferase_domain (AT1): part of
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extender module 1"
27582..28121
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'note= "Acyl transferase domain (AT2): part
    extender module 2"
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/note= "Enoyl reductase domain (ER2): part
extender module 2"
                                                                                                                                                                                                          /note= "Spinosyn biosynthesis protein A"
/rransl_except= (Pos:26940..26942, aa:Pro)
21126..22379
/*tag= r
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               /note= "Spinosyn biosynthesis protein H" complement (18541..19713)
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/note= "Dehydratase domain (DH2): part
module 2"
                                                                    /note= "Spinosyn biosynthesis protein
20168.20995
                                                                                                                                       'note= "Spinosyn biosynthesis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Spinosyn biosynthesis protein
                                                                                                                                                                                                                                                                                                                                                         initiator module"
                                             /*tag= o
/product= spnG
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/product= spnH
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29024..30295
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine
                                                                                                                                                                                                                                                                         ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agent; antagonist; blomass; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggtggagctecgatacgaggteggcgatecgtatgecatecggatgaegttecaeettee 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 GGTCGAGGAACGCCACCAGCGGTGCCGTCCCCGCCGGAACAGCGCACGGTCCGCGCGGA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggitcaagcagaggicatgatgagcticcicgictccgaggagcictcgitccgiaticc 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 407 BP; 60 A; 139 C; 142 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIJKSUNIV LEIDEN.
NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%; Score 53.6; DB 46.9%; Pred. No. 0.068;
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 398 cactgggccgcatcctcgccgaggagcagaacgccg
                         /label- SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luiten RGM
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                            griseus ssgA gene-2.
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                                                                                                                             BP
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces griseus.
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                                                                                                                           AAZ49728 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                            Streptomyces
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ID AAZ4
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278 accgigcgcigitccggggcgggacggcaccgciggiggcgitccicgaccggacggaca 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 tgcgtgcgctgccccaggtaagcgaggccgcgctgctgtccacctgcaaccgtaccgagt 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ88151 encodes AAR74619 Xanthomonas campestris L-glutamyl tRNA reductase. The DNA as part of an expression vector can be used to transform a host cell, for the recombinant prodn. of the protein. The protein can be used in the prodn of vitamin B12, glutamic acid-1-semialdehyde, 5-aminolevulinate, haem, chlorophyll and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 tcggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggtcggcgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 agctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctggaggacg
                                                                                                                                                                                                                                                                                                                             Xanthomonas campestris; L-glutamyl tRNA reductase; vitamin B12;
glutamic acid-1-semialdehyde; 5-aminolevulinate (ALA); haem;
chlorophyll; phycobilin; recombinat production; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragment encoding L-glutamyl tRNA reductase - derived from Xanthomonas sp., useful for production of 5-amino:levulinate, vitamin-B12, chlorophyll, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1549;
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                                                                                        239 cctggtgatgaacaccggtggatgaacgtcgacgaggtgctg 280
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Pred. No. 0.046;
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                                                       ctcggccaggagcacacgctgggtgacttcgacggcaacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1549 BP; 291 A; 516 C; 514 G; 228 T; 0
                                                                                                                                                                                                                                                                                              Xanthomonas L-glutamyl tRNA reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
212..1492
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KK.
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53.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                            campestris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP07031480-A
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                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas
                                                                                                                                                                                                                                                          02-NOV-1995
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                                                                                                                                                                                                                                                                     299; CTGCTGCTGGACGCCGCAGACGACGAAGACGCCGATGGCGCGGGAGCTGCTGGACGGT
                                                                                                                                                                                                                                                                                                                           319 ttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttc
                                                                                        ggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatc
                                                                                                                                                 359 GCCGACGCCGCGGAGCTGCTGCTGCTGGACGCGACGACGACGACGCCGACGCCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 GACGCTGACGCGCGCGGAGCTGCTGCTGGACGGCGCAGACGACGAGACGCCG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New alpha-amylase gene - useful for production of malto-pentaose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas; maltopentaose; alpha-amylase; enzyme; variant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas alpha-amylase variant encoding DNA (FERM BP-6116).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 gacggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaacgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NORQ ) NORINSUISANSHO SHOKUHIN SOGO.
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                                                                                  cggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacag 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a human proteophosphoglycan protein designated hPPG-1. Also describes are methods for the preparation and detection of hPPG-1. The present sequence encodes the Leishmania major PPG protein which is used in comparison with the hPPG-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 gcagaggtcatgatgagcttcctcgtctccgaggagctctcgttccgtattccggtggag 78
                                                                                                                                                 cccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgt
                                                                                                                                                                                                                                                                                                                           118 TCACAGGGCATCGCCGGGAAGGTGGAACGTCATCCGGATGGCATACGGATCGCCGACCT
                                                                                                                                                                                                                                                                                                                                                                                    312 ggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgc 367
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                                                                                                                                                                                                                                                                                                                                                                                                                          CETATCGGAGCTCCACCGGAATACGGAACGAGAGCTCCTCGGAGAGCGAGGAAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; hPPG-1; PPG; proteophosphoglycan; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human phosphoglycan protein and its coded sequence
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Pred. No. 0.073;
); Mismatches 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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P-PSDB; AAB74609.
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Sequences AAX37293-298 represent nucleic acids encoding alpha-amylase variants (AAY17904-Y17909). The variants are derived from the Pseudomonas sp. KO-8940-derived maltopentaose-forming amylase (Shida, O. et al., Biosci. Biochen, Biochen, Vol. S6, 76-80, 1992). The variants have a replacement of the 57th or the 130th amino acid residue in the sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6117, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The enzymes prepared from the alpha-amylase variants produce maltopentaose in a high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 gacctggggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacgg 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 53.4; DB 20; 51.0%; Pred. No. 0.072; ive 0; Mismatches 121;
Claim 4; Page 6-8; 23pp; Japanese.
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Search completed: July 18, 2002, 11:35:47 Job time: 11212 sec

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TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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  TOPOLOGY:
MOLECULE TYPE
S-09-036-987A-1
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Query Match
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  (without alignments)
649.840 Million cell updates/sec
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Patent No. 5212296
Patent No. 5212296
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Sequence 3
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                                                                                                                                    July 18, 2002, 08:23:30 ; Search time 165.56 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-385-028-1
US-08-363-255-1
US-08-383-942C-18
US-08-387-942C-18
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US-09-017-706-7
US-08-034-650-9
US-08-449-015-9
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US-07-642-734C-3
US-08-439-009A-3
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Maximum DB seq
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Perfect score:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-WAR-1998
CLASSIFICATION: 435
US-08-804-198-1

US-07-945-283-3

5215881-3

US-07-945-283-1

US-08-920-812-13

US-08-920-812-13

US-08-921-177-13

US-08-921-177-13

US-08-921-177-13

US-08-920-827-13

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US-09-443-501A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Madduri, Krishnamuthy
APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Ger
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NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09036987A Patent No. 6143526
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Broughton, Mary C.
Crawford, Kathryn P.
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(317)337-4847
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agros
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Length 80161;

DB 3;

Score 54.8;

12.5%;

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239 cctggtgatgaacaccggtggatgaacgtcgacgaggtgctg 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: PLASMID POS3410F57
US-09-017-706-3
                                                                                             ; Sequence 3, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.2%;
Best Local Similarity 51.0%;
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
LOCATION: (85)..(1848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (7)..(1848)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
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                                                                                                                                          169 ctgctgctggacgggctcaacagcccgagcggcgacggcgatgtgcacatcggcccgacc 228
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                                                                                                                                                                               CTGCTGGCCGACGGCTGATCGCCGAGGCGAAGGCGATGTGCGGATCGGCC---CT
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APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER PILING DATE: 1999-08-09
SEARLIER FILING DATE: 1999-08-03-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 0.0059;
0; Mismatches 132;
    ed. No. 0.0059;
Mismatches 132;
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; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1
      Pred.
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Best Local Similarity 52.1%;
Matches 147; Conservative
      52.1%;
                        Matches 147; Conservative
      Best Local Similarity
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US-09-370-700-1
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CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: JP 305071/1997
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEO ID NOS: 14
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Patent No. 6087147
GENERAL INFORMATION:
APPLICANT: 1TO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
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Gaps

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Length 1981; Indels 761

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147 gacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacgg 206
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APPLICANT: ITO, YOSHIFUMI
APPLICANT: ITO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: UNMBER: US/09/017,706A
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT APPLICATION NUMBER: JP 305071/1997
EARLIER APPLICATION NUMBER: JP 305071/1997
EARLIER PILING DATE: 1997-10-21
NUMBER OF SEQ. ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
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US-09-017-706-6
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OTHER INFORMATION: MUTATED GENOMIC DNA
FEATURE:
                                                                    OTHER INFORMATION: MUTATED GENOMIC DNA
                                                                                                              ; OTHER INFORMATION: PLASMID pOS34100L57
US-09-017-706-5
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US-09-017-706-6; Sequence 6, Application US/09017706A
; Sequence 6. Application US/09017706A
; Sequence 6. Application US/09017706A
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LOCATION: (85)..(1848)
      .(1848)
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Best Local Similarity
Matches 126; Conserva
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APPLICANT: ITO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: JP 305071/1997
BARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 5
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FERTURE:
MAME/KEY: mat_peptide
LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
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                                                                                                                                                       TYPE: DNA ORGANISM: Pseudomonas sp., Strain KO-8940
                         305071/1997
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MUTATED GENOMIC DNA
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US-09-017-706-4
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EARLIER APPLICATION NUMBER: JP 3
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 4
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LOCATION: (7)..(1848)
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NAME/KEY: CDS
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                                                                    642 ggccaagcacatcagcccgacggacctgggtgccatcatcgacagcgtcaacgcgcgcac 701
                                                                                                        326
                                                                                                                                           761
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING TITLE OF INVENTION: MALYOPENYAOSE, VECTOR CONTAINING SAID GENE AND TITLE OF INVENTION: TRANSFORMANT FILE REFERENCE: 8361-0003-0 CURRENT APPLICATION UNABER: US/09/017,706A CURRENT FILING DATE: 1998-02-05 EARLIER RPLICATION NUMBER: JP 305071/1997 EARLIER RPLING DATE: 1997-10-21 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       582 gatctccgactacctggtcgacctggtccagatgggcgtcaagggcttgcgcgtcgatgc 641
 gatetecegaetacetegetegaeeteggtecagateggeegteaagggettgegegtegatge 641
                                                                                                                                                                                                               762 gcccagccagtacttcgggctcggcggcgggcaggtcacggtgaccgagttcgcctacgg 821
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                                    cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca
                                                                                                          ggteggegeggaccgtgegetgttecgggegggacggcaccgetggtggcgttectcga
                                                                                                                                             702 cggtgccgcacggccattctggttcctggaggtgatcggcgcgcggggcgaggcggtgca
                                                                                                                                                                                ccggacggacaagctcgtccgccaggagcacacgctgggtgacttcgacggcaa
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LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%; Score 53.4; DB 3;
51.0%; Pred. No. 0.011;
tive 0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: PLASMID: pos3410H139
US-09-017-706-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MUTATED GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09017706A Patent No. 6087147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 51.08
Matches 126; Conservative
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APPLICANT: ITO, YOSHIFUMI
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LOCATION: (7)..(1848)
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327 ccggacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa 386
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                                                                                                                                                               GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ITO, YOSHIFUMI

APPLICANT: ITO, YOSHIFUMI

TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING

TITLE OF INVENTION: MALTOPERATAOSE, VECTOR CONTAINING SAID GENE AND

TITLE OF INVENTION: TRANSFORMANT

TITLE OF INVENTION: TRANSFORMANT

TITLE OF INVENTION: 178ANSFORMANT

TITLE OF INVENTION: 178ANSFORMANT

CURRENT PAPLICATION NUMBER: US/09/017,706A

CURRENT FILING DATE: 1999-2-05

EARLIER APPLICATION NUMBER: JP 305071/1997

SEALLER PILING DATE: 1999-10-21

NUMBER OF SEO ID NOS: 14

SCOFTWARE: PAGENTIN Ver. 2.0

SEO ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53.4; DB 3; Length 1 Pred. No. 0.011; 0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: PLASMID: pOS3410L139
US-09-017-706-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MUTATED GENOMIC DNA FEATURE:
                                                                                                                    Sequence 8, Application US/09017706A Patent No. 6087147
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APPLICANT: BOS, Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VERNIFS, CORDIST.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08034650 Patent No. 5641671
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Best Local Similarity 51.0%;
Matches 126; Conservative
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LOCATION: (85)..(1848)
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822 caaggag 828
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US-08-034-650-9
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2141 GAGTGGGCCGAGCCGTTCTTCGGCGACGAGCGCCCGGCAGCGCCCATGACCTCGAACGG 2200
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             TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. Street, N.W.
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Pred. No. 0.06;
0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,015
FILING DATE: 24-MAY-1995
CLASSIFICATION A 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNK/5970/91731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.3%;
Best Local Similarity 50.9%;
Matches 118; Conservative
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ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kokulis, Paul N. REGISTRATION NUMBER: 1
                                                                                                                                                  CITY: Washington STATE: D.C.
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LOCATION:
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US-08-449-015-9
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TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2261 crcgacececaecreácecegaceaecececececaecaecececececere 2312
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Pred. No. 0.06;
0; Mismatches 114; Indels 0
                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELEPHONE: (202) 861-3000
TELERA: (202) 862-0944
TELER: (314627 CUSH
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                               ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTONEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-449-015-9
; Sequence 9, Application US/08449015
Patent No. 5804409
; GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VERRIPS, Cornelis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.3%;
ilarity 50.9%;
Conservative
                                                                                                                                             COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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1559..2617
                    NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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483..1556
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                         Washington
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Best Local Similarity
Matches 118; Conserv
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LOCATION:
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                                                                                                                              STATE: D
COUNTRY:
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LOCATION: 744..11219
OTHER INFORMATION: /function= "gene="erya""
OTHER INFORMATION: /Product=""ORF1 encoding modules 1 & 2 for OTHER INFORMATION: /Geoxyerythronolide B""
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LOCATION: 2250..350
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
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TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain 1 of module
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LOCATION: 3831..4811
OTHER INFORMATION: /function= "approximate span of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 744..6659
OTHER INFORMATION: ^function= "APPROTHER INFORMATION: MODULE 1"
OTHER INFORMATION: /label= FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1998..2198
   Katz, L
Donadio, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 CGTCACCGGCATGGTGCGCTCGGCCTACGGCGAGGAGCCAGCAACTTCGGCATGAGCGA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 cccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgt 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 ggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgctggg 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 cggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacag 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 CGAGATGTCCGGCTACGGTTTCGATCCGCACGAGCAGACCATCAACCTGACGATCCGCGA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.2%; Score 49; DB 2; Length 115
Best Local Similarity 50.2%; Pred. No. 0.08;
Matches 152; Conservative 0; Mismatches 145; Indels
                                                                                           TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP STERET: P.O.BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-07-642-734C-1/C
US-07-642-734C-1, Application US/07642734C
; Partent No. 5824513
; GENERAL INFORMATION:
APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-7
                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                     22042
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                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                              CITY: 1
STATE:
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NAME/KEY: CDS
LOCATION: 744..11219
COTHER INFORMATION: /function= "gene= "erya""
OTHER INFORMATION: /product= ""ORF1 encoding modules 1 & 2 for OTHER INFORMATION: 6-deoxyerythronolide B""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 2250..3626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/modulel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

LOCATION: 744..1868

LOCATION: 744..1868

COTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase domain 1 of module 1"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1998..2198

COTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain 1 of module 1"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 3831..4811
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                  ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
CITY: Abbott Park
STATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function= "APPROXIMATE SPAN OF MODULE 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
   NAME/KEY: misc_feature
   LOCATION: 5574..6125
   OTHER INFORMATION: /function= "approximate span of
                                                                                                                                                                                                COUNTRY: US
ZIP: 60064-3500
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
INVENTION: Specific Polyketides SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4952.US.D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 11219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 744..659
OTHER INFORMATION: /func
OTHER INFORMATION: /labe
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                          NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                           STATE: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5964 CGGTCAGGTCCAGCTCGCGCGTCAGCTTGCGCGCGCCCGAGCACCTTGGCGC 5905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 tgtgcacatcggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggt 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 ggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccctgtgac 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 ctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcga 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 cggcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcgaccg 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 gacggacaagetcgtgccgctcggccaggagcacacgctgggtgacttcgacg 382
                                                  NAME/KEY: misc_feature
COGATION: 5574..6125
OTHER INFORMATION: /tunction= "approximate span of
OTHER INFORMATION: /tunction= deta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 9906.110454
OTHER INFORMATION: /tunction= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.2%; Score 49; DB 1; Length 11219; Best Local Similarity 50.2%; Pred. No. 0.078; Matches 147; Conservative 0; Mismatches 145; Indels
OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678-.8066
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACPsynthase of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 8262.9305
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08439009A
Patent No. 6004787
GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 5369..656
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module 1"
                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678..11219
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

: LOCATION: 10707..10964

OTHER INFORMATION: /function= "approximate span of

: OTHER INFORMATION: acyl carrier domain of module 2"

US-07-642-734C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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STREET: 1251 Avenue of the Americas
                          New York
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                       CITY: Ne:
STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 ggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgac 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 ctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcga 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 tgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggt 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cggcggaccgtgcgctgttccggggggggggacggcaccgctggtggcgttcctcgaccg 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5904 GACTTGCCCGCTCGATGCGCTCGCCGGTGAGGGTGTCCACGGTGCCGTCGTCG 5852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 gacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacg 382
                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678..11219
OTHER INFORMATION: module 2"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678..8066
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacyl ACPsynthase of module 2"
  OTHER INFORMATION: beta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 9906..10454
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49, DB 3; Length 11219;
Pred. No. 0.078;
0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: 8262..9305
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase domain of module 2" FEATURE:
                                          NAME/KEY: misc_feature
LOCATION: 6369..6626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 10707_.10964
COTHER INFORMATION: /tmction= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAAmura, Etsuo
APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Kitadokoro, Kengo
APPLICANT: Shin, Nasaru
APPLICANT: Teraoka, Hiroshi
TITLE OF INVENTION: No. 566586el Protease
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jamee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08343428
Patent No. 566586
GENERAL INFORMATION:
APPLICANT: Nakamura, Etsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.2%;
Best Local Similarity 50.2%;
Matches 147; Conservative
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1759 GGGCGCGCCCACCGCGTCGGGTACGTGGAGGCCGTGGGCGTACGGGCGGACCGCCGCCGC 1818
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                                                                     COMPUTER REALBLE FORCE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS Dos 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/343,428
FILING DATE: 18-NOV-1994
CLASSIFICATION NUMBER: PCT/J93/00592
FILING DATE: 30-APR-1993
APPLICATION NUMBER: JAPAN 4-126511
FILING DATE: 19-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
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                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: SHGN-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptomyces fradiae
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MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
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NAME/KEY: sig peptide
LOCATION: 435.944
DENTIFICATION METHOD:
US-08-343-428-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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                                                          COMPUTER READABLE FORM:
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Best Local Similarity
New York
                                  10020-1104
                   USA
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                                                                                              APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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Pred. No. 0.25;
0; Mismatches 146; Indels 3
                                                                                                                                                                                                                                         ADDRESSER JACORSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRELIAR PRELAGE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION UNBER:
APPLICATION UNBER: US 08/790,462
ATORNEY AGENT INFORMATION:
NAME: D. DOUGJAS PICE
RECISTRATION NUMBER: 24,514
RELEPHONE: (202 39305350
TELEPHONE: (202 39305350
TELEPHONE: RCA 248593 IDEA UR
INFORMATION POR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
FENTING 1542 base pairs
                 Sequence 16, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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Best Local Similarity 49.7%;
Matches 147; Conservative (
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-09-385-028-16
US-09-385-028-16
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Search completed: July 18, 2002, 11:24:25 Job time: 10855 sec

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Searched:

Run on:

Database

Result

1 2 3 3 4 4 7 7 7 111 112 113 114 117

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AL SUBMISSION

By 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster and melanogaster and provided by Razutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Cantitute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be load/drosophila_Dac.htm.

Location/Qualifiers
             AQ852321 LMAJFV1 AL108460 brossophil AQ846152 LMAJFV1 BH018404 L14841.4 AQ846152 LMAJFV1 BH019836 L5386c.4 BH019836 L5386c.4 BH019816 L5873b.4 BH019916 L5873b.4 AUS95670 AL10840B LTCOOLD AL106674 DROSSOPHIL AL106674 DROSSOPHIL AL1066051 DROSSOPHIL AL1066051 DROSSOPHIL AG137956 TELTAOGON AL1065051 DROSSOPHIL AG152796 PAN LTCOOLD AL1081291 DROSSOPHIL AG152796 PAN LTCOOLD AL10812 PAN LTCOOLD 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO091P 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                            AQB52043
BBG35178
BBG35178
BH019916
BH458211
BF529185
BG859785
AG859785
AG859785
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AG877280
AG817280
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BH020269
BH019836
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CNS006XK
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AL053013
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Drosophila melanogaster
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 source
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LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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   RESULT
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AL066051 Drosophil
AQ851215 LMAJFV1_1
AQ851019 LMAJFV1_1
AQ851316 LMAJFV1_1
AQ851336 LMAJFV1_1
AL192712 Tetraodon
                                                                                                                            (without alignments)
1225.988 Million cell updates/sec
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L11211.d_
Pan trog1
SCL074.G1
L24591.d_
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Drosophil
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AL053013 Drosophil
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                                                                                                                                                                                        438
1 atgcgcgagtcggttcaagc.....aggagcagaacgccggctga 438
                                                                                                        July 18, 2002, 07:26:40 ; Search time 4821.96 Seconds
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AG032885 1
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AQ849196
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                     13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM nucleic - nucleic search, using sw model
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AQ851336
CNS02DOV
C97336
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CNS010EW
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AG032885
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Maximum DB seq length: 2000000000
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em_gss_hum:*
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Match Length DB
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em_estin:*
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em_estov:*
em_estpl:*
em_estro:*
em_htc:*
gb_est1:*
gb_est2:*
gb_htc:*
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12.1
12.1
12.0
11.9
11.7
11.7
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                                                                                                                                                                         Title:
Perfect score:
Sequence:
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52.2
51.2
50.6
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Gaps

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Length Indels

285 654

BASE COUNT ORIGIN

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928 bp DNA linear GSS 03-NOV-1999 nDeb0003C14f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0003C14f, DNA sequence. AQ856496 GSS 6206953
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Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                   535 SMCGKKCGSTTBGSTTTTTTSSGSGYGKGCSSGSBSCSCCSSCSSSSSCSCCCCC 594
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Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
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/cultivar="Wipponbare"
/db_xref="taxon:4530"
/clone="nbeb0003c14f"
/clone=lib="CUGI Rice BAC Library (EcoRI)"
                                                                                             511 others
                                                                                                                                                                                                                              Mismatches 124;
                                                                                                                                                                                    Score 57.8; DB 12;
Pred. No. 0.75;
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Fax: 864 656 4293
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Clemson University Genomics Institute
Clemson University
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Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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High quality sequence stop: 194.
Location/Qualifiers
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
                                                                      : TET3"
61 9
                                                                                                                                                                                    13.2%; Sco
ilarity 14.3%; Pro-
Conservative 152;
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ibrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RRCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                                                                                          Query Match 13.4%; Score 58.8; DB 12; Best Local Similarity 13.8%; Pred. No. 0.51; Matches 49; Conservative 175; Mismatches 128;
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                                                     172
       /clone="BACR19D16"
/note="end : TET3"
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

DEFINITION

CNS0091P

RESULT LOCUS

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FEATURES

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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2. cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Leishmania major
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
1 (bases 1 to 556)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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//lab_nost=-E. Coll billows
//note="Wedcror: pBaCIndigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximatley 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence T7 end of BAC # BACK14N09 of RPCI-98 library from Drosophila melanogaster (fruit AL066051
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Determination of this BAC-end sequence was carried out as part of a
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 928;
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0; Mismatches 140; Indels
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Pred. No. 4
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/clone="LMAJFV1"
/clone=lib="Leishmania major FV1 random genomic library"
/lab_host="ToP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's EcoRV site."
235 c 175 g 105 t
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DNA Sequencing by: Washington University Genome Sequencing Center

If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major

Friedlin strain V1 genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining

Clone material please contact: Natalia S. Akopyants Ph.D.

(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.

Seq primer: -400P from Gibco
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Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Willams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by
                                                                                                                                                                                                                                                                                                                                      shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 ACGAGGACGCCGACGCGGGGGGGGTGCTGCTGGACGCGCGAGACGACGACGACGCCGACG 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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46.6%; Pred. No. 5.6;
tive 0; Mismatches 194;
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/strain="Friedlin strain Vl"
/db_xref="taxon:5664"
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High quality sequence stop: 418.
Location/Qualifiers
1. .556
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Contact: Akopyants, NS /
WashU Leishmania Project
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Library construction: Natalia S. Akopyants, Ph.D.
Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain V1 genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For Information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu)
Geverley@borcim.wustl.edu)
Seq primer: -40UP from Gibco
Class: shotgun
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Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Bistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., McCann, R., Tsagareishvill, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shotgun sequencing: a resource for DNA microarrays and expression
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/clone_lib="Leishmania major FV1 random genomic library"
/lab_host="TOP10 (Invitrogen)"
                                                                                                                                                                                                                                                                                                                                       AQ847989 11. A Leishmania major FV1 random genomic 11brary Leishmania major FV1 random genomic 11brary Leishmania major genomic clone LMAJFV1_LMS3h01 3' similar to contains element 212bp.2 leishmania repetitive element ;, DNA
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WashU Leishmania Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
371 gigacticgacggcaacciggaggacgcactgggccgcatcctcgccgaggagcagaacg
                                                   121 ACGAAGACGCCGACGCGCGGGAGCTGCTGCACGCCGCAGACGACGAGGACGCCGACG
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/strain="Friedlin strain Vl"
/db_xref="taxon:5664"
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Location/Qualifiers
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Fax: 314 286 1810
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Length 414;

DB 12;

Score 52.2;

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LMAJFVI_lm29c04.yl Leishmania major FVI random genomic library Leishmania major genomic clone LMAJFVI_lm29c04 5' similar to contains element V1-ch1_type_II.2 V1-ch1_type_I leishmania repetitive element ;, DNA sequence.
                                                                                                                                                                                                                       /clone_lib="Leishmania major FV1 random genomic library" /clone_lib="Leishmania major FV1 random genomic library" /fab_host="ToPl0 (invitrogen)" / fab_host="Yoctor: pzero-2 (invitrogen); Site_l: ECORV; Genomic DNA was sheared from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline Phosphatase and ligated into pzero-2 vector's ECORV site."
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Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  and/or Stephen M. Beverley
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.larity 47.0%; Pred. No. 9.7;
Conservative 0; Mismatches 218;
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                                                                                                                                        1. .555
/organism="Leishmania
(natalia@borcim.wustl.edu) ar
(beverley@borcim.wustl.edu)
Seq primer: -400P from Gibco
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Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
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LMAA_FVL_Im43e03.x1 Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAA_FV1_lm43e03 3' similar to
contains element V1-chl_type_II.5 V1-chl_type_I leishmania
repetitive element ;, DNA sequence.
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Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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Leishmania major
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ed. No. 6.5;
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1 (bases 1 to 555)
Best Local Similarity 46.3 Matches 171; Conservative
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274 GGACGCCGACGCGCGCGCGCTGCTGCTGCTGGACGCCCAGACGACGACGACGCCGACGC 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Leishmania major"
/strain="Friedlin strain V1"
/db_rafe="Lexon:5664"
/clone="Luka_FFV1_lab_2004"
/clone="Luka_FFV1_lab_2004"
/clone="Luka_FFV1_lab_2004"
/lab_host="TOPIO (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: ECORV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECORV site."
84 a 140 c 204 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(hatalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
Seq primer: -40RP from Gibco
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                l (bases 1 to 474)

Akopyants, M.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., K.

Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A.,

Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M.,

I., Bennett, J., Kole, R., Underwood, K., Cardenas, M., Gibbons, M.,

Barvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y.,

Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M.

A survey of the Leishmania major Friedlin strain v1 genome by shotyun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 cgaggagctctcgttccgtattccggtggagctccgatacgaggtcggcgatccgtatgc 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catccggatgacgttccaccttcccggcgatgcccctgtgacctgggcgttcggccgcga 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gotyctyctygacygyctcaacaycccyaycygcyacyyc---gatytycacatcyyccc 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 CGCAGACGACGACGCCGACGCCGAGGCTACTGCTGCTGGACGACGACGACGACGA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gctgttccggggcgggacggcaccgctgtggtggcgttcctcgaccggaccggacagctcgt 344
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                                                                                                                                                                                                                                                                                                                           Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, 1
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 474;
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21192569
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Pred. No. 12;
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1. .474
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                   REFERENCE
                                           AUTHORS
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                                                                                                                                                                                      TITLE
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   CNSO2DOV 755 bp DNA linear GSS 13-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 260DO6 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 755)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 755)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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                               345 gccgctcggccaggagcacacgctgggtgacttcgacggcaacctggaggacgcactggg 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 GAGGACGAGAGCCTGGTGTACGAGGCCGTGATCGACTGGGTCAAGGCCGACACGGAGCGC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,
Bouncau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Charaterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
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Pred. No. 16;
0; Mismatches 135; Indels
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/db_xref="taxon:99883"
/clone="260D06"
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                                                                                                             437
                                                                                                                                             sequence 1
                                                                                                             405 ccgcatcctcgccgaggagcagacgccggctg
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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/clone_lib="G"
/note="Genoscope s'
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us-09-749-185-1.rst

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/_clone="LMAJFV1_lmd3e09"
/clone="Liba"Leishmania major FV1 random genomic library"
/lab_host="TOP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: ECORV;
/note="Vector: pZero-2 (Invitrogen); Site_1: ECORV;
/note="Vector pZero-2 (Invitrogen); Site_1: ECORV;
/denomic DNA was isolated from stationary phase cells. For
this library, DNA was sheared to give a tight size
/distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECORV site."

136 c 195 g
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Library construction: Natalia S. Akopyants, Ph.D.
Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
                                                                                                      AUB49196
LMAJFV1_Im43e09.yl Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_Im43e09 5' similar to
contains element V1-ch1_type_II.2 leishmania repetitive element;
                                                                                                                                                                                                                                                                                                                                                                      Akopyants, N.S., Cliffcn, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing: a resource for DNA microarrays and expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                             Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
21192569
  346 CCTGATGGGCGAGTTCGTGCCGTGCGACGAGATGCGCGACCTG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49.6; DB 12;
Pred. No. 18;
0; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Leishmania major"
/strain="Friedlin strain Vl"
/db_xref="taxon:5664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Akopyants, NS / Beverley, SM
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (beverley@borcim.wustl.edu)
Seg primer: -40RP from Gibco
Class: shotgun
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AQ849196.1 GI:6053844
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48.6%;
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Matches 136; Conserv
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1. (bases 1 to 558)
Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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Fax: 81-298-38-7468
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Tetraodon ingroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphia; Acanthomorphia; Acanthomorphia; Tetraodontidaes; Tetraodontidaes; Tetraodontidaes; Tetraodontilaes; Tetraodontilaes; Tetraodontilaes; Disses I to 1129
Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
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306 accgctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggag
                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="251L09"
/clone_lib="G"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC - Intrary (Dros BAC) was made by Alain Bliland at CEPH (Centre d'Etude du Dyymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 19;
5; Mismatches 103;
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/organism="Drosophila m./
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN03P19"
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32.8%;
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Best Local Similarity
Matches 77; Conserv
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Length 1129;

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AG032885.1 GI:16559758
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-007M05.F.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoda, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoda, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tei:sla.45-503-9111, Fax:sla-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1313 bp DNA linear GSS 01-NOV-2001
Pan troglodytes DNA, clone: PTB-007M05.F, genomic survey sequence.
AG032885
                                    537 GATGGCGCGGAGCTGCTGCTGGACGCCAAAAACGACGAGGACGCCGACGCGGGGGAGCTG 596
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                                                                                                                                                               477 NAGGACGAAGACGCCGACGCGCGCGCTGCTGCACGCCCCANAGGACGAAGACGCC
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/clone_lib="PTB Chimpanzee Male BAC Library"
389 c 502 g 132 t 225 others
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Pred. No. 20;
0; Mismatches 214; Indels
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Fujiyama, A., Hattori, M., Toyoda, A., T
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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/db_xref="taxon:9598"
/clone="PTB-007M05.F"
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R.Site 2
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Eushamaia.
Eleishmania.
Eleishmania.
I (bases 1 to 629)
Myler, P.J., Vogt, C., Cawthra, J., Klacking, M., Marty, A., Mack, J.,
Myler, P.J., Nguyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal,
G., Nabson, S., Seyler, A., Worthey, E. and Stuart, K.
Leishmania major Friedlin Cosmid End Sequences
U npublished (2000)
Contact: Myler PJ
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-8846
Fax: 206 284-81313
Email: mylerpjespiebri.org
                                                                                                                                                                                                                                                                                                                                                                                                    L11211.d HygT3.1 Leishmania major Friedlin Cosmid Genomic Library Leishmania major genomic clone L11211, DNA sequence.
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// Ab_host="E. coli ED8767"
// Anote="Vector: cLHYG; Site_1: BamHI; Genomic DNA from Leishmania major Friedlin was partially digested with Sau3AI, size selected, and ligated with BamHI-digested cLHYG cosmid vector DNA. 9216 clones were picked and arrayed. Library construction is described in Ivens et al., Genomics Research, 8:135-145 (1998). The cLHYG vector (Acc. No. CVU59231) is described in Ryan et al., Gene, 131:145-150 (1993).
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297 GACGCCGATGCCGCGGAGCTGCTGCTGCTGGACGCCCAGACGACGACGACGCCGACGCC 356
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/clone_lib="Leishmania major Friedlin Cosmid Genomic
Library"
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Pred. No. 20;
0; Mismatches 164;
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/strain="Friedlin"
/db_xref="taon:5664"
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Class: cosmid ends.
Location/Qualifiers
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1797656 seqs, 10463268293 residues hits satisfying chosen parameters:

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Scoring table:

US-09-749-185-2

Title: Perfect score:

Sequence:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

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Total number of

Searched:

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LUITEN RUDOLF GIJSBERTUS MARIA (NL); WEZEL GILLES PHILIPPUS
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AX007218 Sequence
AX007216 Sequence
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AX00545 Streptomy
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D87846 Streptomyce
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AC092558 Oryza sat
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D50051 Streptomyce
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AR103046 Sequence
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E24180 Alpha-amyla
E24181 Alpha-amyla
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Streptomyces gilseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae, Streptomycetaceae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 3 06-3An-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARI(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_htg_hum:* em_htg_inv:* em_htg_other:*

em_sts:* em_un:*

em_vi:*

em_htgo_inv:*

SUMMARIES

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Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces
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Kawamoto,S., Watanabe,H., Hesketh,A., Ensign,J.C. and Ochi,K.
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 1 06-JAN-2000;
UNIV LEIDEN (NL); KRAL BARRND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                          Length 407;

    .>405
    /gene="ssgA"
    /note="strain ATTC of Streptomyces griseus"

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Pred. No. 9.9e-43;
0; Mismatches 0;
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/db_xref="taxon:1911"
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AX007216.1 GI:9995082
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ilarity 100.0%;
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                      /gene="ssgA"
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                                                  Shinichi, K. and Ensign, J.

Shinichi, K. and Ensign, J.

Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus

Unpublished (1995)

E Shaces I to 1513)

E Shinichi, K.

Direct Submission

L Submitted (06-APR-1995) Kawamoto Shinichi, National Food Research
Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2,
Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996)

L 1513
                                                                                                                                                                                                                                                                                           /product="ssga"
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DKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG"
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Expression analysis of the ssgA gene product, associated with sporulation and cell division in Streptomyces griseus Microbiology (Reading, England) 143 (Pt 4), 1077-1086 (1997)
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Pred. No. 7e-43;
0; Mismatches 0;
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/strain="B2682"
/db_xref="taxon:1911"
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/codon_start=1
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Best Local Similarity 100.
Matches 407; Conservative
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                                                               AUTHORS
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RESULT AF195772

RESULT AX007224

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Streptomyces netropsis.
Streptomyces netropsis.
Bacteria: Firmicutes; Actinobacteridae;
Bacteria: Firmicutes; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, K.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms
Patent: WO 0006613-A 9 06-JAN-2000;
UNLY LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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PAT 06-SEP-2000
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/gene="ssgA"
/note="strain ATCC of Streptomyces netropsis"
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DNA
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/organism="Streptomyces
/db_xref="taxon:55404"
407 bp
9 from Patent WO0000613.
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                                                                                                                                                                                                                                                                                                                                                                /product="ssga"
/protein_id="AAG28483.1"
/db_xref="G1:11066163"
/db_xref="G1:11066163"
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GDAPVTWARFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVGADRALFRAGAP
PLVAPLDRTDKSVPLGGEQTLGDFEDSLEAALGKILAEEQNAG"
   BCT 01-NOV-2000
                                                                                                                                                                                                                                                                                                                  /note="similar to Streptomyces griseus SsgA; possible cell division protein"
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                                                                                              Actinomycetales; Streptomycineae, Streptomycetaceae; Streptomyces. (bases 1 to 438)

"In Mezel, G.P., Rousseau, C. and Kraal, B.

"Cloning and sequencing of the Streptomyces netropsis ssgA gene unpublished

"Diversity of 1 to 438)

"Van Wezel, G.P.

"Direct Submission

Submitted (18-07-1999) Biochemistry, University of Leiden, PO Box 9502, Leiden 2300 RA, Netherlands

Location/Qualifiers
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                                                                         Streptomyces netropsis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
   DNA linear BC
gene, complete cds.
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/db_xref="taxon:55404"
1. .438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 298.2; DB 1;
Pred. No. 4.9e-29;
0; Mismatches 68;
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Streptomyces netropsis SsgA (ssgA)
AF195772
AF195772.1 GI:11066162
                                                                                                                                                                                                                                                                                                                                                                                                                                      142 g
                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
                                                              netropsis.
                                                                                                                                                                                                                                                                              /gene="ssgA"
                                                                                                                                                                                                                                                                                                       /gene="ssgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.3%;
Best Local Similarity 83.3%;
Matches 339; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       158 c
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                                                              Streptomyces
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/rraus.____sqa"
/product__sqa"
/protein_id="Cac07387.1"
/db_xref="GI:9995089"
/db_xref="GI:9995089"
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/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFG
/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLTPTD"
// RIVPLGQERSLADFDALLDEALDPTIAEEQNAG"
// RIVPLGQERSLADFDALLDEALDPTIAEEQNAG"
                                                                                                                                                                                                                                Kraal.B., Luiten.R.G. and Van Wezel,G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 7 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
PAT 06-SEP-2000
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                                                                                                                                   Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
1 (bases 1 to 407)
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Pred. No. 3.4e-24;
0; Mismatches 92;
  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Streptomyces/db_xref="taxon:121022"
407 bp
Patent W00000613
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ssgA"
/note="strain ATCC
                                                                                                                    Streptomyces goldeniensis.
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/transl_table=11
                                                                    GI:9995088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ssgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.8%;
Best Local Similarity 77.4%;
Matches 315; Conservative
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BCT 08-JUL-1999

linear

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Jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the cannot be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid Oll Cosmid Oll lies between H24 and D78 on the Asel-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Blibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                AL096823.1 GI:5457267
abaB; bldA regulation; cysA; cystathionine/methionine
gamma-synthase/lyase; gntR-family; integrated element; korSA;
plySR-family; membrane protein; phosphotyrosine protein phosphatase;
pra; pSAM2; ptpA; ssgA; thiamine biosynthesis; thiC;
transcriptional regulator; traSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomy cetales; Streptomy cineae; Streptomy cetaceae; Streptomy ces. [bases 1 to 1544]
[bases 1 to 1544]
Kinashi, M., Misser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-UUL-1999) Streptomyces coelicolor sequencing proje Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1878 E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 15441)
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
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361 GACGAGGCGCTGGACCGCATCCTGGCCGAGGAGCAGAACGCCGGCTG 407
                                                                                                                        Streptomyces coelicolor cosmid 011. AL096823
                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
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Location/Qualifiers
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RELLIDGGPRECGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
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135 c 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to Streptomyces griseus SsgA; possible cell division protein"
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                                                  BCT 01-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Box
                                                                                                                                                                                                                                                                          1 (bases 1 to 408) van Wezel,G.P., Rousseau,C. and Kraal,B.
Cloning and sequencing of the Streptomyces goldeniensis ssgA gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (18-OCT-1999) Biochemistry, University of Leiden,
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
                                AF195770 408 bp DNA linear BCT 0
Streptomyces goldeniensis SsgA (ssgA) gene, complete cds.
AF195770
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                                                                                                                                                                          Streptomyces goldeniensis.
Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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    .408
/organism="Streptomyces goldeniensis"
/db_xref="ATCC:21386"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAG28481.1"
/db_xref="GI:11066159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:121022"
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/product="SsgA"
                                                                                                                        AF195770.1 GI:11066158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ssgA"
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77.4%;
                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1 to 408)
van Wezel,G.P.
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Best Local Simil
Matches 315; (
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                                                                        DEFINITION
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ORIGIN
                                                                                                                                                                                                     ORGANISM
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VERSION
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AUTHORS
TITLE
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RESULT AF195770
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/strain="A3(2)"

project,

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SW.CYSA_STRCO (EMBL: U37580), CySA, S. COCLICOLOR putchive Cystathionine gamma-lyase (392 aa). Similar to many e.g. SW.MEGL_PSEPU (EMBL: U98854), mdeh. Pseudomonas putlda methionine gamma-lyase (398 aa), fasta scores; opt: 608 z-score: 653 6 E(): 4.5e-29, 36,9% identity in 404 aa overlap. Highly similar to TR: 053668 (EMBL: X9139) Streptomyces antibloticus hypothetical protein found upstream of the abaB gene (232 aa) (87.1% identity in 232 aa overlap). Contains Pfam match to PF01653 and overlap. Sy.Met metabolism Plr-dependent enzyme and PS00868 Cys/Met metabolism enzymes pyridoxal-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-tyrosine-phosphatase, len: 164 aa; previously sequenced as SW:PTPA_STRCO (EMBL:U3/580), ptpA, scoulcolor low molecular weight. contains Pfam match protein-tyrosine-phosphatase (164 aa). Contains Pfam match to PP01451 LMWPc, Low molecular weight phosphotyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MYKRVCFVCTGNICRSPMAEAVFRRNEDAGLGHLVEADSAGTG GWHEGEGADPRTEAVLADHGYGLDHARQFQGSWFSRLDLVVALDAGHLRALRRLAPT BRDAAKVRLLRSYDPAVAGGDLDVPDPYYGGRDGFEECLEMVEAASTGLLAAVREQVE GRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
PVFAAHFHLPGDPTGPYTYGRDENPTWTRLESAIGELEAPGEAGUETLVFASGMAAIS
SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALKVAEALRTRPEITGLRYPGLPDDPSHKVASQQMLRYGCVVSFTLPSRARADRFLDA
LRLVEGATSFGGVRSTAERRGRWGGDAVPEGFIRLSVGAEDPDDLVADLLRALDETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IETPSNPGLDVCDVRRLVEAAHAGGALVAVDNTLATPLGQRPLELGADFSVASGTKQL
len: 392 aa; previously sequenced as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGHGDVLLGYVAGRDAGAMAAVRRWRKIVGAIPGPMEAWLAHRSIATLQLRVDRQDST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1533, .2624)
/gene="SCQ11.03c"
/note="Match to PP01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
complement(2031, .2075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 256.6; DB 1; Length 15441; Pred. No. 3.3e-24; 0; Mismatches 94; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2693. 3187)
/gene="SC011.04c"
/note="SC011.04c, ptpA, low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"putative cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00868 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
complement(2693 ...3187)
/gene="SCQ11.04c"
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protein-tyrosine-phosphatase"
/protein_id="CAB46959.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / farma-synthase/lyase"
/protein_id="CAB46958.1"
/db_xref="G1:5457270"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SCQ11.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                         attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=cysA
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Matches 313; Conserv
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complement(360. .1265)

/gene="SCQ11.02c" abaB, probable lysR-family
/note="SCQ11.02c, abaB, probable lysR-family
transcriptional regulator, len: 301 aa; previously
sequenced as TR:Q53869 (EMBL:U37580) s.coelicolor
lysR-like procein (301 aa). Highly similar to
SW:ARAB_STRAT (EMBL:X91393), araB, Streptomyces
antibioticus transcriptional regulatory protein (301 aa),
fasta scores; opt: 1581 z-score: 1813.2 E(;; 0, 80.3%
identity in 300 aa overlap. Similar to many other
transcriptional regulators. Contains probable
helix-turn-helix motif at aa 17-38 (Score 1659, +4.84 SD).
Contains Pfam match to PF00126 HTH., Bacterial regulatory
helix-turn-helix protein, lysR family and PS00044
Bacterial regulatory proteins, lysR family signature"
                                                                                                                    Complement(<1. .289)
/gene="SCO11.01c" hypothetical protein, partial CDS, len:
/gene="SCO11.01c" hypothetical protein, partial CDS, len:
>95 aa; unknown function, previously sequenced as TR:053870 (EMBL:07580), S.coelicolor hypothetical protein ORSF downstream of phosphotyrosine protein phosphatase (159 aa). Weak similarity to the N-terminus of TR:069888 (EMBL:AL023797) Streptomyces coelicolor hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDLALLRTFVTVHRAGSFTRAAALLGLSQPAVTSQIRTLERQLG
RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEJAETGLEDDSTLRTLHLAGPPEFTA
ERALPALGELTGEDGQAFALRASFGNAEETLEGLAAGHHDLAIGTTRPRGALHTATPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTVRPVVKRTARAVLLDGDHLILIKRTKPGVDPYWVTPGGGVEP
DDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDEVHVLVATPHWAERAGVEDVRDTDASALKHVPVVEVHESLPFVGRYMASVFDARPA
SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
RTGTLAMPHIARAHEWLLRAAADWN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1518. .2696)
/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative lysR-family transcriptional regulator"
/protein_id="CAB46957.1"
/db_xref="GI:5457269"
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                                                                                                                                                                                                                                                                                                                                                                                  protein (172 aa), fasta scores; opt: 158 2-score: 206.4 E(): 0.00036, 46.2% identity in 65 aa overlap. Continues as SCH24.40c in cosmid H24 (EMBL:AL049826)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1. .4279)
/note="sequence corresponding to EMBL:U37580 from 1 to
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/note="overlap with Streptomyces coelicolor cosmid H24
(EMBE.AL049826) from 41528 to 41625"
complement(360. .1265)
/gene="SCOII.02c"
/note="abaB"
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/gene="SCQ11.02c"
/note="March to PF00126 HTH_1, Bacterial regulatory
hote="March to PF00126 HTH_1, Bacterial regulatory
helix-turn-helix protein, lysR family Score 145.96"
complement(1125. .1217)
/gene="SCQ11.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein_id="CAB46956.1"
/db_xref="G1:5457268"
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/gene="SCQ11.03c"
                                                            complement(1. .289)
/gene="SCQ11.01c"
                                 /clone="cosmid Q11"
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/label=SCQ11.01c
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/label=abaB
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RELLVBGVLDAAGDGDVRVCPVGQTATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
QCLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
1219 c 192 g 80 t
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division protein"
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gtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgacc 120
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetales; Streptomycineae; Streptomycesa 1 to 566)
To an Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces albus ssgA gene Unpublished
                                                                       241 ggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccgg
                                                                                                                                             301 acggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
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van Wezel,G.P.
Direct Submission
Submitted (18-OCT-1999) Biochemistry, University, Leiden 2300 RA, Netherlands
Location/Qualifiers
1 .566
/organism="Streptomyces albus"
//db_xref="taxon:1888"
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Pred. No. 1.3e-21;
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/db_xref="G1:11066161"
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74.2%;
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16. .20
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26. .433
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RELLVEGVEDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGRAPLLAFLDRTD
RGLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
1 150 c 1139 g 61 t
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
                                                                                      5714
240
                                                                                                                          ggcgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcgaccgg 300
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                                                                       acggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctg
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/db_xref="taxon:1962"
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Patent: WO 0000613-A 5 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL);
(NL); NL ORGANISATIE VOOR WETENSCHAP
VAN (NL)
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/db_xref="GI:9995087"
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5 from Patent W00000613.
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1. .>405
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ilarity 74.2%;
Conservative
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source

FEATURES

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DEFINITION

RESULT AX007220

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

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where these have been used to deduce the initiation codon. Gane prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4766-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/ jun/cgi.bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg., gtg., trg or (att.)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cennot be identified we choose the most upstream initiation codon. IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. If may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid BigA lies between and overlaps cosmids E6 and E56 on the Asole genomic restriction fragment. Location/Qualifiers source //strain=*A3(2)"	/db.zrei="ftaxon:100226" /db.zrei="ftaxon:100226" /gene="SCE19A.01" /gene="SCE19A.02" /gene="SCE19A.03" /gene="SCE19A.03	/protein_id="CAB50983.1" //db_xxef="Gl:5531351" //db_xxef="Gl:5531351" //db_xxef="Gl:5531351" //db_xxef="Gl:5531351" //db_xxef="Gl:5531351" //db_xxef="Gl:5831351" //db_xxef="Gl:5831351" //db_xxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //db_yxef="Gl:5831351" //dre="SCE194.03c" //dr
	SCE19A LOCUES SCE19A LOCUES SCE19A LOCUES SCEPAN AL09682. BETERBACK BETERBACK BETERBACK BETERBACK BETERBACK BETERBACK BETERBACK BETERBACK AL09682. AL10096ALORNAL MARCOLIOLA A3(2) AL09682. AL09682. AL1008AL AL09682. AL10096ALORNAL MARCOLIOLA A3(2) AL09682. AL09682. AL10096ALORNAL MARCOLIOLA A3(2) AL09682. AL0	Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web. (URL: http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given

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2660. .3955 /gene="SCE19A.06"

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Query Match
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/gene="SCE19A.04c"
/fonte="SCE19A.04c"
/fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCEI9A.05c, hypothetical protein, len: 77 aa; unknown function. similar to parts of many sugar permeases eg. TR:1996159 (EMBL:105013), malx, vibrio furnissii pTS (phosphoenolpyruvate-dependent sugar phosphotransferase system) permease for glucose (523 aa), fasta scores; opt: 77 z-score: 287.9 E(): 1.1e-08, 48.1% identity in 77 aa overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB"
                                                                                                                                                                                                                                                                                            /product="putative secreted protein"
/protein_id="CAB50984.1"
/protein_id="CAB50984.1"
/protein_id="G1:5531352"
/protein_id="G1:5531352"
/translation="MASRHRERETVTAVATVATIALTAGLTTGCDAVDKALDCVRT ADAIADSVTELQQAVENADDFTQWEESLNSIDKNLDRIGDQTDNTDVNKAVDDLGKAV DNNRTSVEDETPLSPPLSPPLAPAGELTKVCTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEGVPRWRKGSGEGWYTAEYAMLPRATNTRGDRESVKGRIGGRTHEISRLIGRSLRAU
IDYKALGENTVVLDCDVLQADGGTRTAAITGAYVALADAVAWAQGRKLIKANRKPLTG
YVSAVSVGYUTVGTPLLDLRYEEDVRATDMNVVCTGDGRFVEVQGTAEAEPFRADELN
TLLDLATAGCTELAELQRKALDATLER"
complement (1511. 2185)
/gene="SCE194.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'translation="MASKAEKIVAGLGGIDNIDEIEGCITRLRTEVNDPALVNEAALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MSRIDGRTPQQLRPVTIERGWSKHAEGSVLVSFGDTKVLCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exoribonuclease family, score 266.70, E-value 3.1e-76" complement(1805. .1843) //gene="SCE19A.04c" //gene="PS01277 Ribonuclease PH signature"
positional base preference and amino acid composition. Contenis probable N-terminal signal sequence and appropriately positioned PS00013 prokaryotic membrane liboprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1201. .1233)
/gene="SCE19A.03c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Journal and the contry PF00367 PTS_EIIB, phosphotransferase system, EIIB, score 43.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to entry PF01138 RNase_PH, 3/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative ribonuclease PH"
/protein_id="CAB50985.1"
/db_xref="G1:5531353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAHGVVKMGTAIQVVIGTDADPIAAEIEDMM
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/product="hypothetical protein"
/protein_id="CAB50986.1"
/db_xref="GI:5531354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCE19A.05c"
/note="SCE19A.05c"
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/note="bf--
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/gene="SCE19A.05c"
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/gene="SCE19A.04c"
                                                                                                                                                                                                                           /transl_table=11
/label=SCE19A.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attachment site"
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                                                                                                                                                      lipoprotein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane protein; membrane transferase; protein-export membrane protein; regulator; secreted protein; sugar transferase; threonine-tRNA synthetase; transport system inner membrane protein. Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996) 97000351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acetyltransferase; acyltransferase; adenine
phosphoribosiltransferase; DNA helicase; DNA polymerase III;
elongation factor; endodeoxyribonuclease; GTP pyrophosphokinase;
                                                                                                               (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20202 CGGACGATCCCTACGCCGTGCACATCACCTTCCACATCGACTCCGGCCACCCGGTGCACT 20261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20382 ceaaceaceacecercereaacececeacececaaceaceaceareaceaceaceacea 20441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20442 CCCTGCGGGCGGTGCCGCGGGACCGAGGCGCGCACCGCATCGGGATCGACGGCTGG 20501
                                                       possible PTS transmembrane component,
                                                                                                                                                                                                                                                                                                                                                        20142 TCAGGCTCGTCCTGTCGCCCGAGAGCGCCATTCCGGTGCCGGCCCGGCTCGGCTACCACA 20201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 38640)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctgg 361
                                                                                                                                                                                                                                                                                                                                                                                                                   62 teggegateegtatgeeateeggatgaegtteeacetteeeggegatgeeetgtgaeet 121
                                                                                                                                                                                                                                                                                             2 tgagcttcctcgtctccgaggagctctcgttccgtattccggtggagctccgatacgagg 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 gegeggaccgtgegetgttccggggegggacggcaccgetggtggcgttcctcgaccgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgcacateggecegaeegageeegaggeeteggagatgteeacateeggeteeaggteg
                                                                                                                                                                          Length 35284;
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                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                             DB 1;
                                                                                                                                                                                                   Pred. No. 7e-06;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                      len: 431 aa; similar to many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38640 bp
Streptomyces coelicolor cosmid L2.
AL137778
                                                                                                                                                                             Score 110.4;
2660. .3955
/gene="SCE19A.06"
/note="SCE19A.06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seeger, K.J. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL137778.1 GI:6822206
                                                                                                                                                                             27.1%;
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                                                                                                                                                                                                         55.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 aggacgcactgggccg 377
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                         Best Local Similarity
Matches 210; Conserv
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COMMENT

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identical to previously sequenced SW.RELA_STRCO (EMBL:X87267) Streptomyces coelicolor GTP_STRCO (EMBL:X87267) Streptomyces coelicolor GTP_STRCO (EMBL:X87267) Streptomyces coelicolor GTP_STRCO (EMBL:X872829) Streptomyces antibioticus RelA protein, 841 aa; fasta scores: opt: 4969 z-score: 4966.2 E(): 0; 90.3% identity in 848 aa overlap and to SW.RELA_CORGL (EMBL:AF038651) Corynebacterium glutamicum GTP pyrophosphokinase (EC 2.7.6.5) RelA, 760 aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.7% identity in 774 aa overlap. Contains Pfam match to entry PRO1842 ACT, ACT domain and match to Prosite entry PS00017 APP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /yord="SCL2.04c, apt, adenine phosphoribosiltransferase, /yord="SCL2.04c, apt, adenine phosphoribosiltransferase, len: 182 as; identical to previously sequenced SW: APT_STRCO (EMBL:X87267) Streptomyces coelicolor adenine phosphoribosyltransferase (EC 2.4.2.7) Apt, 182 as and highly smilar to SW: APT_ECOLI (EMBL:M14040) Escherichia coll adenine phosphoribosyltransferase (EC 2.4.2.7) Apt, 183 as, fasta scores: opt: 600 z-score: 682.8 E(): 1.2e-30; 54.8% identity in 168 as overlap. Contains Pfam match to entry PF00156 Pribosyltran, Phosphoribosyl Lransferase domain and match to Prosite entry PS00103 Purine Pyrinial inc phosphoribosyl transferases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3273...7460)

Complement(3273...7460)

S.coelicolor secD, secF & apt genes"

complement(378...3781)

complement(3904...4568)

Complement(3904...4568)

EMBL: 887267 S.coelicolor apt & relA genes"

complement(3956...4453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPDEAQPLTAAKPESASAAKPAPSAPQAKNDTHGPIQHAPAA
PVDKPAEQQPRPKPLPAERPQNAPVVRAPAGQPARSGSSNRVRARLARLGVQRANPYN
PVLEPLLRIVRGNDPKIETSTLRQIERAYQVAERWHRGQKRKSGDPYITHPLAVTTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AELGMDPATLMAGLLHDTVEDTEÝGLEDLRRDFGDVYTLLVDGYTKLDKVKFGEAAQA
ETVRKMYVAMAKDPRVLVIKLADRLHNMRTMRYLKREKQEKKARETLEIYAPLAHRLG
MNIIKWELEDLAFAILYPKMYDEIVRLVAERAPKRDEYLAVVTDEVQQDLRAARIKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTGRPKHYYSSYQKMIVRGRDFAEIYDLVGIRVLVODVRDCYAALGTYHARWNPYGR
FKDYIAMPKFNWYQSLHTTVIGPGGKPVELQIRTFDMHRRAEYGIAAHWKYKQEAVAG
ASKVRTDAPKSSGKSKDDHLNDMAWLRQLLDWQKETEDPGEFLESLRFDLSRNEVFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAGPSRDWLGFVKSPRARNKIRAWFSKERRDEAIEOGKDAIVRAMRKQNLPIQRIL
TGDSLVTLAHEMRYSDISALYAAIGEGHVSAPNIVOKLVQALGGEAATEEIDESVPP
SRGRCRKRRANADPGVVVKGVEDVWVKLARCCTPVPGDPIIGFVTRGSGVSVHRSDCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPKGDVIALPAGATPVDFAYAVHTEVGHRTIGARVNGRLVPLESTLDNGDLVEVFTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVDSLSREPERILEVEWAPTQSSVFLVAIQVEALDRSRLLSDVTRVLSDQHVNILSAA
VQTSRDRVATSRFTFEMGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
                                                                                                                                                                                                                                                                                                                           len: 847 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF01842 ACT, ACT domain, score 63.10, E-value 6e-15" complement(2378. .2401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                   /note="previously sequenced region SW:SCAPTRELA
EMBL:X87267 S.coelicolor apt & relA genes"
complement(1229. .3772)
                                                                                                                                                                                                                                                                                                                               relA, GTP pyrophosphokinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="adenine phosphoribosiltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="GTP pyrophosphokinase"
/protein_id="CAB70915.1"
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/gene="relA"
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                                                                                                                                                                                                                                            complement(1229. .3772)
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                                                                                                                                                                                                                                                                                                                           /note="SCL2.03c,
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                                                                                                                                                                                                                                                                                      /gene="relA"
                                                                                                                                                                                                               /gene="relA'
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                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                           Surfand)

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/Cgilbu/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream initiation codon. If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the most sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a consider of the considered clone. It may be shorter because we only sequence of the consider of the considered clone. It may be shorter because we arrange for a consider of the considered clone. It may be shorter because we arrange for a consider of the considered clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVDHLREQVDAHHAVGDLEALRARLDQLVALVETRREERKAQRAKOSBEARGAKEALV
AEAEELARSDQWRAAGERLRSLVDTWKGLPRLDRKSDDELWHRESHARSAFSKRRRQH
FAQLDAQREEARRIKERLVSEAEALSNSTDWGPTAARYRDLMSEWKAAGRAQREHEDD
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SVNERWEAIGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGPTPRHARVPRA"
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                                                                                                                        Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                  (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
Notes:
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/organism="Streptomyces coelicolor A3(2)"
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/protein_id="CaB70914.1"
/db_xref="G1:6822208"
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/protein_id="CAB70913.1"
/db_xref="G1:6822207"
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/gene="SCL2.02"
/note="SCL2.02, unknown, len: 46 aa"
/codon_start=1
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/db_xref="taxon:100226"
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/trans1_table=11
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/gene="SCL2.01"
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/partial
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                                                                                                                                                                                                                                                                                                                                                                                                          strand).
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SVSDAERRLAGLERASGARLGVYAYDTGSGRTVAYRADELFPMCSVFKTLSSAAVLRD
LDRNGEFLSRRILYTODDVEQADGAGFETGKPONLANAQUTVEELCEVSITASDNCAA
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/translation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
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amino acid transport integral membran protein; branched amino acid
binding secreted protein; branched amino acid transport system
binding protein; branched amino acid transport system permease;
integral membrane protein; ion transport integral membrane protein;
polysaccharide biosynthesis protein; regulator; regulatory protein;
secreted amidase; secreted peptidase; secreted protein; sigma
factor; transcriptional regulator; transcriptional regulatory
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 32704)
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beta-lactamase precursor
Eur. J. Biochem. 166, 345-350 (1987)
87275916
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="beta-lactamase"
                                                                                                                                                    /organism-"Streptomyces
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/gene="beta-lactamase"
/note="inverted repeat"
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540 c 496 g 1
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243. .1187
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Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
                                                                                                                                                                                 /strain="G"
/db_xref="taxon:1888"
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/transl_table=11
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64.0%;
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                                                                                          FEATURES
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                         /db_xref="G1:6822210"
/these continued to continue contin
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Debottay, P., Dusart, J., De Meester, F., Joris, B., Van Beeumen, J., Erpicum, T., Frere, J.-M. and Ghuysen, J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G
                                                                                                                                                                                                                                        /note="Pfam match to entry PF00156 Pribosyltran,
Phosphoribosyl transferase domain, score 150.30, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCL2.05c, secF, protein-export membrane protein, len: 373 aa; identical to previously sequence SW.SECF_STRCO (EMBL.X8599) Streptomyces coelicolor protein-export membrane protein SecF. 373 aa and similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15030 TGGCCTCGTTGTGTCGAGCGAGTCCTCCTGCCTGTCCCCGAGGCCTGCGGTACGACA 35089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35150 GGGTCTTCGCCCGCGACCTGCTCGCCGAAGGTCTCCACCGTCCCACCGGCACCGGCACG 35209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35210 recensivendecesteceseasteaeseceassecencesestestecareserecaserece 35269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 toggogatecgtatgccatecggatgaegttecacetteecggegatgeeectgtgaeet 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 gggcgttcggccgcgagctgctgctgctggacgggctcaacagcccgagcggcgacggcgatg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggtcg 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 gcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccgga 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cggacaagctcgtccgctcggccaggagcacacqctgggtgacttcgacggcaacctgg 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                      /gene="apt"
/note="PS00103 Purine/pyrimidine phosphoribosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.2%; Score 106.8; DB 1; Length 38640;
54.6%; Pred. No. 1.9e-05;
iive 0; Mismatches 177; Indels 0;
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Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STMLACBG 1410 bp DNA S.albus beta-lactamase gene, complete cds.
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'protein_id="CAB70916.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="seck"
complement(4501. .5622)
/gene="seck"
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                                                                                                                                                                                                                                                                                                                                         complement(4103. .4141)
                                                                                                                                                                                                                                                                                                                                                                                                                          transferases signature
complement(4468. .4503)
complement(4501. .5622)
                                                                                                                                                                                 complement(3980. .4429)
                                                                                                                                                                                                                     /gene="apt'
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M28303.1 GI:153338
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Gaps 81

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BCT 04-AUG-2000

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/ULTAINSTATE OF 12.14
// CLEARS LETE OF 12.14
// COMPLEMENTY LINPAGTES RICGTDAFLEK LFDEFASSR "
COMPLEMENT (3297. 7058)
// GENE="SC8A11.04c" POBABLE SECRETED PEPTIGNS PER COMPLEMENT (3297. 7058)
// GENE="SC8A11.04c" PROBABLE SECRETED PEPTIGNS PER COMPLEMENT (3297. 7058)
// COTE = "SC8A11.04c" PROBABLE SECRETED PEPTIGNS SECRETED PEPTIGNS SECRETED PEPTIGNS SECRETED PEPTIGNS SECRETED (1.124)
// COTE = "SC8A11.04c" PROBABLE SECRETED SECRETED (1.124)
// COTE = "SC8A11.04c" PEPTIGNS SECRETED (1.124)
// COTE = "SC8A11.04c" PEPTIGNS SECRETED S
                                                                                                                                                                                                       /translation-"IGARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
VRARILORAAGNPLALVELPRAAQGISPPLDDLPLTGRLEFAREASRTDSLTRECRTFL
VLAAEPPPELMOLLDVASRLAGSEYVYALOBAVDAGLVVLTGRTPEFRHPLMRSAI
VLAAEPPPEPPLHOLLDVASRLAGSEYVYALOBAVDAGLAVLTGRTPEFRHPLMRSAI
VTRATVADRISTHAALATLEGSPGRRLVHLAAATLGPDDELAGOLERFADDAGKRGO
LAAAVPALRQAGELVHDPRRQTGLLVRAAELASFINDRVQAQILLNRADLAEPGFTER
ARLMLVSDKAAFEPDBEPORRYODMIDAAAGAFDVGSTSVABNILWRAAARCFFQDGDA
RVRAQAAAELDRWKPDDPAPHVLTVANTEPYRFGTDLIARLEKLRFDREDGRLLHYL
GSGSMATGDVGRATTYLAQAARTSWRSQGRLGLLARSLAGSWPRLYTGQLAQAREESAE
GIALABETGEMIVWLGLKATSALTAVLRGEREAARSVRELRAHSLESPYMPRASVMAQ
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LVELDELDARLDSEMHYVARTYSTAVAPDOTAREOCYDSALSALDPYRPTRAEHLH
CHGRRLRRQRRNVDARRYELRLRDEPRVGAQPWADNAREQLEAAGESOGRRRPSKGE
SLTVQERQIAELASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2093. --2176
/gene="SCBA11.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                                                                                               /product="putative transcriptional regulator (fragment)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 49.10, E-value
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/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
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/product="putative regulator"
/protein_id="CAC01575.1"
/db_xref="GI:9716214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.02c"
                                                                                                                                 /protein_id="CAC01573.1"
/db_xref="G1:9716212"
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/gene-"SC8A11.03"
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/gene="SC8A11.01"
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2787, 3257
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signature"
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//octe="SCBA11.01"
//octe="SCBA11.01, possible transcriptional regulator
//octe="SCBA11.01, possible transcriptional regulator
(fragment), len: >750 as; similar to TR:095124
(fragment), len: >750 as; similar to TR:095124
(fragment), len: >750 as; similar scores:
0pt: 818 z -score: 913.7 E(): 0; 32.6% identity in 775 as
opt: 818 z -score: 913.7 E(): 0; 32.6% identity in 775 as
overlap. Contains Pfam match to entry PF00196 GerE,
Bacterial regulatory proteins, luxR family and match to
Prosite entry PS000625 Bacterial regulatory proteins, luxR
family signature. Also contains a possible
helix-turn-helix motif at residues 699. .720 (+3.25 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If the cannot be identified we choose the most IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Blbb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
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Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                     Unpublished (a) 32704)

a. (bases 1 to 32704)

Cerdeno, M., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
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jun/cgi-bin/frameplot.pl. CAUTION:
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domain and matches to Prosite entries PS00136 Serine proteases, subtilase family, aspartic acid active site, PS00137 Serine proteases, subtilase family, histidine active site and PS00138 Serine proteases, subtilase family, serine active site. Also contains possible N-terminal region signal peptide sequence"
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/protein_id="CAC01576.1"
/db_xreff="GI:9716215"
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/gene="SC8A11.04c"
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correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                  carboxypeptidase; D-amino acid oxidase; ddah, dimethylarginine dimethylaminohydrolase; dehydrogenase; efflux protain; endonuclease; enoyl CoA hydratase; IPP isomerase; metallopeptidase; oxidoreductase; racemase; regulator; thiolase; transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk RR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                                                                           Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 37245).
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):478(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996) 97000351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 37245)
Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
ABC transporter; amino acid permease; BCCT family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptomyces coelicolor A3(2)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 105
/note="Nominal overlap with cosmid 4C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .859)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="cosmid 5F2A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SC5F2A.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(83. .85
/gene="SC5F2A.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 37245)
Oliver, K. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ddah
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complement(3245. .4879)
/gene="SC5F2A.03c"
/gene="SC5F2A.03c"
/gene="SC5F2A.03c, probable ABC transporter, len: 544aa;
/gene="SC5F2A.03c, probable ABC transporter, len: 544aa;
similar to many involved in antibiotic resistance egs.
TR:054381 (EMBL:X79146) from the lincomycin-production
gene cluster of streptomyces inconnesis 78-11 (578 aa)
fasta scores; opt: 1624, z-score: 1696.3, E(): 0, (50.3%
identity in 541 aa overlap). Contains two Pfam matches to
entry PF00005 ABC tran, ABC transporter, two Prosite
matches to PS00017 ATP/GTP-binding site motif A (P-loop)
and Prosite match to PS00211 ABC transporters family
signature. Also contains a possible coiled-coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRPDVLLLDEPTNNLDVYARRRLYAAVESWPGVMVVVSHDRELLDRVDQIADLRAGSV
TWYGGNLTAYEEALAVEGEAAERWYRVAESDLRROKRELADAQVVLARRRRYGQKMYD
TWREPRAVMYKLRARTAQQSAGGYRIMHEEKLAGAKERLDDAVEAVEDDEIRVDLPYT
AVPPGRTYLTLIRALELAYGAKAGGLDLHGPERIALLGRNGAGKTTLRTUAGELAYD
AGEATAHVPLRFLPQRLDVLDDGLTVAENVARFAPGATNNRIRALLARFLFRGARADO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSTSPTSLTCTSISFAWPDGTEVFDGLDVAFGPGRTGLVGLNGAGKSTLLKLIAGRLTPADGTVRVAGQVGYLPQNVTLDTALRVDEALGIDGRRAALHAIEAGDVRREEHFETVGDDWDVEERALATLGELGLDHIGLDRTVGEVSGGESVLLRLAALLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAATLSGGERFRAALAALMLAEPAPQLLMLDEPTNNLDMASVRQLTGALEAYEGALLV
SABUDEPLESSLGITRWLLLEEGELREITPEAVGYSA"
complement (3290, 3787)
/gene="SCSF2A.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4739. .4762)
/gene="SC5F2A.03c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6297 GCGTCTCGTCGCCGCCGCCGCGTATGCCGAGCATTCCCGCCACCCTGCACTACGACCG 6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6117 CGGCGACGTCCGGGTGCGCCGTACGCGTACGACCGCACCG-----TCCTGGAGTT 6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 cggcgatccgtatgccatccggatgacgttccaccttcccggc-----gatgcccc 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 tgtgacctgggcgttcggccgcgagctgctggtggacgggctcaacagcccgagcggcga 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccaggtcggcgcggaccgtgcgctgttccgggggggacggcacgctggtggcgttcct 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 gagottoctcogtctccgaggagctctcgttccgtattccggtggagctccgatacgaggt 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00211 ABC transporters family signature."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6237 CGCCGACCCGTTCGCCGTCCGCATGACCTTCCCGGCCCCGGCCACCCTCGAGGCCGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6177 GETCTGCTGGACCTTCTCCCGCGAGCTGCTCATCGCCGGGATGCAGGAGCCGAACGGCCA
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/gene="SC5F2A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79.2; DB 1;
Pred. No. 0.058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative ABC tra
/protein_id="CAB40670.1"
/db_xref="GI:4584467"
/db_xref="SPTREMBL:09X7M6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4232. .4783)
/gene="SC5F2A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/trans1_table=11
/label=SC5F2A.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4942. .5850
/gene="SC5F2A.04"
4942. .5850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        around 250aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.5%;
54.6%;
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Best Local Similarity
Matches 212; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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                           CDS
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complement(976.3234)
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//gene="SCSF2A.02c"
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LAFMDPVTTTCHDCEGRRFREEVLRLTVDGRSVADVLAMTAGQALGFFSDPGVRRRLR
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ALLDRLVDAGNTVVVVEHNLDVVAHADRVIDLGPDGGRDGGRVIFEGTPRELLAARGS
                     dimethylaminohydrolase, len: 258 as; hydrolyses asymmetrically methylated arginine with preference for dimethylated arginine over monomethylated arginine (experimental). Similar to TR:D1038106 (EMBL:AB001915) NG.NG-dimethylated and dimethylated arginine sapiens (288 as) fasta scores; opt: 323, z-score: 384.7, codon_start=1
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transporter, score 101.40, E-value 1.7e-26."
/gene="SC5F2A.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="dimethylarginine dimethylaminohydrolase"
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/label=ddah
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Streptomyces grise Pseudomonas alpha-Pseudomonas alpha-Pseudomonas alpha-Pseudomonas alpha-

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mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agonist; antagonist; biomass; ds.
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                                                       AAX37297
AAX37298
AAQ14465
AAF74867
AAD17184
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/label= SsgA_protein
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                The present sequence is a DNA (ATCC 21345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigratine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bloinsecticide; receptor agent; antagonist; blomass; ds.
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                                                                                      Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                               Sequence 407 BP; 60 A; 139 C; 142 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Score 407; DB 21;
Pred. No. 2.5e-68;
0; Mismatches 0;
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELLJK ONDERZO.
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                                                                                                                              Disclosure; Fig 5; 60pp; English.
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Best Local Similarity 100.
Matches 407; Conservative
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                                                              P-PSDB; AAY44649
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid oulture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antiblocits, antitumour agents, imminosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraline agents, herbicides, antiparastitc agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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100.0%; Pred. No. 2.5e-68;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                            (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                      "SsgA protein"
                                                                                                                                                                                                                                                                                                                                                                                                  Luiten RGM
                                       Location/Qualifiers
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Best Local Similarity 100.
Matches 407; Conservative
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Streptomyces griseus.
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us-09-749-185-2.rng

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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, eryme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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tgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgac 180
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/label= SsgA_protein
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                                                                                                                                                                                                                                   ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antimisaria; agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agent; antagonist; blomass; ds.
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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Pred. No. 7.6e-48;
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                                                                                                                                                                                                Streptomyces netropsis ssgA gene.
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                                                                              BP
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                           Streptomyces netropsis.
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P-PSDB; AAY44650.
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                                           Gaps
                                                          9
                                                                   mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 3004; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                                                                                                                       1 atgagettectegtetecgaggagetetegtteegtatteeggtggageteegataegag
                                                                                                                                            tgggcgttcgggcgggagttgctcatcgacggaggtccgcgggccgtgcggggacggggac
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                                                                                                                                                                                                                                                                                                                                                                                         ssgA; liquid culture; filamentous bacteria; secondary metabolite;
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                        Length 407;
                                          Indels
                                                                                                                                                                                                                                                                407
                                                                                                                                                                                                                                                                56 A; 135 C; 145 G; 71 T; 0 other;
                  Score 259.8; DB 21;
Pred. No. 1.3e-40;
...trhes 92;
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                                         0; Mismatches
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/label= SsgA_protein
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1..405
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                        63.88;
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                                 Similarity 77.4 .5; Conservative
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                                                                                                                                                                                                                                                                                                                        AAZ49729 standard;
BP;
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Sequence 407
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mat_peptide
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                                         Matches 315;
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Best Local
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                                                                                                                              The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antiblotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entitumour signal antimigraine agents, hebblicides, antiparaslitc agents, runnant growth promoters, bloinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 gtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccttgtgacc 120
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transgenic plant; insect resistance;
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 239; DB 21
Pred. No. 1.1e-36
                                                                                 60pp; English.
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macrolide; insecticidal; ds.
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74.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 74.2'
Matches 302; Conservative
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ID AAF88315 standard;
                                                                                    Disclosure; Fig 5;
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polyketide synthase; biosynthesis; transgenic plant; insect resistance;

S. spinosa DNA fragment SEQ ID 1.

28-AUG-2001 (first entry)

Forosamine; trimethylrhamnose;

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of Identify, inactivate or modulate genes involved in the biosynthesis of adding forosamine or trimethylrhamnose to a spinosyn or polyketide adding forosamine or trimethylrhamnose to a spinosyn or polyketide caylycone; and (IV) for recombinant production of the corresponding enzymes, which are used for production of transgenic plants that express or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are also be used to raise specific antibodies, useful for identifying companies and a gene bank. Cells transformed with (I) may produce to expression clones in a gene bank. Cells transformed with (I) may produce (II). This sequence represents a genomic DNA fragment of the S. Spinosa comment of the significant of the signifi
                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45624 BP; 7933 A; 14913 C; 14940 G; 7838 T; 0 other;
                                                                                                                                                                                                                   Salas JA;
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   99DE-1057268
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                                                                                                                                                                                                                                                                                      WPI; 2001-267102/28.
                                                                                                                                             (FARB ) BAYER AG.
29-NOV-1999;
                                                                                                                                                                                                                Eberz G,
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ï 21031 GIGGAGCTGCGGTACGACAGCCGCAATCCGTACGAGATCTCCATGAAGCTCAACGTAGGC 20972 20971 ACGGACGGTCAGGTGGACTGGGTGATCGCCCGCGACCTGCTGGCCGGGCGTGATCGCC 20912 20855 20854 GTGATCGAGATGAGCTCGCCGTCGGGGCAGGCCTCCTTCGAGGTGAATGCTGACCAGCTT 20795 20794 GCGGACTTCTTGAACGACACCTACGACGTGGTCGAACCTGGTGATGAACACCGGTGGATG 20735 223 cacatocogotoccaggitoggogogogogotoctoticoggogogogogocogotog 282 163 ccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtc 222 283 giggegitectegaceggaceggacagetegigeegeteggecaggageacacegetgggt 342 43 giggagciccgatacgaggicggicgatccgtatgccatccggatgacgitccaccitccc 102 Gaps 103 ggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacagc 20911 GAGGCAGGCGAAGGCGATGTGCGGATCGGCC---CTCGACGGGGTTTTCCGGGGTTGGTC Length 45624; .; ; 0; Mismatches 156; Indels 20734 AACGICGACGAGGIGCIGAGCCAGCIGCTCTCGCACAACCI 20694 343 gacttcgacggcaacctggaggacgcactgggccgcatcct 383 DB 22; Score 75.4; DB 22 Pred. No. 5.5e-06; Query Match 18.5%; Best Local Similarity 53.4%; Matches 182; Conservative (셤 ò g οy g ò g ŏ g õ q

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AAF88312 standard; DNA; 50000 BP

AAF88312

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to clamify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide aliopersone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of the corresponding enzymes, including production of transgenic plants that express of derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying captone of the saccharopolyspora with (I) may produce (II) at significantly increased levels or produce new derivatives of genome which contains the coding regions for proteins involved in formation of the saccharopolyspora proteins involved in the second of the saccharopolyspora proteins procured the saccharopolyspora spinosa spi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzymes for spinosyn blosynthesis, useful for insecticidal spinosyns and their derivatives
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Pred. No. 5.5e-06;
0; Mismatches 156;
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Best Local Similarity 53.4%;
Matches 182; Conservative
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//note= "Spinosyn blosynthesis protein A"
/transl_except= (Pos:26940..26942, aa:Pro)
21126..2379
/*tag= r
//note= "Beta-ketosynthase domain (KSi): part of the
11nitiator module"
                                                                                                                                                                                                                                                                                                                                                                                                       part of
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/note= "Acyl carrier protein domain (ACP1): part of
extender module 1"
38916..35374
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/note= "Beta-ketoreductase domain (KR1): part of
extender module 1"
28404..28649
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/note= "Acyl transferase domain (AT1): part of
initiator module"
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/note= "Enoyl reductase domain (ER2): part of
extender module 2"
34082..34621
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/note= "Beta-ketosynthase domain (KS1): part
extender module 1"
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/note= "Acyl carrier protein domain (ACP1):
initiator module"
24102..25349
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/note= "Acyl transferase domain (AT1): part
extender module 1"
27582..28121
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extender module 2"
30629..31621
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           /product= spnJ
/note= "Spinosyn biosynthesis protein
16556..17743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product- spnC
/note- "Spinosyn biosynthesis protein
29024..30295
                                                                      protein
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                                                                     /note= "Spinosyn biosynthesis complement (17749.18501)
                                                                                                                  /note= "Spinosyn biosynthesis
complement (18541..19713)
                                                                                                                                                               /note= "Spinosyn blosynthesis
20168..20995
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21111..28898
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module 2"
                                                /*tag= m
/product= spnI
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  Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode: insect; polyketide; polyketide synthase; PKS; extender module; initiator module; acyl transferase domain; AT; acyl carrier protein; ACP; beta-kerosynthase domain; KS; KR; dehydratase domain; DH; enoyl reductase domain; ER; beta-ketoreductase;
DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes
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complement (4168..5325)
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10436..11434
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                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Keto acyl reductase"
complement (3416..4165)
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complement (1135..1971)
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AAQ88151 standard; DNA; 1549

AAQ88151

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/note= "Acyl carrier protein domain (ACP4): part of extender module 4" 44966..59752
                                           /note= "Acyl carrier protein domain (ACP2): part of extender module 2"
                                                                                                                                                                                                                                   of
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/note= "Acyl carrier protein domain (ACP3): part
extender module 3"
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/*tag= ad
/ote= "Beta-ketoreductase domain (KR2): part
extender module 2"
34886..30295
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/note= "Beta-ketoreductase domain (KR3): part
extender module 3"
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/note= "beta-ketoreductase domain (KR4): part
extender module 4"
44431..44676
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/note= "Beta-ketoreductase domain (KR5): part
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50009..50254
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extender module 5"
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/note= "Beta-ketosynthase_domain (KS4): part
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/note= "Acyl transferase domain (AT3): part
extender module 3"
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/note= "Acyl transferase domain (AT4): part
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/note= "Dehydratase domain (DH5): part of
module 5"
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/note= "Acyl transferase domain (AT5):
extender module 5"
                                                                                          Spinosyn biosynthesis protein
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/note= "Beta-ketosynthase c
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37108..38097
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15077..46348
                                                             5419..44931
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Xanthomonas campestris; L-glutamyl tRNA reductase; vitamin B12; glutamic acid-1-semialdehyde; 5-aminolevulinate (ALA); haem; chlorophyll; phycobilin; recombinat production; ds.

Location/Qualifiers 212..1492

Xanthomonas campestris.

/*tag=

JP07031480-A.

03-FEB-1995

(COSM-) COSMO SOGO KENKYUSHO KK

WPI; 1995-109535/15.

P-PSDB; AAR74619.

93JP-0184709 93JP-0184709

27-JUL-1993; 27-JUL-1993;

Xanthomonas L-glutamyl tRNA reductase.

(first entry)

02-NOV-1995

AAQ88151;

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teggecegacegagecegagggeeteggagatgtecacateeggeteeaggteggeggg 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                           AAQ88151 encodes AAR74619 Xanthomonas campestris L-glutamyl tRNA reductase. The DNA as part of an expression vector can be used to transform a host cell, for the recombinant prodn. of the protein. The protein can be used in the prodn. of vitamin B12, glutamic acid-1-semialdehyde, 5-aminolevulinate, haem, chlorophyll and
                                                                                                                                                                                                                                                                                                              DNA fragment encoding L-glutamyl tRNA reductase - derived from Xanthomonas sp., useful for production of 5-amino:levulinate, vitamin-B12, chlorophyll, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.4; DB 16;
Pred. No. 0.057;
); Mismatches 101;
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Best Local S
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Length 80161;

DB 20;

13.5%; Score 54.8; DB 20; 52.1%; Pred. No. 0.04; tive 0; Mismatches 132;

Conservative

Best Local Similarity Matches 147; Conserv

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Query Match

79 atccggatgacgttccaccttcccggcgatgccctgtgacctgggcgttcggcgcgag 138

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                                                                                                                                                                                                                                                                                                                                       ssgA: liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agent; antagonist; blomass; ds.
                                                                     367
                                                                                              315 tgcgtgcgctgccccaggtaagcgaggccgcgctgctgcacctgcaaccgtaccgagt
           248 accytycyctyttccgggcgggacggcaccyctggtggcgttcctcgaccggacggaca
                                                                   agctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaacctggaggacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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/product= "SsgA protein"
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Length 438;

21;

53.6; DB No. 0.085;

Score Pred.

13.2%;

Ouery Match Best Local Similarity

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Sequences AAX37293-298 represent nucleic acids encoding alpha-amylase variants (AAY17904-117909). The variants are derived from the Pseudomonas sp. KO-8940-derived maltopentaose-forming amylase (Shida, O. et al., Blosci. Blotech, Blochem. Vol. 56, 76-80, 1992 ). The variants have a replacement of the 57th or the 130th amino acid residue in the sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6117, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The enzymes prepared from the alpha-amylase variants produce maltopentaose
                                                                                                                                                                                                                      188
                                                                                      cggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgacctg 122
                                                                                                                                                                           ggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgatgt 182
                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                             187 TGAGCCCGTCCAGCAGCTCGCGGCCGAACGCCCAGGTCACAGGGGCATCGCCGGGA 128
                                                                                                                                                                                                                                                                                                                                                        243 cgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcgaccggac 302
                                         GCGTGTGCTCCTGGCCGAGGCACGAGCTTGTCCGTCCGGTCGAGGAACGCCACCAGCG 308
                                                                                                                                                                                                                                                                                                                                                                                                 89
gagetteetegteteegaggagetetegtteegtatteeggtggageteegataegaggt 62
                                                                                                                                                                                                                                                                   183 gcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggtcgg
                                                                                                                                 307 GTGCCGTCCCCGCCCGGAACAGCGCACGGTCCGCGCCGACCTGGAGCCGGATGTGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                   127 GGTGGAACGTCATCCGGATGGCATACGGATCGCCGACCTCGTATCGGAGCTCCACCGGAA
                                                                                                                                                                                                                      247 CICCGAGGCCCTCGGGCTCGGTCGGCCGATGTGCACATCGCCGTCGCCGCTCGGGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                               303 ggacaagetegtgeegeteggeeaggageacaegetgggtgaettegaeggeaace 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 TACGGAACGAGCTCCTCGGAGACGAGGAGCTCATCATGACCTCTGCTTGAACC 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas alpha-amylase variant encoding DNA (FERM BP-6116).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 6-8; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NORQ ) NORINSUISANSHO SHOKUHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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Gaps

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Indels

Mismatches 121;

0;

Conservative

126;

Matches

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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6117, 6117, 6118 or 6114. The variants can be used to transform plants to produce maltopentaose. The enzymes prepared from the alpha-amylase variants produce maltopentaose
                                                        gacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacgg 176
                                                                                                             177 cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca 236
                                                                                                                                          761
                                                                                                                                                                                                                          coggacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa 356
                                                                                 582 gatctccgactacctggtcgacctggtccagatgggcgtcaagggcttgcgcgtcgatgc 641
                              Gaps
                                                                                                                                                                      ggtcggcggaccgtgcgctgttccggggggggggggcaccgctggtggcgttcctcga
                                                                                                                                                                                         New alpha-amylase gene - useful for production of malto-pentaose
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Length 1981;
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1981 BP; 343 A; 679 C; 678 G; 281 T; 0 other;
 DB 20;
                           121;
Score 53.4; DB :
Pred. No. 0.087; 0; Mismatches 1:
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                                                                                                                                                                                                                                                                                                                                                                               AAX37294 standard; DNA; 1981 BP.
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13.1%;
51.0%;
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              Similarity 51.0 (6; Conservative
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P-PSDB; AAX17905.
                                                                                                                                                                                                                                                                                                   cctggag 363
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                           Matches 126;
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  Query Match
                 Best Local
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Length 1981;

53.4; DB 20; No. 0.087;

Score ?

13.1%; 51.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                          gacctggggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcggcgg 176
                          642 goccaagcacatcagcccgacggacctgggtgccatcatcgacagcgtcaacgcgcgcac 701
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                                                                                             cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca
                                                                                                                                                                                                                               702 cggtgccgcacggccattctggttcctggaggtgatcggcgcgccgggcgaggcggtgca
                                                                                                                                                                                      ggtcggcgcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (FERM
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Pred. No. 0.087;
0; Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX37295 standard; DNA; 1981 BP
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51.08;
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Best Local Similarity 51.09
Matches 126; Conservative
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P-PSDB; AAY17906.
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ggccaagcacatcagcccgacggacctgggtgccatcatcgacagcgtcaacgcgcgcac 701

cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca

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ccggacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa

ggtcggcgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcga

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Sequences AAX37293-298 represent nucleic acids encoding alpha-amylasse variants (AAX17904-Y17909). The variants are derived from the Pseudomonas sp. KO-8940-derived maltopentaose-forming amylase (Shida, Oet al, Blosci. Blotech, Blochem. Vol. 56, 76-80, 1992). The variants have a replacement of the 57th or the 130th aminon acid residue in the sequence as compared to the wild-type. The sequences are deposited under the accession numbers FERM BP-6116, 6119, 6115, 6117, 6118 or 6114. The enzymes prepared from the alpha-amylase variants produce maltopentaose. The in a high yield.
                                                                                                                                                                                      ccggacgacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacggcaa 356
                                                                                                                                                                                                                762 geceagecagtaettegggeteggeggegggeaggteaeggtgaeegagttegeetaegg 821
 gacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcgacgg
                                                                              cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca
                                                                                                                         ggtcggcggaccgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcga
                              gatetecgaetacetggtegaeetggtecagatgggegteaagggettgegegtegatge
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                                                                                                                                                                                                                                                                                                                                                         BP.
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Pseudomonas; maltopentaose; alpha-amylase; enzyme; variant; ss

97JP-0305071. 97JP-0305071

21-OCT-1997; 21-OCT-1997;

11-MAY-1999

JP11123081-A

Pseudomonas

Synthetic.

Pseudomonas alpha-amylase variant encoding DNA (FERM BP-6118).

(first entry)

27-JUL-1999

AAX37297;

AAX37297 standard; DNA; 1981 BP.

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Pred. No. 0.087;
0; Mismatches 121; Indels
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1larity 51.0%;
Conservative
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P-PSDB; AAY17908.
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Best Local Similarity
Matches 126; Conserv
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13.1%; Score 53.4; DB 20; 51.0%; Pred. No. 0.087; tive 0; Mismatches 121;

Query Match
Best Local Similarity 51.0°
Matches 126; Conservative

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Search completed: July 18, 2002, 11:36:11 Job time: 11236 sec

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Sequence 9,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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              Compugen Ltd
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-09-051-019-1
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Listing first 45 summaries
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Sequence 1, Appli
Sequence 3, Appli
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Patent No. 5215881
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Sequence 13,
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                                                 Sequence 13,
                                          Sequence 1,
                                                           Sequence
                      5215881-1
5215881-1
5215881-3
0S-07-945-3
0S-08-920-812-13
0S-08-921-177-13
0S-08-921-177-13
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0S-08-920-828-13
0S-08-439-009A-3
0S-08-439-009A-3
0S-09-443-501A-2
0S-09-443-501A-2
0S-08-804-227C-7
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ALIGNMENTS

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APPLICANT: Baltz, Richard H.
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Cardway, Kathryn P.
APPLICANT: Medduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
COUNTRY: USA
ZIP: 46268
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: PSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PAtentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50,608
Sequence 1, Application US/09036987A Patent No. 6143526 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-MAR.1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REPRENCE/DOCKET NUMBER: 50,6
TELECOMMUNICATION INFORMATION:
TELECHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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Length 80161; э; Э Score 54.8; 13.5%; g

52.1%;

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237 ggtcggcgggaccgtgcgctgttccgggcgggggggcaccgctggtggcgttcctcga 296
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TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: JP 305071/1997
SEARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PECENTIN Ver. 2.0
SEQ ID NO 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
  cctggtgatgaacaccggtggatgaacgtcgacgaggtgctg 280
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Patent No. 6087147

GENERAL INFORMATION:
APPLICANT: ITO, YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABI
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
TITLE REPREBUCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Pseudomonas sp., Strain KO-8940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MUTATED GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: PLASMID POS3410F57
US-09-017-706-3
                                                                                                              ; Sequence 3, Application US/09017706A; Patent No. 6087147; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%;
51.0%;
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Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                     79 atcoggatgacgitccaccitcccggcgatgcccctgtgaccigggcgttcggccgcgag 138
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                        Gaps
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APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathry C
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Turedway, Patti J
APPLICANT: Turedway, Patti J
APPLICANT: Turedway, Patti J
APPLICANT: Waldron, Clive
TILE REFERENCE: 50489 DIVI
CURRENT APPLICANTON NUMBER: US/09/370,700
EARLIER APPLICATION NUMBER: US/09/370,700
EARLIER PLILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 39
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Pred. No. 0.0067;
0; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Saccharopolyspora spinosa US-09-370-700-1
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Best Local Similarity 52.1 Matches 147; Conservative
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TYPE: DNA

FEATURE: FEATURE:

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WESULT 6
US-09-017-706-6
S-09-017-706-6
Sequence 6, Application US/09017706A
Patent No. 6087147
GENERAL INDOFFMATION:
TITLE OF INVENTION: A-AWILASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT ETLING DATE: 1998-02-05
EARLIER PILING DATE: 1998-02-05
EARLIER PILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
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                             OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
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US-09-017-706-6
                                                                  OTHER INFORMATION: MUTATED GENOMIC DNA PEATURE:
                                                                                                                ; OTHER INFORMATION: PLASMID POS34100L57
US-09-017-706-5
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LOCATION: (85)..(1848)
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Matches 126; Conservat
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Matches 126, Conserva
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APPLICANT: ITO, YOSHIFDMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: TRANSFORMANT
TITLE OF INVENTION: TRANSFORMANT
FILE REPERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
BARLIER FILING DATE: 1999-10-21
NUMBER: OF SEQ ID NOS: 14
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LOCATION: (85)..(1848)
OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
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illarity 51.0%; Pred. No. 0.014;
Conservative 0; Mismatches 121;
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CURRENT FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: JP 305071/1997
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 14
SOFWWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1981
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US-09-017-706-4
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US-09-017-706-5
Sequence 5, Application US/09017706A
; Patent No. 608/147
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                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (7)..(1848)
FEATURE:
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Best Local Similarity
Matches 126; Conserva
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Query Match 13.1%;
Best Local Similarity 51.0%;
Matches 126; Conservative
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LOCATION: (85)..(1848)
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Patent No. 6087147
GENERAL INFORMATION:
APPLICART: ITO. YOSHIFUMI
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
TITLE OF INVENTION: MALTOPENTAOSE, VECTOR CONTAINING SAID GENE AND
TITLE OF INVENTION: TRANSFORMANT
FILE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
CURRENT FILING DATE: 1998-02-05
EARLIER PILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.0
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582 gatctccgactacctggtcgacctggtccagatgggcgtcaagggcttgcgcgcgtcgatgc 641
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OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC:
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US-09-017-706-7
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LOCATION: (85)..(1848
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LOCATION: (7)..(1848)
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                                                                                                                                    HAVING ABILITY FOR HIGHLY PRODUCTOR CONTAINING SAID GENE AND
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Sequence 9, Application US/08034650
Sequence 9, Application US/08034650
GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
APPLICANT: FREMKEN, Leon G.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: PREMER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53.4; DB 3; Length 1 Pred. No. 0.014; 0; Mismatches 121; Indels
Sequence Application US/09017706A
; Sequence No. 6087147
; GEMERAL INFORMATION:
GEMERAL INFORMATION:
GEMERAL INFORMATION:
TITLE OF INVENTION: A-AMYLASE GENE HAVING ABII
TITLE OF INVENTION: TRANSFORMANT
FILLE REFERENCE: 8361-0003-0
CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CHRENT FILING DATE: 1998-02-05
; EARLIER PILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SCFUTANRE: PALENTIN Ver. 2.0
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US-09-017-706-8
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112 cctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggc 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 ctccaggtcggcgcggaccgtgcgctgttccggggcggggacggcaccgctggtggcgttc 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 gacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccgg
                     PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2261 · CTCGACGCGCGGCGGACCGGCGCGCGCGCGCGCGCGCGCTGCATG 2312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49.6; DB 1; Length 2
Pred. No. 0.071;
0; Mismatches 114; Indels
                                                                                                                                                 STATE: 1 1013 L. SLIEEL, N.W.

STATE: D.C.

LOUNTRY: USA

ZIP: 20036-5601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,015

FILING DATE: 24-MAY-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 07/727,235

FILING DATE: 03-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: ROKULIS, Paul N.

REGISTRATION NUMBER: 16,773

REGISTRATION NUMBER: 16,773

REGISTRATION NUMBER: 16,773

REGISTRATION NUMBER: 16,773

REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNK/5970/91731
                                                                 NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSS:
ADDRESSE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08387942C
Patent No. 5939289
GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PNK,
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0344
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%;
illarity 50.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 118; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
US-08-449-015-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT. 11
US-08-387-942C-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 gacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccgg 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 cctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggc 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctccaggtcggcgcggaccgtgcgctgttccggggcggggacggcaccgctggtggcgttc 291
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 ctcgaccggacggacaagctcgtgccgctcggccaggagcacacgctgggtg 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 2900;
                                                                                                                  COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114;
                                                                                                                                                                                                                                                                                                                                                                                                PRICASSILICATION 1433
PRICASSILICATION DATA
PPLICATION NUMBER: US 07/727,235
FILING DATE: 03-2016-1991
FILING DATE: 03-2016-1991
AFTILING DATE: 03-2016-1991
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERRING-COCKET NUMBER: PNK/5970/91731
TELECOMMUNICATION INFORMATION:
TELEFRANC (202) 861-3000
TELEFRAN: (202) 822-0944
TELES: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2%; Score 49.6; DB
ilarity 50.9%; Pred. No. 0.071;
Conservative 0; Mismatches 1
                                                                 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-449-015-9
Sequence 9, Application US/08449015
Patent No. 5804409
GENERAL INFORMATION:
APPLICANT: BOS. Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VERRIPS, Cornelis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
1559..2617
                     NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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ORGANISM: Saccharopolyspora erythraea
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 11219 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1998..2198
                                                                                                                                                                                                                                                               ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  Katz, L
Donadio, S
                                                                                                                                                                                                     CITY: Abbott Park STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                  ns
                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 cccgagcggcgacggcgatgtgcacatcggcccgaccgagcccgagggcctcggagatgt 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 tgacttcgacggcaacctggaggacgcactgggccgcatcctcgccgaggagcagaacgc 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 cggcgatgcccctgtgacctgggcgttcggccgcgagctgctgctggacgggctcaacag 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 ggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacacgctggg 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 CGAGATGTCCGGCTACGGTTTCGATCCGCACGAGCCACCATCAACCTGACGATCGCGGA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 CAGCGTGGCCCACGACA----ACGGCCTCGACGGCTTCGTCGCCGACTACCAGGTCGG 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 CGTCACCGGCATGGTGCGCTCGGCCTACGGCGAGGACCAGCAACTTCGGCATGAGCGA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.0%; Score 49; DB 2; Length 1155; Best Local Similarity 50.2%; Pred. No. 0.094; Matches 152; Conservative 0; Mismatches 145; Indels
          TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: 52 CORRESPONDENCE ADDRESS: SIRCH, STEWART, KOLASCH & BIRCH, LLP STREET: P.O. BOX 747 CITY: FALLS CHURCH
                                                                                                                                                                                                                                                        COUPTIER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C
FILING DATE: 09-MAY-1995
CLEASIFICATION: 09-MAY-1995
ATTORNEY/AGRAT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-642-734C-1/C
; Sequence 1, Application US/07642734C
; Patent No. 5824513
v. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-7
VALLA, SVEIN
                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                22042
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546 CGG 548
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                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
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NAME/KEY: misc_feature
LOCATION: 744.659
.OTHER INFORMATION: /function= "APPROXIMATE SPAN OF
OTHER INFORMATION: /Label= FUNCTION
OTHER INFORMATION: /Label= FUNCTION
OTHER INFORMATION: /Label= FUNCTION
NAME/KEY: CDS
LOCATION: 744.11219
OTHER INFORMATION: /function= "gene= "erya"
OTHER INFORMATION: /product= "ORF! encoding modules 1 & 2 for
OTHER INFORMATION: 6-deoxyerythronolide B""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 2250..3626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/module1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 744..1868
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
APPLICANT: Donadio, S
PEDLICANT: Mcalpine, J B
TITLE OF INVENTION: Excembinant DNA Method for Producing TITLE OF INVENTION: Expthromycin Analogs
TORRESPONDENCE ADDRESS: 27
CORRESPONDENCE ADDRESS: ADDRESSEE: Edward H. Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /function- "approximate span of OTHER INFORMATION: acyl carrier domain 1 of module 1"
                                                                                                                                                                        ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 3831..4811
OTHER INFORMATION: /function= "approximate span of
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DANCKERS, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/POCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FEATURE:

NAME/KEY: CDS

LOCATION: 744.11219

OTHER INFORMATION: /function= "gene= "eryA""

OTHER INFORMATION: /product= "'ORF1 encoding modules 1 & 2 for OTHER INFORMATION: 6-deoxyerythronolide B""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 2250..3626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACP synthase domain/modulel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 744..1868
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain 1 of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 3831..4811
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1998..2198
LOCATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 1 of module
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 744..6659
OTHER INFORMATION: /function= "APPROXIMATE SPAN OF
OTHER INFORMATION: MODULE 1"
OTHER INFORMATION: /label= FUNCTION
                                    NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F. Weinstock
STREET: Abbort Laboratories D377/AP6D-2 One Abbott
STREET: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 5574..6125
OTHER INFORMATION: /function= "approximate span of
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
COMPUTER: IRM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPATION OF THE STATE
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REFERENCE/DOCKET NUMBER: 46,943
REFERENCE/DOCKET NUMBER: 46,943
REFERENCE/DOCKET NUMBER: 4952.US.DI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
TITLE OF INVENTION: Specific Polyketides NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 3831..4811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                       CITY: Abbc
STATE: IL
                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 tgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggt 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgac 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 cggcgcgcgcgcgtgcgctgttccgggcgggacggcaccgctggtggcgttcctcgaccg 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 gacggacaagctcgtgccgctcggccaggagcacacctgggtgacttcgacg 352
                                                                         NAME/KEY: misc_feature
LOCATION: 5574..6125
OTHER INFORMATION: _function= "approximate span of
OTHER INFORMATION: _bcta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 9906.110454
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.0%; Score 49; DB 1; Length 11219; Best Local Similarity 50.2%; Pred. No. 0.088; Matches 147; Conservative 0; Mismatches 145; Indels
    OTHER INFORMATION: acyltransferase 2 domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

NAME/KEY:

LOCATION: 6678..11219

OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 2"
FEATURE:

NAME/KEY: misc_feature
LOCATION: 6678..8066

OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoacyl ACPsynthase of module information: /function= inf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08439009A
Patent No. 6004787
GENERAL INFORMATION:
APPLICANT: Donadio, S
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 6369..6526
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

: LCCATION: 10707..10964

: OTHER INFORMATION: /function= "approximate span of

: OTHER INFORMATION: acyl carrier domain of module 2"

US-07-642-734C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-439-009A-1/c
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1699 GACCGCGCGCGCGGATCGTGCCGCACGCACGCGTCGTCATGCCCCCGCGTGGTCCACGCC 1758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgatgtgcacatc 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 ggcccgaccgagcccgagggcctcggagatgtccacatccggctccaggtcggcggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.8%; Score 48; DB 1; Length 2064; nilarity 53.1%; Pred. No. 0.14; Conservative 0; Mismatches 90; Indels
                                                                                                                           COMPUTER: IBM Compatible SYSTEM: MS Dos 5.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/343,428
FILING DATE: 18-NOV-1994
CLASSIFICATION NUMBER: PCT/J93/00592
FILING DATE: 30-APR-1993
APPLICATION NUMBER: JAPAN 4-126511
FILING DATE: 19-MAY-1992
ATTONNEY/AGENT INFORMATION:
NAME: Halley, Jr., James F.

REGISTRATION NUMBER: 27794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by experiment
1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 54/34
REFERENCE/DOCKET NUMBER: 54GN-7
TELECOMMULICATION INFORMATION:
TELEPHONE: (212)596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces fradiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: -35 signal
LOCATION: 359..364
IDENTIFICATION METHOD:
NAME/KEY: -10 signal
LOCATION: 378..383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IDENTIFICATION METHOD:
; NAME/KEY: sig peptide
LOCATION: 435.944
; IDENTIFICATION METHOD:
US-08-343-428-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1879 Trcccccccrc 1890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                              New York
                                                                                      10020-1104
                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CORIGINAL SOURCE:
                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 102;
                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcga 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cggcgcggaccgtgcgctgttccggggcggggacggcaccgctggtggcgttcctcgaccg 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ggtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgcccctgtgac 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 tgtgcacatcggcccgaccgagcccgaggcctcggagatgtccacatccggctccaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gacggacaagctcgtgccgctcggccaggagcacacgctgggtgacttcgacg 352
                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 6678.8066
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 2"
FEATURE:
OTHER INFORMATION: beta-ketoreductase domain of module 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function= "approximate span of beta-ketoreductase domain of module 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 3; Length 11219;
Pred. No. 0.088;
0; Mismatches 145; Indels
                                       NAME/KEY: misc_feature
LOCATION: 6369..6626
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain 2 of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

: ICCATION: 10707..10964

OTHER INFORMATION: /function= "approximate span of

: OTHER INFORMATION: acyl carrier domain of module 2"

US-08-439-009A-1
                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LACATION: 6678.11219
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shin, Nasaru
APPLICANT: Teraoka, Hiroshi
TITLE OF INVENTION: No. 566586el Protease
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jamee T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08343428
Patent No. 5665586
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nakamura, Etsuo
APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Kitadokoro, Kengo
APPLICANT: Shin, Nasaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.0%;
Best Local Similarity 50.2%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 9906..10454
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Susan B. Jensen
APPLICANT: Susan B. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
TITLE OF INVENTION: Acid Biosynthesis
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
CITY: Washington
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIPFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CAGGGGGAGCGCTCGCTCGCGCGACCCTGGTGCACGCCCCTCGGTCGCGCCCGACCGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GOGGIGGOGGOCTCCTCACCGGCGCCCCACCACCGCGGGGCTCGCCGGTGAGATCTAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 crestrorisciscorecresancerrarancine arecorreces creares and an area and an area area.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 ctggtggcgttcctcgaccggacggacaagctcgtgccgctcggccaggagcacac 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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Pred. No. 0.29;
0; Mismatches 146; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION STATES
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-7M-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTARATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELEFONON: (202 389-666
TELEFAN: (202) 39305350
TELEFAN: (202) 39305350
TELER: RCA 24859 IDEA UR
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
                  Sequence 16, Application US/09385028 Patent No. 6232106 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-385-028-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.48;
49.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 49.73
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
US-09-385-028-16
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Search completed: July 18, 2002, 11:24:51 Job time: 10881 sec

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Perfect score: Sequence: Scoring table:

Searched:

OM nucleic

Run on:

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AL Cascape.

AL Submission

Direct Submission

AL Submitted (0.2-Unv.1999) Genoscope - Centre National de Sequencage :

Direct Submission

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and melanogaster in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RRCI-99 and was constructed by partial ESCRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's Pl and bow to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                            A0852043 LMAJFV1_1
B8635178 B8635178
B8635178 B8635178
B8635178 B86351815
B86351815
B8635181 AGENCOURT
B859785 102409601
B8659785 102409601
AG057280 Pan trog1
ALS88142 ALS88142
ALO66742 Drosophil
AG043477 Pan trog1
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AG032939 Pan trog1
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BH018881 L2031k.d_
AQ845292 LAMJFV1_1
BH019456 L3651.d_H
AZ131579 OSJNBb011
             AQ851019 LMAJFV1_1
BH020269 L7165c.d_
BH019193 L24591.d_
BH019836 L5336c.d_
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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AQ851336 LMAJFV1_1
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AL192712 Tetracodon
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nbeb0003C14f CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0003C14f, DNA sequence.
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I (bases I to 928)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 cgcggaccgtgcgctgttccggggcgggacggcaccgctggtggcgttcctcgaccggac 302
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                  14.0%; Score 57; DB 1
ilarity 14.3%; Pred. No. 1.2;
Conservative 161; Mismatches
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Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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  /db_xref="taxon:7227"
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- Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegaw and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595 SCSSYCCSSBSSKCSSTSBSCSCCCSSKSVCGTSCSSSSSCSSSSSTSSSSTS 654
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Pred. No. 0.87;
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/clone="BACR19D16"
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VERSION KEYWORDS SOURCE

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AUTHORS

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                                                                                   on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of All Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the clemson University BAC/EET Resource Center (www.genome.cdu)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence T7 end of BAC # BACK14N09 of RPCI-98 library from Drosophila melanogaster (fruit ALD), genomic survey sequence.
/note="Vector: pBACIndigo; Site_1: EcoRI; Site_2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Determination of this BAC-end sequence was carried out as part of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gacctgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgg 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 GAGCTCGGTGTTCTCCATGGAGGAGATCCTGCGCCCACCAACAACTTCTCGCCGGCGCT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 cgatgtgcacatcggcccgaccgagcccgagggcctcggagatgtccacatccggctcca 236
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 935)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 928;
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Pred. No. 5.5;
0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 others
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoss in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leishmania major.
Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 others
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Matches 111; Conservative 104; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  897 GSCSGGGGSCCSCSCGCSSCSSSCSCCCCCGS 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53; DB 1
Pred. No. 5.5;
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/clone="BACR14N09"
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1 (bases 1 to 556)
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REFERENCE

COMMENT

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ORIGIN
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MEDLINE
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AQ847989
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DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.

(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.

Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV; Geomato DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA posymerase, dephosphorylated with Shrimp Alkaline Phosphatase and ligated into pZero-2 vector's EcoRV site." 175 g 105 t
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Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmit, A., Person, B., Theising, B., Ritter, E., Ronko, J., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvill, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S. M. A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing: a resource for DNA microarrays and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .556
/organism="Leishmania major"
/strain="Friedlin strain VI"
/db_xref="taxon:5664"
/clone="LMAPY1_Lim44f10"
/clone=lib="Leishmania major FV1 random genomic library"
/lab_host="TOP10" (Invitrogen)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 TGGACGCCGCAGAAGACGAAGACGCCGACGCGCGGAGCTGCTGCTGGACGGCGCCAGACG 302
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                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                               / Beverley, SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                      Other_GSSs: lm44f10.y1
Contact: Akopyants, NS /
WashU Leishmania Project
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       AUTHORS
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DNA Sequencing by: Washington University Genome Sequencing Center If using this information please cite:

N.S. Akopyants and S.M. Bewerley 'A survey of the Leishmania major Eriedlin strain VI genome by shotgun sequencing' and the Washington University Genome Sequencing Center For Information on obtaining clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib-"Leishmania major FV1 random genomic library"
/clone_lib-"Leishmania major FV1 random genomic library"
/lab_host="ToPl0 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_l: ECORV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECORV site."
a: 125 c 179 g 33 t
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1 (bases I to 414)

1 (bases I to 414)

Kissinger, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L., Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenss, M., Gibbons, M., Bowers, Y., McCann, R., Tsagareishvill, R., Wilson, R. and Beverley, S.W. A survey of the Leishmania major Friedlin strain vi genome by shotgun sequencing: a resource for DNA microarrays and expression
341 gigacticgacggcaacciggaggacgcacigggccgcatccicgccgaggagcagaacg 400
                                                            121. ACGAAGACGCCGACGCGGGGGGGCTGCTGCTGGACGCGCAGACGACGACGACGCCGACG 62
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Location/Qualifiers
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AQ847989.1 GI:6052637
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Length 414;

DB 12;

Score 52.2;

12.8%;

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CNS02DOV 755 bp DNA linear GSS 13-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 260D06 of library G from Tetraodon nigroviridis, genomic survey
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei,
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 755)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 GCTGCTGCTGGTGGACGCCCAGACGACGACGCCCGACGCCGCGGGGCTGCTGCTGGACGC 213
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    Beverley Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 474;
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(natalia@borcim.wustl.edu) and/or Stephen M. (beverley@borcim.wustl.edu)
Seq primer: -40RP from Gibco
Class: shotgun
High quality sequence stop: 399.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                              /strain="Friedlin strain Vl"
/db_xref="taxon:5664"
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Pred. No. 14;
0; Mismatches
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DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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  Pred.
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Contact: Akopyants, NS /
WashU Leishmania Project
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Rissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Rissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising. B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Glbbons, M., Harvey, N., McCann, R., Tsagareishvill, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain v1 genome by shotgun sequencing: a resource for DNA microarrays and expression
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                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="C60023_lare]
/clone="C60023_lare]
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/clone=lib="Raice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
/note="Vector: pBluescript II SK+ phagemid to the SalI-NotI site of pBluescript II SK+ phagemid."

188 c 209 g 86 t 4 others
               National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
1961. 81-298-38-7441
Fax: 81-298-38-7446
Email: tsasak'@br.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
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Pred. No. 19;
0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
   Contact: Takuji Sasaki
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                   2 (bases 1 to 755)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                      Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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t 3 others
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Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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/db_xref="taxon:99883"
/clone="260D06"
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Pred. No. 18;
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238 c 266 g 111
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Best Local Similarity 49.2%;
Matches 131; Conservative
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                                          Weissenbach, J.
Charaterization and
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CNSO2AGC 1129 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 251L09 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                           Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon. 1 (bases 1 to 1129)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Unpublished
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1009)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
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32.8%; Pred. No. 21;
tive 55; Mismatches
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Tetraodon nigroviridis
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/note="end : SP6"
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                                                                                                                                                                                            Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain V1 genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: piero-2 (Invitrogen); Site_1: EcoRV; Chote="Vector: piero-2 (Invitrogen); Site_1: EcoRV; this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA POLYMerase, dephosphorylated with Shrimp Alkaline.
Phosphatase and ligated into plero-2 vector's EcoRV site."
116 c 195 g 10 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Friedlin strain VI"
/db_xref="taxon:5664"
/clone="LMAJFV1_Im43e09"
/clone="Lb="testshmania major FV1 random genomic library"
/lab_host="TOP10 (Invitrogen)"
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                                           Washu Leishmania Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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0; Mismatches 144;
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                         Contact: Akopyants, NS / Beverley, SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Leishmania major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 302.
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                                                                                                                                                                                                                                                                                                                                                                                           (beverley@borcim.wustl.edu)
Seq primer: -40RP from Gibco
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                     Email: est@watson.wustl.edu
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ilarity 48.6%;
Conservative
                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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Length 1009;

243 others

FEATURES

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2 (bases 1 to 1313)
Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                   Location/Qualiflers
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SacI
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                                                                                                                                                            Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
1. 1129
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-007M05.F.
Pan troglodytes
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                                                   Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                   Bouneau, L., Fisher, C.,
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             Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="251L09"
/clone="15=151"
/note="Genoscope sequence ID : COAG251CF055P1-end
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Fuliyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Best Local Similarity 46.7%;
Matches 157; Conservative 0
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AWB001.G03F000328 ITEC AWB Wheat Melotic Stage Library Triticum aestivum cDNA clone AWB001.G03, mRNA sequence.
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (02-AUG-2001), Genomic Sciences Center (GSC); and Chemical Research (RTKEN), Genomic Sciences Center (GSC); and Chemical Enternourge (GSC); Theorem (E-mail:chimpbes@gsc.riken.go.jp, ORL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Was generated during the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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/clone_lib="PTB Chimpanzee Male BAC Library"
1 389 c 502 g 132 t 225 others
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Pred. No. 22;
0; Mismatches 214;
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-007M05.F"
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Search completed: July 18, 2002, 10:12:46 Job time: 9966 sec
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/clone_lib="ITEC AWB Wheat Meiotic Stage Library"
/tissue_Lype="excised florets"
/dev_stage="excised florets"
/dev_stage="meiotic stage no later than metaphase I"
/note="Vector: pSport 1 (Life Technologies cat. no.
1848-013); Site_l: Sall; Library constructed in pSport 1.
Directionally cloned using the Superscript Plasmid System for CDNA synthesis and plasmid cloning. M13 Reverse
sequencing primer used to obtain 5' sequence data. 1.4
18 c 143 g 50 t
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticae; Triticum.

1 (bases 1 to 437)
                                                                                                                                                                                                                                                                              Special Research Centre, Basic and Applied Plant Molecular Biology Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA Feb: 61 8 8303 7368
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                                                                          Anderson, O. A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Hermann, R.G., Holton, T., Jacquenin, J. M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)
Contact: Langridge P
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                                                                                                                                                                                                                                                                                                                                                             Email: plangridge@waite.adelaide.edu.au
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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Pred. No. 27;
0; Mismatches 132;
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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AL108460.1 GI:5628764
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49.2%;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ehi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.

1 (bases 1 to 1101)
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN37L08"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
н	704	100.0		21	AAY44649	Streptomyces drise
~	909	86.1		21	AAY44652	Streptomyces netro
က	556	79.0		21	AAY44651	Streptomyces golde
4	464	65.9		21	AAY44650	Streptomyces albus
S	84	11.9		22	ABG24744	Novel human diagno
9	83.5	11.9		21	AAG12893	Arabidopsis thalia
7	83.5	11.9		21	AAG27402	Arabidopsis thalia
80	81	11.5		18	AAW14287	Human deleted in p
σ	81	11.5		21	AAY70071	Human tumour suppr
10	81	11.5	552	21	AAY69622	Human Smad4. Homo
11	81	11.5		19	AAW85025	Smadd-green floure

(UYLE-) RIJKSUNIV LEIDEN. (NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.

99WO-NL00395.

25-JUN-1999; 26-JUN-1998; Luiten RGM;

Van Wezel GP, Kraal B, Lu WPI; 2000-147269/13 N-PSDB; AAZ49727, AAZ49728

	12	81	11.5	0	19	AAW85013	Smad4-green floure
	13	75.5	0	1046	17	AAW02156	smic
	14	വ	0	1046	21	AAY 52304	Vibrio furnissii p
	15 16	7.7	10.5	400	7 0	AAU56775 ABB64343	Propionibacterium Drosophila melanod
	17	72	\circ	1248	70	AAY43569	Amino acid sequenc
	18	72	0	1248	20	AAY23960	Fragment 7 of the
	19	72	\circ	1248	21	AAY67527	FHA fragment 7 pol
	070	7 (⊃ <	3596	7.	AAY8/40/	Bordetella pertuss
		71 .5	\sim	212	717	AAB06133	Firamentous naemag Human DPC4 Smad co
		71.5	0	234	20	AAW96221	Smad4/DPC4 protein
		71.5	0	971	22	AAU50418	Propionibacterium
	25	71	0	837	71	AAB12381	N-terminal domain
		71	0	1248	19	AAW69594	Filamentous haemag
		70.5	\circ	787	22	ABB71973	Drosophila melanog
		0 69	n 0	2448	77	ABB33020	arabidonsis thalia
		69.5	0.0	259	22	AAB59590	Human carbonic anh
		69.5	6.6	317	21	AAG24693	Arabidopsis thalia
		69.5	6.6	364	21	AAG24692	Arabidopsis thalia
		69.5	6.6	1298	22	ABB61948	Drosophila melanog
	34		9.8	752	22	AAU49339	Propionibacterium
	35	68.5	9.7	361	21	AAY75618	Neisseria gonorrhe
	36	89	9.7	143	21	AAY81424	Cellulomonas fimi
	37	89	9.7	323	22	AAU61464	Propionibacterium
	38	89	7.6	401	22	AAU35669	Haemophilus influe
	J. C.	90	7.0	410	77	ABB61295	Ω.
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						ALIGNMENTS	
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£	AAY44649		ndard	standard; Protein		135 AA.	
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占	18-AP	8-APR-2000	(firs	(first entry)	γ.		
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KW KW KW KW	SsgA; mycel hypoc herbi bioin	SsgA; liquid culture; mycelium; antibiotic, hypocholesterolaemic herbicide; antiparasi bioinsecticide; recep	d culturitibiot erolaem entiparide; re	ture; fi. otic, and emic agen arasitic receptor	lame titu nt; age age	d culture; filamentous bacteria; secondary metal intibiotic, antitumour agent; immunosuppressive erolaemic agent; enzyme inhibitor; antimigraine antiparasitic agent; ruminant growth promoter; ide; receptor agonist; antagonist; biomass.	secondary metabolite; nosuppressive agent; ; antimigraine agent; wth promoter; ; biomass.
XX SO	Strep	Streptomyces gri	s grise	sens.			
V A	W0200	WO200000613-A1	-A1.				
X G	06-JA	06-JAN-2000.					
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Reducing branching and microorganisms used to
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Matches 116; Conserv
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                                                  The present sequence is S. griseus Ssgh protein. Ssgh reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgh gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme funhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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0
                                                                                                                                                                                             Length 135;
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100.0%; Pred. No. 5.7e-72;
tive 0; Mismatches 0;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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                                English.
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Best Local Similarity 100.
Matches 135; Conservative
                                Fig 5; 60pp;
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The present sequence is S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycel in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, berbicides, antiparastic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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Pred. No. 7.5e-61;
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85.9%;
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ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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       Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, ronzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                   SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellun; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter;
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                                                                                                                                                                                                                                                     Length 135;
                                                                                                                                                                                                                                                                                                         17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                       Score 556; DB 21;
Pred. No. 3.5e-55;
                                                                                                                                                                                                                                   79.0%; Sco. 78.5%; Pred. No. 3... 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY44650 standard; Protein; 135 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-NL00395
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                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 EDALGRILAEEQNAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Wezel GP, Kraal B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces albus G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-147269/13.
N-PSDB; AAZ49729.
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                               Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200000613-A1.
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                                                                                                                                                                                                                                                                                                         Matches 106;
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                                                                                                                                                                                                                                                          Query Match
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                Gaps
                                                                                                                                                        VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                  1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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   Length 135;
                                           Indels
     Score 464; DB 21;
Pred. No. 9.7e-45;
                                           18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 55103; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #24735.
                                                                                                                                                                                                                                                                                                                                                                   ABG24744 standard; Protein; 321 AA.
       65.9%;
65.9%;
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23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
Query Match
Best Local Similarity 65.9°
Matches 89; Conservative
                                                                                                                                                                                                                                   EDALGRILAEEQNAG 135
                                                                                                                                                                                                                                                         ddalnrslaeegsag 135
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N-PSDB; AAS88931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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990S-0134256.
990S-0134218.
990S-0134221.
990S-0134370.
990S-0134768.
990S-0134941.
990S-0135353.
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9905-0137502
9905-0137724
9905-0138640
9905-0138640
9905-0139119
9905-0139452
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990S-0136392.
990S-0136782.
990S-0137222.
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99US-0139459.
99US-0139460.
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990S - 0.139462

990S - 0.139463

990S - 0.139763

990S - 0.139817

990S - 0.139817

990S - 0.140353

990S - 0.140823

990S - 0.141287

990S - 0.141287

990S - 0.14287

990S - 0.14383

990S - 0.14433

990S - 0.14433
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99US-0145085.
99US-0145087.
99US-0145089.
            111-MAY -1999)
14-MAY -1999)
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14-MAY -1999)
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21-MAY -1999)
22-MAY -1999)
25-MAY -1999)
25-MAY -1999)
26-MAY -1999)
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10-JUN-1999;
14-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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28-JUN-1999;
29-JUN-1999;
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16-JUL-1999;
16-JUL-1999;
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18-JUN-1999;
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18-JUN-1999;
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23-JUN-1999;
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08-JUL-1999;
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22-JUL-1999;
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           diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                  ---REL-LLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGA----DRALFRAGTAPLVA 96
 polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                         42;
                                                                                                                                                                              22; Length 321;
                                                                                                                                                                                                         52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 12181.
                                                                                                                                                                                                                                 1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG
                                                                                                                                                                                                                                                                                                                                           97 FLDRIDKLVPLGQEHTLGDF----DGNLEDAL-GRILAE 130
                                                                                                                                                                                                                                                                                                                                                            ; Score 84; DB 2;
; Pred. No. 0.39;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG12893 standard; Protein; 456 AA
                                                                                                                                                                            11.9%;
27.7%;
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99US-012548.
99US-0125788.
99US-012624.
99US-0126785.
99US-0128234.
99US-0128234.
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99US-0130891.
99US-0131449.
99US-0131480.
99US-0132404.
99US-0132485.
99US-0132485.
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                                                                                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                   321 AA;
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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23-APR-1999;
23-APR-1999;
28-APR-1999;
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06-MAY-1999;
06-MAY-1999;
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04-MAY-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                     242
                                                                                                                                                                     Gaps
                                                                                                                                                                                       4 LVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGR-----ELLLDGLNSPSG 57
                                                                                                                                                                                                                                             31;
                                                                                                                                              11.9%; Score 83.5; DB 21; Length 456; 25.0%; Pred. No. 0.7; ive 22; Mismatches 52; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 32224.
                                                                                                                                                                                                                                                                                                                                                AAG27402 standard; Protein; 456 AA
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99US-0126264.
99US-0126785.
99US-012874.
99US-012874.
99US-012874.
99US-013077.
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990S-0130891.
990S-0131449.
990S-0132048.
          990S-0160981.
990S-0160989.
990S-0161406.
990S-0161406.
990S-0161359.
990S-0161360.
990S-0161361.
990S-0161992.
990S-0161993.
   99US-0160980
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99US-0132485
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                                                                                                                                                                     35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                          Local Similarity
                    22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
116-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
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05-MAY-1999;
06-MAY-1999;
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990S-0145145.
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990S-0145913.
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990S-0145918.
990S-0146388.
990S-0146388.
990S-0146388.
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990S-0147260.
990S-0147303.
990S-0147416.
990S-0147935.
990S-0148171.
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990S - 0148319
990S - 0148685
990S - 0148684
990S - 0149175
990S - 0149723
990S - 0149929
990S - 0149929
990S - 0149929
990S - 015984
990S - 0151065
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990S - 0151080
990S - 0151080
990S - 0151303
990S - 0153758
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99US-0156596.
99US-0157117.
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99US-0158029.
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99US-0159293.
99US-0159294.
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99US-0159638.
99US-0159584.
99US-0160741.
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990S-0160768.
990S-0160770.
990S-0160814.
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21-OCT-1999;
21-OCT-1999;
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03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
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25-AUG-1999;
26-AUG-1999;
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13-AUG-1999;
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20-AUG-1999;
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08-0CT-1999;
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90S-0132487 90S-0132863 90S-013286 90S-0134218 90S-0134219 90S-0134370 90S-0134370 90S-0134370	990S-0135629. 990S-0136392. 990S-0136392. 990S-0137522. 990S-0137522. 990S-0137524. 990S-013754. 990S-0138647. 990S-0138847. 990S-0139453. 990S-0139453. 990S-0139453. 990S-0139453. 990S-0139453. 990S-0139453. 990S-0139455. 990S-0139455. 990S-0139455. 990S-0139455.	90S - 0139750 90S - 0139763 90S - 01398763 90S - 0140354 90S - 0140354 90S - 0140825 90S - 0141287 90S - 0141287 90S - 0142920 90S - 014364 90S - 014364	90S-0144086 90S-0144086 90S-0144331 90S-0144332 90S-0144333 90S-0144334 90S-0144334 90S-0144336 90S-0144632 90S-0144684 90S-0146884 90S-0146884 90S-0146884 90S-0146884 90S-0145088
6 MAY - 1999; 7 - MAY - 1999; MAY - 1999; 4 - MAY - 1999; 4 - MAY - 1999; 8 - MAY - 1999; 8 - MAY - 1999; 9 - MAY - 1999; 1 - MAY - 1999; 1 - MAY - 1999; 1 - MAY - 1999;	24 • MAY 1999; 27 • MAY 1999; 28 • MAY 1999; 28 • MAY 1999; 28 • MAY 1999; 30 · JUN 1999;	8 JUN-1999; 8-JUN-1999; 8-JUN-1999; 3-JUN-1999; 3-JUN-1999; 8-JUN-1999; 8-JUN-1999; 1-JUL-1999; 1-JUL-1999; 8-JUL-1999;	6.70L-1999; 6-70L-1999; 9-70L-1999; 9-70L-1999; 9-70L-1999; 9-70L-1999; 0-70L-1999; 0-70L-1999; 1-70L-1999; 1-70L-1999; 2-70L-1999; 2-70L-1999; 2-70L-1999;
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90S - 0145192 90S - 0145145 90S - 0145218 90S - 0145224 90S - 0145913 90S - 0145919 90S - 0145919 90S - 0145919 90S - 0145951 90S - 0145951 90S - 0145951 90S - 0145951	9905-0147303- 9905-0147303- 9905-0147303- 9905-0147416- 9905-0147416- 9905-0147935- 9905-0148171- 9905-0148171- 9905-0148341- 9905-0148368- 9905-0148368- 9905-0149368- 9905-0149426- 9905-0149426- 9905-0149426- 9905-0149426- 9905-0149426- 9905-0149923- 9905-0149923- 9905-0149929- 9905-0149929- 9905-0149929-	905-0151065 908-0151086 908-0151080 908-0151030 908-0151330 908-015378 908-0154018 908-0154039 908-0154039 908-0154039 908-0154039 908-0154039 908-015559 908-015559 908-015559 908-015659 908-015659 908-015659 908-015659	905-0158029 905-0158232 905-0158233 905-0159293 905-0159295 905-0159233 905-0159331 905-0159634 905-0159634 905-0160741 905-0160741 905-0160741
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by administering an agent that: (a) modulates DPC4 expression, by administering an agent that: (a) modulates DPC4 expression, by according an agent that: (a) modulates DPC4 expression, specifically a sense DPC4 sequence (particularly in the form of a vector, i.e. by gene therapy), but also an antisense sequence where DPC4 protein is over expressed or (b) minics the activity of DPC4. DPC4 presence dabsence of human chromosome 1861.1 fragments. When a homozygous deletion is detected in this region, an agent can be administered that accumulates within, or kills, only cells which contain such a deletion. This agent exploits the absence of an enzyme deletion, i.e. it has a highly selective action.
 (in vivo or in vitro) proliferative diseases, especially pancreatic carcinoma, bile duct, bladder or colorectal cancer, Crohn's disease, colitis-associated neoplasia or chronic ulcerative colitis. These conditions, where associated with a homozygous deletion, can be treated
                                                                                                                                                                                                                                                                                                                           -----ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                               ------VHIG---PTEPEGLGDVHIRLQVGADRAL
                                                                                                                                                                                                                                                     Ouery Match 11.5%; Score 81; DB 18; Length 552; Best Local Similarity 25.7%; Pred. No. 1.7; Matches 38; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour suppressor protein, Dpc4.
                                                                                                                                                                                                                                                                                                                                                                                                                  87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                             408 fvqsyyldreagrap----gdavhkiyp 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY70071 standard; Protein; 552 AA.
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N-PSDB; AAZ51013.
                                                                                                                                                                                                                 552 AA;
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                                                                                                                                                                                                                                                                                                                             137 llkellsrgvpvdsesesg-----tpliwaaghdqknavevllehnanpna 182
                                                                                                                                                                                                                                                                                                         DGDVHIGP----TEPEGLGDVHIRLQVGADRALFRAGTAPL----VAFLDRTDKLVPLG 108
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                       LVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGR-----ELLLDGLNSPSG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;
tumour suppressor gene; proliferative disease; bile duct; bladder;
colorectal; cancer; Crohn's disease; colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human deleted in pancreatic cancer locus 4 - DPC4 - polypeptide.
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treatment of proliferative
                                                                                                                                                                                                 Length 456;
                                                                                                                                                                                                                             Indel's
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                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                11.9%; Score 83.5; DB 25.0%; Pred. No. 0.7; ive 22; Mismatches
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35;
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5-OCT-1999;
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25-0CT-19
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Cell proliferative disorder; nuclear localisation factor; neoplasm; Dpc4; Delted in Pancreatic Carcinoma; locus 4; Smad-binding element; SBE; tumour suppressor; transforming growth factor-beta; TGF beta; anti-cancer drug; treatment; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of a cell proliferative disorder by administration of tumor suppressor polypeptide Dpc4 (Smad4) coupled to a nuclear localization
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                      using a chimeric Dpc4 (Deleted in Pancratic Carcinoma, locus 4) polypeptide coupled to a nuclear localisation factor. Upon localisation to the nucleus and binding to Smad-binding element (SBB), Dpc4 shows tumour suppressor action. This method can also be used for identifying transforming growth factor beta (TGF beta) inducible genes, modulators of Dpc4 nuclear localisation and in screening for anti-cancer drugs. Dpc4 can be used in the treatment of neoplasms and in gene therapy. The present sequence is that of human Dpc4 tumour suppressor protein. Note: It is indicated in the claims section that the present peptide sequence is sequence Id No: 1 and elsewhere in the specification as
             discloses a method of treating cell proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smad4; MADH4; DPC4; TGF-beta signalling pathway; transcription factor; expression inhibition; antisense therapy; tumour formation; inflammation.
                                                                                                                                                                                                                                                                                                      304 vhnelafqppisnhpapeywcsiayfemdvqvge-----tfkvpsscpi-----vtv 350
                                                                                                                                                                                                                                                                                                                                               ------VHIG---PTEPEGLGDVHIRLQVGADRAL 86
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                             5 VSEELSFRIPV-------ELRYEVGDPYAIRMIFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense inhibition of the human Smad4 gene, useful for diagnosing, preventing and treating conditions associated with Smad4 expression e.g. inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents human Smad4. The Smad proteins are a family of cytosolic proteins which are involved in TGF-beta
                                                                                                                                                                                                                         DB 21; Length 552;
1.7;
                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                         Score 81; D
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                       AAY69622 standard; Protein; 552 AA.
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                                                                                                                                                                                                                                                   38; Conservative
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                                                                                                                                                                                                                                                                                                                                50 DGLNSPSGDGD---
                                                                                                                                                                                                                                       Best Local Similarity
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proteins (such as bone morphogenetic protein (BMP), activin and TGF-betas themselves) phosphorylate Smad proteins, which then home or ref-betas themselves) phosphorylate Smad proteins, which then home or transcription. Smad4 (also known as MADH4 and DPC4) is a shared heterodimerisation partner for the pathway restricted members of the Smad4 family (Smad1-3, 5 and MADH6) and is known as the common mediator. The N-terminus of Smad4 promotes the binding of the Smad complex to DNA, and the C-terminus provides an activation signal required for the complex to stimulate transcription. The invention relates to antisense complex to stimulate transcription. The invention relates to antisense complex to stimulate to the human Smad4 gene, which inhibit its expression. A series of oligonucleotides (AAZ59749-2598) were designed to trajet different regions of the human Smad4 RNA, and were analysed for their effect on Smad4 mRNA levels by quantitative real-time PCR. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with Smad4 expression, such as tumour formation, inflammation and certain infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
superfamily signal transduction. On ligand binding, TGF-beta superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VSEELSFRIPV------ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Smad4 gene; fusion protein; green fluorescent protein; GFP; intracellular signalling; chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 81; DB 21; Length 552; 25.7%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 1.7;
16; Mismatches
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Chimeric - Homo sapiens.
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   552 AA;
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Tullin S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catabolism
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW02156;
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                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW02156
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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                                      The present sequence represents a human Smad4-green flourescent protein fusion product. The fusion protein is used in an assay that exemplifies the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is obtained by recording the variation, caused by the molecule, on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light emission is processed to provide information that correlates spatial distribution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, especially to screen for potential therapeutic agents or toxins, and to identify new drug targets.
                                                                                                                                                                                                                                                                                            304 vhnelafqppisnhpapeywcsiayfemdvqvge-----tfkvpsscpi-----vtv 350
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining effect on signalling pathways in live cells from redistribution of luminophores - specifically fusions of green fluorescent protein with a signalling component, and new apparatus, particularly for identifying toxins and potential therapeutic agents
particularly for identifying toxins and potential therapeutic agents
                                                                                                                                                                                                                                                                     ----ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                 50 DGLNSPSGDGD------VHIG---PTEPEGLGDVHIRLQVGADRAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Smad4 gene; fusion protein; green fluorescent protein; GFP;
intracellular signalling; chimera.
                                                                                                                                                                                                                                                  :99
                                                                                                                                                                                                                          DB 19; Length 798; 2.8;
                                                                                                                                                                                                                                                28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thastrup 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smad4-green flourescent protein fusion product.
                                                                                                                                                                                                                         Score 81; DB; Pred. No. 2.8; 16; Mismatches
                     Example 17; Pages 176-178; 326pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scudder K,
                                                                                                                                                                                                                                                                                                                                                             F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                  408 fvqsyyldreagrap----gdavhkiyp 431
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW85013 standard; Protein; 806 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Aequorea victoria.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                          11.5%;
25.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-DK00145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                              Query Match
Best Local Similarity 25...
Best Local 8% Conservative
                                                                                                                                                                                                                                                                    VSEELSFRIPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO-NORDISK AS
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                                                                                                                                                                                           798 AA;
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Tullin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW85013;
                                                                                                                                                                                            Sequence
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                                                 The present sequence represents a human Smad4-green flourescent protein fusion product. The fusion protein is used in an assay that exemplifies the invention. The specification describes how quantitative information about the influence of a molecule on a cellular response is obtained by recording the variation, caused by the molecule, on mechanically intact living cells, in the spatially distributed light emitted from a luminophore present in the cells. The variation in light emission is processed to provide information that correlates spatial distribution to the degree of the molecule. The method is used to identify agents that (in)directly affect intracellular signalling, especially to screen for potential therapeutic agents or toxins, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Periplasmic chitodextrinase; periplasmic Beta-N-acetylglucosaminidase; Beta-N-acetylglucosamidase; chitin; oligosaccharide; catabolic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitin biosynthetic enzymes end I, exo I and exo II - are periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) and aryl beta-N-acetyl:gluco:amidase(s), respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 DGLNSPSGDGD-------VHIG---PTEPEGLGDVHIRLQVGADRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 81; DB 19; Length 806; 25.7%; Pred. No. 2.8; ive 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ပဲ
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Example 17; Pages 108-109; 326pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662 fvqsyyldreagrap----gdavhkiyp 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW02156 standard; Protein; 1046 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 68-71; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                       to identify new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Periplasmic chitodextrinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US02332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.7'
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          806 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VSEELSFRIPV --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio furnissii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT36387
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WO200181581-A2
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                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                    AAU56775;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                           RESULT. 15
                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                         Chitodextrinase; periplasmic; endI; Endo-I; chitin; chitosan; endoenzyme;
                                                                                                                                                                                                                                                                                                                                                                                beta 1-4 N-acetylglucosamine; GloNc; degradation; catabolism;
oligosaccharide; agriculture; medicine; nitrogen fixing nodules;
disease resistance; induction; fungicide; antimetastatic;
Lewis lung carcinoma; immune system, macrophage; activation; production;
        Periplasmic chitodextrinase (AAW02156), periplasmic Beta-N-acetylglucosaminidase (AAW02157) and aryl Beta-N-acetylglucosaminidase (AAW02158) can be used to produce chitin Oligosaccharides with the structure (GIONAc)n where n is 2 or higher, by contacting them with soluble chitin. The enzymes are encoded by the genes end!, exoI and exoII respectively. They are all genes involved in the catabolic pathway of chitin.
                                                                                                                                                                                         920 vafslpawktlpagdtyeldmvyylpisgpanysvningvdyafkfeqpdlpladlssgn 979
                                                                                                                                                 19; Gaps
                                                                                                                                                                     LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Periplasmic localisation signal peptide"
                                                                                                                            Length 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31..1046 ... //note= "Mature periplasmic chitodextrinase"
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keyhani NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding periplasmic chitodextrinase endoenzyme
                                                                                                                            DB 17;
                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                    Vibrio furnissii periplasmic chitodextrinase.
                                                                                                                           Score 75.5; DB
Pred. No. 17;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roseman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Columns 33-40; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                     AAY52304 standard; Protein; 1046
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                                                                                                                            10.7%;
30.5%;
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                                                                                                                                                                                                               53 NSPSGDGDVHIGPTEPEGLGDV
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                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                          Query Match 10.7
Best Local Similarity 30.5
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chitlaru E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-022280/02.
                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant protein
                                                                                              1046 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio furnissii
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                                                                                                                                                                                                                                                                                                           AAY52304;
                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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                            chitin to Glonac. End of grants of the control of t
contrast to other organisms, which only require two enzymes to degrade
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bhatia A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
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rter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75.5; DE Pred. No. 17; 8; Mismatches
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Jen S, Carter
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30.5%;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by particular proteins include SAPHO syndrome (synovitis, acne, practicular). Hypertosis and osteomyelitis), uveltis and endophthalmitis. The particular presence or absolved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies contacting the capterision and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as therefore treat P. acnes infections. The antibodies may also be used as chagnostic agents for determining P. acnes presence, for example, by contame linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed printed in the printed in electronic format directly from WIPO at the print of the printed and the printed printed printed in electronic format directly from WIPO at the printed and the printed print
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.; Query Match 10.5%; Score 74; DB 22; Length 400; Best Local Similarity 28.2%; Pred. No. 7.1; Matches 35; Conservative 15; Mismatches 56; Indels 18; Gaps 12 RIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGL 71 g ŏ ò

72 GDVHIRLQVGADRALFRAGTAPLVA---FLDRTDKLVPLGQEHTLG-----DFDGNLEDA 123

124 LGRI 127 δ

В

173 ldrv 176

Search completed: July 18, 2002, 14:15:01 Job time: 10331 sec

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50 DGLNSPSGDGD-------VHIG---PTEPEGLGDVHIRLQVGADRAL 86
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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S-09-096-776B-9
S-08-984-618-10
S-08-386-727-2
S-08-600-452A-2
S-09-413-814-93
S-09-413-814-80
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Maximum Match 100%
Listing first 45 summaries
                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 MSFLVSEELSFRIPVELRYE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kern, Scott E.
APPLICANT: Hahn, Stephan A.
ITILE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: A JO25 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: 425 EXECULIVE SQUARE, SULLE 1400
CITY: La Jolla
COMPRY: USA
ZUONTRY: USA
ZUONTRY: USA
ZUE: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,821
FILING DATE: 19-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REFERENCE/DOCKET NUMBER: 07265/079001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2:
SEQUIBLE CHARACTERISTICS:
US-09-500-358-3
US-09-498-809-3
US-08-984-618-9
US-08-836-943-2
US-08-804-227C-4
US-09-313-409-7
US-09-356-409-7
US-09-568-480-7
US-09-568-486-7
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US-09-355-115-7
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Patent No. 5712097
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Best Local Similarity 25.7
Matches 38; Conservative
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RESULT 4
US-08-701-582D-14
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STATE: CA
COUNTRY:
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28; Indels . 66; Gaps
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                                                                                                                                                                Sequence 2, Application US/08915214
Patent No. 5814457
GENERAL INFORMATION:
GENERAL INFORMATION:
TYLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,214
FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%; Score 81; DB 2;
25.7%; Pred. No. 0.27;
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07265/079001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-7AN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/07900
TELECOMMUNICATION INFORMATION:
                                                87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                         1 | 1 | 1 | 1 | 4 | 431 | 408 FVQSYYLDREAGRAP----GDAVHKIYP 431
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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Best Local Similarity 25.7'
Matches 38; Conservative
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-----VHIG---PTEPEGLGDVHIRLQVGADRAL 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 81; DB 2; Length 552; 25.7%; Pred. No. 0.27; ... 16; Mismatches 28; Indels
GENERAL INFORMATION:
APPLICANT: Kern, Scott E.
APPLICANT: Hahn, Stephan A.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: A 1225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: WRANN, Jeffrey
APPLICANT: ATISANO, Lilian
APPLICANT: SCHERER, Stephen W.
TITLE OF INVENTION: MADR2 TUMOUR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                   ZIP: 92037

MORDTUR READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38,347
ER: 07265/079001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERNCE/DOCKET NUMBER: 07265/0790C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 F-----RAGTAPLVAFLDRTDKLVP 106
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; Patent No. 6017755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.5
Best Local Similarity 25.7
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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USA
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APPLICANT: de Lencastre, Herminia
APPLICANT: Tomasz, Alexander
TITLE OF INVENTION: AUXILLIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
                                        304 VHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGE-----TFKVPSSCPI-----VTV 350
                                                                                                     191.YLYQSGKGHTIQEVRIVKGLNNP--DLDAAVGEDLAQQLRD-ELELVKGASNEFDKELFL 247
    -ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
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                                                                                  -----VHIG---PTEPEGLGDVHIRLQVGADRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600-1-213 CIP
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                                                                                                                                                                                                         408 FVQSYYLDREAGRAP ---- GDAVHKIYP 431
                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08984618 Patent No. 6251647 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07bul
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CAMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 26.8
Matches 41; Conservative
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      5. VSEELSFRIPV -
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CLASSIFICATION:
                                                                                  50 DGLNSPSGDGD-
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US-08-984-618-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 552
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                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 81; DB 3;
; Pred. No. 0.27;
16; Mismatches
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CURRENT APPLICATION NUMBER: US/09/096,776B
CURRENT FILING DATE: 1998-06-12
PRIOR PEPLICATION NUMBER: US 60/049,990
PRIOR PILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: US 60/053,040
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-01-18
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: REA, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 024916-004
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                    APPLICATION NUMBER: US/08/701,582D
FILING DATE: 22-AUG-1996
CLASSIFICATION: 435
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                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Miyazono, Kohei
APPLICANT: Kawabata, Masahiro
TITLE OF INVENTION: SMAG6 AND
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.5%
Best Local Similarity 25.7%
Matches 38; Conservative
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Best Local Similarity 25.78
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VSEELSFRIPV-----
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-701-582D-14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-096-776B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
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Patent No. 6225064
GENERAL INFORMATION:
APPLICANT GESSLISCHAFT fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Indels
                       APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: 13-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75.5; DB 2;
Pred. No. 2.7;
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT TRFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07662/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      980 GGGTGGGTTEP---GDV 998
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30.5%;
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LENGTH: 1046 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
   CHITLARU, EDITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloecker, Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 30.5
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-600-452A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brandt, Petra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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ZIP: 92037
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: KEYHANI, NEMAT O.
APPLICANT: CHTTLARU, EDITH
APPLICANT: ROWE, CHRIS
APPLICANT: YU, CHARLES
TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
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Pred. No. 2.7;
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89 AGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOBBS, ANN S.
REGISTRATION NUMBER: 36,830
REFERENCE/DOCKET NUMBER: 4130/206916
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-861-3000
TELEFAX: 202-822-0944
TELEFAX: 202-821-3000
TELEFAX: 201-821-3000
TELEFAX: 201
                                                              248 AGEITPVFF---GTALGNFGVDHML---DGLVE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08600452A; Sequence 2, Application US/08600452A; Patent No. 5985644; GENERAL INFORMATION: APPLICANT: BASSLER, BONNIE; APPLICANT: KEYHANI, NEMAT O.
                                                                                                                                                                                                                          Sequence 2, Application US/08386727
Patent No. 5792647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       980 GGGTGGGTTEP---GDV 998
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30.5%;
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BASSLER, BONNIE
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Best Local Similarity 30.59
Matches 25, Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-386-727-2
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STATE: D.C.
COUNTRY: USA
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APPLICANT: ROSEMA
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TOPOLOGY:
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APPLICANT: Bloecker, Helmut
APPLICANT: Cloo, Paul M
APPLICANT: Cloo, Paul M
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Holle, Gerhard
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: Heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
                                                                                                                                                                                                                                                                                                                                                         869 MOVIGRIESSLGIRTTLRTLFEHPTLAQLASHLSSGAASTSAAAATALERGLTRPDGPSS 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       875 MQVLGRIESSLGIRTTLRTLFEHPTLAQLASHLSSGAASTSAAAATALERGLTRPDGPSS 934
                                                                                                                                                                                                                                                                                                                1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
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                                                                                                                                                                                                                                                                                                                                                                                                                            61 VHIG-PTEP----EGLGDVHIRLQVGADRALFRAG-TAPLVAFLD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VHIG-PTEP----EGLGDVHIRLQVGADRALFRAG-TAPLVAFLD 99
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                                                                                                                                                                                                                                Score 73; DB Pred. No. 22; 7; Mismatches
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EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 93
LENGTH: 3072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
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Pred. No. 2
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US-08-348-353-17
Sequence 17, Application US/08348353
Patent No. 593217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80, Application US/09413814
Patent No. 6225064
                                                                                                                                              ; ORGANISM: Sorangium cellulosum US-09-413-814-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Sorangium cellulosum US-09-413-814-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.4%;
Best Local Similarity 31.4%;
Matches 33; Conservative
                                                                                                                                                                                                                                Query Match 10.4%;
Best Local Similarity 31.4%;
                                                                                                                                                                                                                                                                         33; Conservative
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                                                                                                                             TYPE: PRT
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53 LALDGGAGVALQSAKASGTLHVQGGEHLDLGTLAAVGAVDVNGTGDVRVAKLVSDAGADL 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1248;
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TILLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPAGE OPERATING SYSTEM: PC-DOS/MS-DOS CORTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600-1-097CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 72;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/348,353
FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08465965
Patent No. 5968512
GENERAL INFORMATION:
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STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                    STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                      NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 17:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-348-353-17
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                   STATE: New Jersey COUNTRY: U.S.A. ZIP: 07601
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Best Local Similarity
Matches 29; Conserva
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US-08-857-076-114
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Patent No. 6015560
GENERAL INFORMATION:
APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF ENVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 1248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%; Score 72; DB 27.6%; Pred. No. 8.7; tive 11; Mismatches
                                                                                                      PELLOR DION DATE:
PELLOR DATE: 30-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
CLASSIFICATION DATA:
APPLICATION DATA:
PRIOR DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/465,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson, David
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEFAN: 201-487-5800
TELEFAN: 201-343-1684
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 411 Hackensack Avenue
CITY: Hackensack
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APPLICATION NUMBER: US
          CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensers STATE: New Jersey COUNTRY: U.S.A.
ZIP: 07601
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Best Local Similarity
Matches 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE:
US-08-465-965-17
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----IGPTEPEGLGDVHIRLQVGADRALF 87
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APPLICANT: Paradis, Suzanne
APPLICANT: Paradis, Suzanne
APPLICANT: Paradis, Suzanne
APPLICANT: Morris, Jason
APPLICANT: Morris, Jason
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351001
CURRENT APPLICATION NUMBER: US/08/857,076C
CURRENT FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 1248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 RAGTAPLVAFLDRTDKLVPLGQEH-TLGDF--DGNLEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600-1-097CIP1DIV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                  FILING DATE: 30-NOV-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 33-MAY-1994
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION UMBER: 07/695,613
PRIOR APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON, DAVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72;
FILING DATE: 06-JUN LOSSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
TITME DATE: 30-NV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 114, Application US/08857076C
; Patent No. 6225120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 LLLDG-----LNSPSGDGDVH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATENT NO. "STELL STATE OF THE SENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
APPLICANT: Kimura, Koutarou
APPLICANT: Patterson, Garth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 27.69
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-966-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-857-076-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 114
LENGTH: 212
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                                                                                                                                                                                         51 IERARLHIGKGVQLECKGEGDVWVRCL--SDHAVFVQSYYLDREAGRAP----GDAVHKI 104
                                             Gaps
                                                                                                            |: :||: || || || 5 EMDVQVGE-----TFKVPSSCPI------VTVDGYVDPSG-GDRFCLGQLSNVHRTEA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 EELSFRIPV-ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLD-GLNSPSGDGDVHIG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Vinkemeier, Uwe
APPLICANT: Warefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 13
ADDRESSEE: Klauber & Jackson
Ouery Match 10.2%; Score 71.5; DB 4; Length 212; Best Local Similarity 27.0%; Pred. No. 0.98; Matches 33; Conservative 13; Mismatches 25; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                  16 ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.1%; Score 71; DB Best Local Similarity 28.2%; Pred. No. 6.7; Matches 37; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                           US-09-012-710-12; Sequence 12, Application US/09012710; Patent No. 6087478; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hackensack
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                             105 YP 106
                                                                                                                                                                                                                                                    105 VP 106
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Search completed: July 18, 2002, 14:16:06 Job time: 9696 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 18, 2002, 11:38:30 ; Search time 73.98 Seconds (without alignments) 175.345 Million cell updates/sec

US-09-749-185-3

704 1 MSFLVSEELSFRIPVELRYE......FDGNLEDALGRILAEEQNAG 135 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283138 segs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 3: :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query	Ouery Match Length	DB	ID	Description
-	546	77.6	136	7	T37179	probable regulator
7	219	31.1	142	~	T36147	
3	190	27.0	138	~	T35247	probable regulator
4	140	19.9	142	7	T35319	probable regulator
2	84.5		548	7	E84182	type II secretion
9	84	11.9	261	~	T19428	hypothetical prote
7	83.5	11.9	259	7	A22612	carbonate dehydrat
89	81	11.5	324	7	A69648	2-keto-3-deoxygluc
6	81	11.5	552	7	S71811	probable transcrip
10	79.5	11.3	408	7	AD3237	┰
11	78.5	11.2	260	7	152551	
12	78.5	11.2	1101	7	S15271	endoglucanase C (E
13	78	11.1	529	7	E91295	peptide chain rele
14	78	11.1	529	N	I59305	translation releas
15	78	11.1	529	7	G86136	peptide chain rele
16	78	11,1	069	7	D75487	v-type ATP synthas
17	77.5	11.0	260	7	A43641	carbonate dehydrat
18	77.5	11.0	913	7	T35718	hypothetical prote
	77	10.9	795	٦	A70322	endopeptidase La (
	77	10.9	819	7	T45690	receptor-like prot
21	77	10.9	827	Н	A36895	endopeptidase La (
22	76.5	10.9	757	7	G97472	penicillin-binding
23	76.5	10.9	757	~	AC2691	penicillin binding
24	•	10.7	902	7	G83635	probable ClpA/B-ty
25	75.5	10.7	1046	7	T30199	chitinase (EC 3.2.
. 26	^	10.7	160	7	E83610	conserved hypothet
27		10.4	265	7	C70963	hypothetical prote
28	73.5	10.4	346	_	н69789	probable alcohol d
59		10.4	484	(1	S68694	~

translation releas probable acetylorn	hypothetical cytos peptide chain rele	probable 9-cis-epo	2-oxoacidferredo	endopeptidase La-l	peroxisome biogene	probable ATP-depen	filamentous hemagg	aminonucleoside an	Clp ATPase [import	CDA peptide synthe	hypothetical prote	DNA-Binding Protei
D75381 D95388	AE3254 AD1072	A86425 T44993	G69170	T01765	S71090	G70951	S21010	S68981	AE0358	T36180	H70678	157557
77	00	7 7	-	Н	7	7	٦	7	7	7	~	7
538	389	339	512	1096	980	1101	3591	558	891	2117	291	837
10.4 10.4	10.4	10.4	10.3	10.3	10.2	10.2	10.2	10.2	10.2	10.2	10.1	10.1
73.5	73	73	72.5	72.5	72	72	72	71.5	71.5	71.5	71	71
30 31.	33 33	3.4	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
R; Seeger, K.; Haris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A; Reference number: 221598
A; Accession: T37179
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-136 <SEE>
A; Cross-references: EMBE:AL096823; PIDN:CAB46964.1; GSPDB:GN00070; SCOEDB:SCQ11.09
A; Exceptinental source: strain A3(2)
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                 probable regulator - Streptomyces coelicolor
RESULT
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Gaps ; 0 Length 136; Indels Query Match 77.6%; Score 546; DB 2; Lu Best Local Similarity 77.8%; Pred. No. 6.3e-47; Matches 105; Conservative 12; Mismatches 18;

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1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60 δ q

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EDALGRILAEEQNAG 135 121 δ

В

probable regulator - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000 C;Accession: T36147 R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the BMBL Data Library, July 1999 A;Reference number: 221598 A;Reference number: 221598 A;Reference number: 221598 A;Accession: T36147 A;Molecule type: DNA A;Residues: 1-142 <SEE> A;Cross-references: EMBL:AL096852; PIDN:CAB51005.1; GSPDB:GN00070; SCOEDB:SCE19A.24 A;Experimental source: strain A3(2) C;Genetics:

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Similarity 26.6
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                   122 DALGRILAE 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: gspE1
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    C; Genetics:
                                                                                                                                                                                                                                                                                 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable regulator - Streptomyces coelicolor
C:Specias: Streptomyces coelicolor
C:Specias: Streptomyces coelicolor
C:Accession: T35247
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, April 1999
A:Reference number: 221573
A:Accession: T35247
A:Scentus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAB40672.1; GSPDB:GN00070; SCOEDB:SC5F2A.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-142 <OLI>
A;Residues: 1-142 <OLI>
A;Cross-references: EMBL:AL049863; PIDN:CAB42928.1; GSPDB:GN00070; SCOEDB:SC5H1.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable regulator - Streptomyces coelicolor (5.5pecies: Streptomyces coelicolor (5.5pecies: Streptomyces coelicolor (5.5pecies: Streptomyces coelicolor (5.5pecies: Streptomyces coelicolor (5.4ccession: T35319 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000 (5.4ccession: T35319 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000 (5.4ccession: T35319 Ds.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, Submitted to the EMBL Data Library, May 1999 A; Reference number: Z21575 A; Accession: T35319 A; Accession: T35319 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                           VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHT-LGDFDGN 119
                                                                                                                                                                                                                                                                                   -----SGELRRF 107
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                      1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
                                                                                                                                                                                                 48 LLDGLNSPSGDGDVHIGP-----TEPEGLGDVHIRLQVGADRALFRAGTAPLVAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSFLVSEELSFR------IPVELRYEVGDPYAIRMTFHLPG---DAPVTWAFGREL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
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9
A;Gene: SCOEDB:SCE19A.24
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL049587; PIDN:CAB40672.1; GSPDB:GN00070; % Experimental source: strain A3(2) C;Genetics: A;Gene: SCOEDB:SC5F2A.05c C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24 C;Superfamily: Streptomyces
                                                                                    Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
                                                                                  31.1%; Score 219; DB 2;
37.7%; Pred. No. 1.6e-14;
tive 22; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%; Score 190; DB 2; ilarity 31.3%; Pred. No. 1.1e-11; Conservative 19; Mismatches 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 LDRTDKLVPLGQEHTLGDFDGNLEDAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|||:| || : : : LQAAGELVPVGLEHLQLDLDHDLAELM 134
                                                                                  Query Match
Best Local Similarity 37.78
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                             120 LEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                                     ::| | :||
132 IDDGLAELLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: DNA
Residues: 1-138 <OLI>
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Best Local Similarity
Matches 46; Conserv
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type II secretion system protein [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: E84182
C;Accession: E84182
S, My, W.V; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky J. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Freltas, T. Bonson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A.Reference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C24H11.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19428
R;Lloyd, C.
                                                                                                                                                                                                                                                                                                                                                                                                       GLGDVHIRLQVGAD-----RALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 FDVPVRIYRTPGDDADAFTTTYAVREPDRLPGDDARIAACKDRIWTNGVATGDSDAGDDH 243
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                 21. RFPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRP-ESR 79
                                                                                                                                                                                                                                           12 RIPV--ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FRIPVELRYEVGD-----PYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGD-GDVH
                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 548;
                                                                                                                     Length 142;
                                                                                                               Query Match 19.9%; Score 140; DB 2; Length 142
Best Local Similarity 31.0%; Pred. No. 1e-06;
Matches 40; Conservative 20; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, November 1996 A; Reference number: 219123 A; Accession: T19428 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%; Score 84.5; DE 26.6%; Pred. No. 1.7; iive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 .LGQEHT ------LGDF -----DGNLED 122
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A. Authors: Yoshida A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A. Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A. A. Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A. Reference number: A69580; MUID:98044033
A. Accession: A69648
A. Status: preliminary; nucleic acid sequence not shown; translation not shown A. Molecule type: DNA
A. Residues: 1-324 <KUN>
A. Residues: 1-324 <KUN>
A. Cross-references: GB. 299115; GB. AL009126; NID:92634478; PIDN:CAB14128.1; PID:926346
A. Experimental source: strain 168
C. Genetics:
A. Genetics:
A. Genetics:
C. Superfamily: ribokinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the TGF-beta
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Sylear

Sylear

Sylear tenance names: tumor supressor DPC4

C; Species: Homo sapiens (man)

C; Species: Homo sapiens (man)

C; Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 10-Dec-1999

C; Accession: S71811

R; Zhang, Y; Feng, X.H.; Wu, R.Y.; Derynck, R.

Nature 383, 168-172, 1996

A; Title: Receptor-associated Mad homologues synergize as effectors of the TGF-be

A; Reference number: S71891

A; Reference number: S71891

A; Accession: S71811

A; Status: not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: 1-552 czMA

C; Superfamily: human transcription regulator MAD-4

C; Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 ADWFFPGIAEGELLTGEKTPEGIADYYLKKGASFVAIKLGKEGAYFKTGTSE--GFLEGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VHIG---PTEPEGLGDVHIRLQVGADRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DGDVHIGPTEPEGLGDVHIR-----LQVGADRALFRAGTAPLVAFLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 IPVELRYEVGDPYAIRMTFHL------PGDAPVTWAFGRELLLDGLNSPSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 RIDKLVPLGQEHTLGDFDGNLEDALGRIL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 RVDRVV-----DIVGAGDGFAVGVISGIL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F-----RAGTAPLVAFLDRIDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 FVQSYYLDREAGRAP----GDAVHKIYP 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 34; Conserv
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Matches 38; Conserv
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Cispecies: Cispec
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                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                               A;Cross-references: EMBL:Z81475; PIDN:CAB03913.1; GSPDB:GN00021; CESP:C24H11.6
A;Experimental source: clone C24H11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carbonate dehydratase (EC 4.2.1.1) III - horse
N;Alternate names: carbonate dehydratase III
C;Species: Equus caballus (domestic horse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 25-Apr-1997
C;Accession: A22612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 GDP----VTSHLLPSGRVPIGHVF----LRGDNGPVSTDSRHFGPV-PEALVQIRLSLR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTYGGALKQPDG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDPYAIRMTFHL--PGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 PYAIRMTFHLPGDAPVTWA----FGRELLLDGLNSPSGDGDVHIGP-----TEPEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-259 <WEN>
Cs. Superfamily: carbonate dehydratase; carbonic anhydrase homology .
Cs. Superfamily: carbonated amino end; carbon-oxygen lyase; hydro-lyase; zinc C:Reywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; zinc F;4-258/Domain: carbonic anhydrase homology <CAH>
F:1/Modified site: acetylated amino end (Ala) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 VGADRALFRAGTAPLVAFLDRTDKLVPLGQEHT ----LGDFDGNLEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 259;
                                                                                                                                                                                                                                                                                                                                                           Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Wendorff, K.M.; Nishita, T.; Jabusch, J.R.; Deutsch, H.F.
J. Biol. Chem. 260, 6129-6132, 1985
A:Title: The sequence of equine muscle carbonic anhydrase.
A:Reference number: A22612; MUID:85207593
                                                                                                                                                                                                                                                                                                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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                                                                                                                                                                                                                                                                                                                                                        11.9%; Score 84; DB 2; 28.7%; Pred. No. 0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.84;
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                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
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                                                                                                                                                                             A;Gene: CESP:C24H11.6
A;Map position: 3
A;Introns: 25/1; 56/3; 126/1; 194/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%;
ilarity 27.1%;
Conservative 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                 A; Residues: 1-261 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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Best Local S
Matches 33
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endoglucanase C (EC 3.2.1.-) - Cellulomonas fimi
C;Species: Cellulomonas fim
C;Date: 21-Nov-1993 **Bequence_revision 26-May-1995 **text_change 01-Dec-2000
C;Accession: S15271; A43636
R;Coutinho, J.B.; Moser, B.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Mol. Microbiol. 5, 1221-1233, 1991
Mol. Microbiol. 5, 1221-1233, 1991
A;Fitle: Nucleotide sequence of the endoglucanase C gene (cenC) of Cellulomonas fimi, A;Reference number: S15271; MUID:92065819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E91295
peptide chain release factor RF-3 [imported] - Escherichia coli (strain O157:H7, subs C;Species: Escherichia coli (C;Species: Escherichia coli (C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
A; Title: Identification of an abundant S-thiolated rat liver protein as carbonic anhy A; Reference number: $13896; MUD: 9112820
A; Accession: $13896
A; Status: preliminary
A; Molecule type: protein
A; Residues: $25, X', 27-34, 38, 'T', 40-42, 'XX', 45-46, 'S', 48-51, 'X', 53-56, 'RVV', 74, 'XXTFX'
C; Superfamily: carbonate dehydratase; carbonic anhydrase homology
C; Reywords: blocked amino end; carbon-oxygen lyase; hydro-lyase
F; 5-259/Domain: carbonic anhydrase homology <CAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1101 <COU>
A; Cross references: EMBL:X57858; NID:948847; PIDN:CAA40993.1; PID:9580980
A; Ross references: EMBL:X57858; NID:948847; PIDN:CAA40993.1; PID:9580980
A; Note: the authors translated the codon GAC for residues 361, 380, 400, 550, 670, e
B; Moser, B.; Gilkes, N.R.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Appl. Environ. Microbiol. 55, 2480-2487, 1989
A; Title: Purification and characterization of endoglucanase C of Cellulomonas fimi, A; Reference number: A43636; MUID:90103465
                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 RALFRAGTAPLVAFLDRTDKLVPLGQEHTL------GDFDGNLEDALGRILAEE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 RMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQV----GAD
                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 PYAIRMTFHLPGDAPVTWA----FGRELLLDGLNSPSGDGDVHIGP----
                                                                                                                                                                                                                                                                                                                                                                     11.2%; Score 78.5; DB 2; 27.1%; Pred. No. 2.6; tive 14; Mismatches 37;
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Best Local Similarity 27.4%; Pred. No. 15;
Matches 32; Conservative 15; Mismatches
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C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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A; Molecule type: mRNA
A; Residues: 1-260 (RES)
A; Cross-references: GB:M22413; NID:g203224; PIDN:AAA40846.1; PID:g203225
A; Cross-references: GB:M22413; NID:g203224; PIDN:AAA40846.1; PID:g203225
A; Cross-references: GB:M22413; NID:g203224; PIDN:AAA40846.1; PID:g203225
A; Tibe: Carbonic anhydrase III in obese Zucker rats.
A; Reference number: A48856
A; Molecule type: protein
A; Residues: 19-45;120-128
A; Residues: 19-45;120-128
A; Residues: 19-45;120-128
A; Residues: 19-45;120-128
A; Residues: Sig-148;101
A; Rivagase, T: Sugiyama, T: Kawata, S:; Tarui, S:; Deutsch, H.F.; Taniguchi, N.Comp. Biochem: Physiol. B 99, 193-201, 1991
A; Tibe: Analyses of polypeptides in the liver of a novel mutant (LEC rats) to hereditar
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A; Molecule type: protein
A; Residues: 19-28, X', 30-33 < NAG>
A; Residues: 19-28, X', 30-33 < NAG>
A; Experimental source: Long-Evans Cinnamon
B; Chai, Y. C.; Jung, C.H.; Lii, C.K.; Ashraf, S.S.; Hendrich, S.; Wolf, B.; Sies, H.; Thc
Arch. Blochem. Blophys. 284, 270-278, 1991
                              R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells, Rarp, P.; Romero, P.; Zhang, S. Science 294, 2.317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                  ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
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N;Alternate names: carbonic anhydrase III
C;Species: Rattus norvegicus (Norway rail
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change II-May-2000
C;Accession: I22551; A48856; B61530; S13896
R;Kelly, C.D.; Carter, N.D.; Jeffery, S.; Edwards, Y.H.
Biosci. Rep. 8, 401-406, 1988
A;Title: Characterization of CDNA clones for rat muscle carbonic anhydrase III.
                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <KUR>
A;Cross-references: GB:AE008690; PIDN:AAL46314.1; PID:g17744099; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 PSG-----DGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 QIEHDQRYRLADEFVNALKALWRSDEPVTFSGKSPWRIKEGFITPKPRFGRPLISATGS 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 PIIVCRDTDQEAQEYYGAIVAAVEQRNVG 315
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A; Accession: 152551
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A:Reference number: A61530; MUID:92070082
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11.3%
Best Local Similarity 24.8%
Matches 37; Conservative
      C; Accession: AD3237
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Matches 41; Conserv
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                             K.; Han, C.G.
H.
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R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362
A;Accession: S56599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation releasing factor RF-3 [validated] - Escherichia coli
N;Alternate names: peptide chain release factor 3; translation termination factor RF-3
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 02-Feb-2001
C;Accession: 159305; S56599; S63518; F65252; 159306; S33336
R;Mikuni, O.; Ito, K.; Moffat, J.; Matsumura, K.; McCaughan, K.; Nobukuni, T.; Tate, W. Proc. Natl. Acad. Sci. U.S.A. 91, 5798-5802, 1994
A;Title: Identification of the prfc gene, which encodes peptide-chain-release factor 3 A;Reference number: 159305; MuID:94286525
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A; Residues: 2-19 <MOR>
R; Blattner, F.R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Accession: F65252
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A;NOte: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Mortensen, K.K.; Hansen, H.F.; Grentzmann, G.; Buckingham, R.H.; Sperling-Petersen,
Eur. J. Biochem. 234, 732-736, 1995
                    R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A; Ttle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Scession: E91295
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                       A Molecule type: DNA
A; Residues: 1-529 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB38756.1; PID:g13364811; GSPDB:GN00154
A; Experimental source: strain 0157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: ECS5333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 LTFMNKLDRDIRDPMELLDEVENELKI-----GCAPITWPIGCGKLFKGVYHLYKDET 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 YLYQSGKGHTIQEVRIVKGLNNP--DLDAAVGEDLAQQLRD-ELELVKGASNEFDKELFL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- REL-LLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGA-
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A;Molecule type: DNA
A;Residues: 1-529 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78; DB 2;
Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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26.8%;
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Best Local Similarity
Matches 41; Conserv
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A; Residues: 1-529 <BUR>
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C; Accession: E91295
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A;Status: .nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-529 < RLAT>
A;Cross-references: GB:AE000508; GB:U00096; NID:Q2367382; PIDN:AAC77328.1; PID:g17908
A;Experimental source: strain K-12, substrain MG1655
A;Grentzmann, G; Brechemier-Baey, D; Heurque, V; Mora, L; Buckingham, R.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5848-5852, 1994
A;Title: Localization and characterization of the gene encoding release factor RF3 in
A;Reference number: IS9306; MUID:94286335
A;Accession: 159306
A;Reference rounder: LS9306
A;Accession: IS9306
A;Molecule type: DNA
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-314, 'L', 316-529 < RE2>
A;Cross-references: EMBL:226313; NID:q435273; PIDN:CAA81223.1; PID:q435274
A;Genetics:
C;Genetics:
C;Superfamily: translation elongation factor Tu homology
C;H-145/Domain: translation elongation factor Tu homology
C;H-145/Domain: translation elongation factor Tu homology
C;H-145/Region: ucleotide-binding motif A (P-loop)
F;142-145/Region: GTP-binding NKXD motif
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R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Mature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-529 <STO>
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005174; NID:g12519399; PIDN:AAG59555.1; GSPDB:GN00145; UWGP:A;Experimental source: strain 0157:H7, substrain EDL933 C;Genetics: A;Gene: prfC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.1%; Score 78; DB 2; Length 529;
.larity 26.8%; Pred. No. 7.1;
Conservative 18; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 529;
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Search completed: July 18, 2002, 14:17:33 Job time: 9543 sec

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01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metažoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                       P56907
P43928 |
P54283 |
P47862 |
Q99ab6 |
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P42515 |
Q005824 |
Q50641 |
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ZINC (CATALYTIC).
ZINC (CATALYTIC).
B3EECDFF89BFED02 CRC64;
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            YW84_MYCTU
NUD1_RHIME
RF3_HAEIN
                                               CCBA_RAT
AQP3_RAT
CSD_AERPE
TCMG_STRGA
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HRCA_MYCTU
SYH_MYCTU
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Best Local Similarity 27.19
Matches 29, Conservative
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MOD_RES
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                hits satisfying chosen parameters:
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SMA4_RAT
CAH3_RAT
GUNC_CELFI
RF3_ECOLI
VATI_DEIRA
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GYS_NEUCR
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seq length: 200000000
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Maximum DB
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EMBL; AK004804; BAB23576.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Richel B., Lewis S., Matsuo Y., Nikaido I., Ring B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithaw B., Washi H., Roberki S., Marshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., M. Hayashizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYCOKING GTOWTH FACTOR REV. 11:49-58(2000).

-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA (TRANSPORTION: COMMON MEDIATOR OF SIGNAL TRANSPORTION BY TGF-BETA (TRANSPORTING GROWTH FACTOR) SUPERFAMILY; SWAD4 IS THE COMMON SUPPRESSOR.

-!- SUBJUT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).

-!- SUBJUT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).

-!- SUBJUT: MAY FORM TRIMERS WITH RECEPTOR-BEGULATED SMAD (R-SMAD).

-!- SUBJUT: MAY FORM TRIMERS WITH RECEPTOR-SMILARITY).

-!- SUBJUT: MAY FORM TRIMERS WITH RECEPTOR-SMILARITY N.

-!- SUBJUT: MAY FORM TRIMERS WHEN COMPLEXED WITH R-SMAD (BY MIGRATION.)
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=4/J; IISSUE-Lung;
MEDLINE-97311184; PubMed-9166592;
Anna C.H., Devereux T.R.;
Anna C.H., Devereux T.R.;
"Sequence and chromosomal mapping of the mouse homolog (Madh4) of the
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against DPP homolog 4) (Deletion target in pancreatic carcinoma 4 homolog)
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weinstein M., Yang X., Deng C.-X.; "Functions of mammalian Smad genes as revealed by targeted gene disruption in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- SIMILARITY: BELONGS TO THE DWARFIN/SMAD FAMILY.
-!- SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
-!- SIMILARITY: CONTAINS 1 DWB/MH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20175825; PubMed-10708952;
                                                                                                                                                                                                                                                                                                                                                                                   Mamm. Genome 8:443-444(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 67-551 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              human DPC4/MADH4 gene.";
                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY )
                                                                                                                            MADH4 OR DPC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVIEW
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EMBL; U79748; AAB57905.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the Bacillus subtilis chromosome region between the serA and Kdg loci cloned in a yeast artificial chromosome."; Microbiology 142:2005-2016(1996).

-!- CATALYTIC ACTIVITY: ATP + 2-dehydro-3-deoxy-D-gluconate = ADP + beta-L-arabinose I-phosphate.
-!- PATHMAX: PECTIN DEGRADATION.
-!- SAMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 DGLNSPSGDGD------VHIG---PTEPEGLGDVHIRLQVGADRAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34; Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) (2-keto-3-deoxygluconokinase) (3-deoxy-2-0XO-D-gluconate kinase) (KDG kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                            11.6%; Score 82; DB 1; Length 551; 26.4%; Pred. No. 0.95;
                                                                                                                                                                                                                                                                                                                                                 28; Indels
                                                                                                                                                                                                                  S -> A (IN REF. 2).
R -> P (IN REF. 2).
0835EF88D9C1C980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AA.
                                                                                                                            Multigene family
                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                   POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 F-----RAGTAPLVAFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVQSYYLDREAGRAP----GDAVHKIYP 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-168 / MARBURG;
MEDLINE-96349105; Pubmed-8760912;
           MGD; MGI:894293; Madh4.
InterPro; IPR001132; Dwarfin.
InterPro; IPR003619; Dwarfin_A.
                                                                                                                                                                                                                                                       60417 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L47838; AAB38479.1; -. EMBL; 299115; CAB14128.1; -.
                                                                   Pfam; PF00968; Dwarfin; 1.
                                                                                                                            Transcription regulation;
                                                                                                                                                                                                                                                                                                                                Best Local Similarity 26.49
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                    SMART; SM00523; DWA; 1
SMART; SM00524; DWB; 1
                                                                                                                                                                              320
450
257
292
551 AA;
1DD1
                                                                                                                                                                                                                                                                                                                                                                                     5 VSEELSFRIPV --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDGK_BACSU
P50845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serror P.;
                                                                                                                                                                                                   DOMAIN
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DOMAIN
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KDGK_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
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Dev. 11:3157-3167(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massague J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVIEW
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    Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y., Feng X.-H., Wu R.-Y., Derynck R.; ^{\circ}Receptor-associated Mad homologues synergize as effectors of the TGF-
                                                                                                                                                                                                                                                                                                                                                                                191 ADWFFPGIAEGELLTGEKTPEGIADYYLKKGASFVAIKLGKEGAYFKTGTSE--GFLEGC 248
                                                                                                                                                                                                                                                                                                               137 IPPALSAEMKD-----FTYHVMNDMRNAGKTISFDPNVRPSLWP-DQATMVHTINDLAGL 190
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                        13 IPVELRYEVGDPYAIRMTFHL------PGDAPVTWAFGRELLLDGLNSPSG- 57
                                                                                                                                                                                                                                                                                                                                                           ------DGDVHIGPTEPEGLGDVHIR-----LQVGADRALFRAGTAPLVAFLD-- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against MADP homolog 4) (beletion target in pancreatic carcinoma 4) (hSMAD4).
MADH4 OR SMAD4 OR DPC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-97253203; PubMed-9098646;
Moskaluk C.A., Hruban R.H., Schutte M., Lietman A.S., Smyrk T.,
Fusaro L., Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98051189; PubMed-9389648;
Lib F., Pouponnot C., Massague J.;
"Dual role of the Smad4/DPC4 tumor suppressor in TGFbeta-inducible
transcriptional complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequencing of DPC4 in the analysis of familial pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fischer A., Yeo C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DPC4, a candidate tumor suppressor gene at human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal brain;
MEDLINE=96144684; PubMed=8553070;
MADLINE=96144684; PubMed=8553070;
MADLINE=96144684; Rozenblum E., Weinstein C.L., Fischer A., Yehruban R.H., Kern S.E.;
                                                                                                                                                                                     Score 81; DB 1; Length 324;
Pred. No. 0.64;
5; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                          6345AAD7AEDA0759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT CARCINOMA HIS-493.
                 InterPro; IPR002173; PĒKB.
Pfam. PF00294; pĒKB.1.
PROSITE: PS00583; PFKB_KIMASES_1; FALSE_NEG.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 AA
                                                                                                    Transferase; Kinase; Complete proteome.
SEQUENCE 324 AA; 35035 MW; 6345AAD7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 RVDRVV----DIVGAGDGFAVGVISGIL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                         RTDKLVPLGQEHTLGDFDGNLEDALGRIL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=96371046; PubMed=8774881;
                                                                                                                                                                                                                            26;
                                                                                                                                                                                     11.5%; 22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 271:350-353(1996).
                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human)
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMA4_HUMAN
Q13485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carcinoma.
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TYPE PECTA SIGNATURE OF SMEAD PROCEIDS.";

CYCOKING GTOWTH FACTOR REV. 11:15-22(2000).

CYCOKING GTOWTH FACTOR SUPERFAMILY; SNAD4 IS THE COMMON GROWTH FACTOR SUPERFAMILY; SNAD4 IS THE COMMON GROWTH FACTOR SUPERFAMILY; SNAD4 IS THE COMMON GROWTH FACTOR SWAD2 SWAD4/FAST-1 COMPLEX CYON DAY AND PROVIDES AN ACTIVATION FUNCTION REQUIRED FOR SMAD1 OR SWAD2 TO STIMULATE TRANSCHEPTION. MAY ACT AS A TUMOR SUPPRESSOR.

CYON DAY OF THE SWAD AND THE CYTOPLASM IN THE ABSENCE OF LIGAND; MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD.

CYON DESCRIPTION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD.

MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD.

CYON DISEASE: DEFECTS IN MAD14 ARE A CAUSE OF PARCREATIC CARCINOMA.

CYON DISEASE: DEFECTS IN DAY WHILD DOMAIN.

CYON DISEASE: DEFECTS IN MAD14 ARE A CAUSE OF PARCREATIC CARCINOMA.

CYON DISEASE: DEFECTS IN MAD14 ARE A CAUSE OF PARCREATIC CARCINOMA.

CYON DISEASE: DEFECTS IN MAD14 ARE A CAUSE OF PARCREATIC CARCINOMA.

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CYON DISEASE: DEFECTS IN MAD14 ARE A CAUSE OF PARCREATIC CARCINOMA.

CYON DISEASE: DEFECTS IN MAD14 ARE A CAUSE OF PARCREATIC CARCINOMA.

CYON DISEASE: DEFECTS IN MAD14 ARE A CAUSE OF PARCREATIC CARCINOMA.

CYON DISEASE: DEFECTS OF THE DWANTHIN SHAD SAMILY.
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CHARACTERIZATION OF SAD DOMAIN.
MEDIINE-2010/2728; PubMed-10636916;
MEDIINE-2010/2728; PubMed-10636916;
MEDIINE-2010/2728; PubMed-10636916;
Hill C.S., Shioda T., Roberts A.B., Lechleider R.J.;
"The Smad4 activation domain (SAD) is a proline-rich, p300-dependent transcriptional activation domain.";
J. Biol. Chem. 275:2115-2122(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 285-552.
MEDLINE-20113477; PubMed-10647180;
Oin B., Lam S.S., Lin K.;
"Crystal structure of a transcriptionally active Smad4 fragment.";
Structure 7:1493-1503(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.S., de Caestecker M.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 319-543.
MEDLINE-97357157; Pubmed-9214508;
Shi Y., Hata A., Lo R.S., Massague J., Pavletich N.P.;
"A structural basis for mutational inactivation of the tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Verschueren K., Huylebroeck D.; "Remarkable versatility of Smad proteins in the nucleus of transforming growth factor-beta activated cells.";
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Chacko B.M., Qin B., Correia J.J., Lam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Annu. Rev. Biochem. 67:753-791(1998)
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Nat. Struct. Biol. 8:248-253(2001)
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Trhe Smad pathway.";
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Nature 388:87-93(1997).
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SMAD (CO-SMAD) (BY SIMILARITY).
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                                                      SIMILARITY).
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070437;
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            (See http://www.isb-sib.ch/announce/
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against MADH4 OR SWAD4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIO Y., Awata T.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA
(TRANSFORMING GROWTH FACTOR) SUPERFAMILY; SMAD4 IS THE COMMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (P1g).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                            SAD.

DWB.

POLY-ALA.

D -+ W (IN PANCREATIC CARCINOMA).

/FTIG=VAR_011380.

7EE3C4647712DA90 CRC64;
                                                                                                                                                                                                                            Pfam; PF00968; Dwarfin; 1.
SMART; SM00523; DWA; 1.
SWART; SM00524; DWB; 1.
Transcription regulation; Phosphorylation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 81; DB 1; Length 552; 25.7%; Pred. No. 1.2;
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modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@lsb-sib.ch).
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                                        EMBL, AF045447, AAC03051.1; --
EMBL, AF045438; AAC03051.1; JOINED.
EMBL, AF045449; AAC03051.1; JOINED.
EMBL, AF045441, AAC03051.1; JOINED.
EMBL, AF045441, AAC03051.1; JOINED.
EMBL, AF045441, AAC03051.1; JOINED.
EMBL, AF045444; AAC03051.1; JOINED.
EMBL, AF045445; AAC03051.1; JOINED.
EMBL, AF045446; AAC03051.1; JOINED.
EMBL, AF045446; AAC03051.1; JOINED.
EMBL, AF045446; AAC03051.1; JOINED.
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InterPro; IPR003619; Dwarfin_A.
                                                                                                                                                                                                                                                                         Disease mutation; 3D-structure
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1YGS; 08-NOV-98.
1DD1; 24-NOV-99.
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Matches 38; Conserv
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Q9GKQ9;
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Miyakita A., Okuno S., Watanabe T.K., Oga K., Tsuji A., Hishigaki H.,
Suto T., Nakagawa K., Nakahara Y., Higashi K.;
"Molecular cloning of rat Smad4 gene.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against MADH4 OR SMAD4.
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                                                                                                                                                                  SIMILARITY: BELONGS TO THE DWARFIN/SWAD FAMILY. SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN. SIMILARITY: CONTAINS 1 DWB/MH2 DOMAIN.
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SMART; SM0523; DWA; 1.
TRANST; SM00524; DWB; I.
Transcription regulation; Multigene family.
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SEQUENCE FROM N.A.
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INIT_MET
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                          and Smad4 and their
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Osaki M., Tsukazaki T., Ono N., Yonekura A., Hirota Y., Miyazaki Y., Shindo H., Sonta S., Yamashita S.; "conha cloring and chromosomal mapping of rat Smad2 and Smad4 and the. expression in cultured rat articular chondrocytes."; Endocr. J. 46:695-701(1999).
                                                                                  SMAD (CO-SMAD) (BY SIMILARITY).

-!- SUBUNIT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).

INTERACTS WITH C-SKI, MSGI AND ATF2 (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: IN THE CYTOPLASM IN THE ABSENCE OF LIGAND;

MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGLNSPSGDGD------VHIG---PTEPEGLGDVHIRLQVGADRAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p14141; 054961;
01-JAN-1990 (Rel. 13, Created)
15-JUL-1999 (Rel. 38, Last aquence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VSEELSFRIPV-------ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLL 49
                                                           -!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA (TRANSFORMING GROWTH FACTOR) SUPERFAMILY; SMAD4 IS THE COMMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 81; DB 1; Length 552; 25.7%; Pred. No. 1.2; ive 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ALA.
7AE0540AB4DF0E77 CRC64;
                                                                                                                                              SIMILARITY).
-!- SIMILARITY: BELONGS TO THE DWARFIN/SMAD FAMILY.
-!- SIMILARITY: CONTAINS 1 DWA/7411 DOMAIN.
-!- SIMILARITY: CONTAINS 1 DWB/7412 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       ranscription regulation; Multigene family.
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                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001132; Dwarfin.
InterPro; IPR003619; Dwarfin_A.
Pfam; PF00968; Dwarfin; 1.
SMART; SM00523; DWA; 1.
                                                                                                                                                                                                                                                                                                        EMBL; AB010954; BAA83092.1; -.
                                                                                                                                                                                                                                                                                                                    AF056002; AAC12781.1; -. Q13485; 1DD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.78
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         321
451
452 AA;
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                                                                                                                                                                                                                                                                                                                    EMBL;
HSSP;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C STRAIN-WASTAIR; TISSUE-LIVET;

MEDLINE-20361776; PubMed-10900145;

MEDLINE-20361776; PubMed-10900145;

MEDLINE-20361776; PubMed-10, Akazawa D., Hatsumura M., Ishida T.,

Natsusue K., Yamada H., Oguri K.;

Matsusue M., Ishida T.,

Matsusue M., A.,

Matsusue M., Ishida T.,

Matsusue M., A.,

Matsusue M.,

Mat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Gaps
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                                                                                                                                                                                                                                                                                                                                                    Mallis R.J., Jung C.-H., Chatterjee T.K., Fisher R.A., Thomas J.A., "cbNA sequence of rat liver carbonic anhydrase III.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                          Edwards Y.H.;
rat muscle carbonic anhydrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 259;
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ZINC (CATALYTIC).
ZINC (CATALYTIC).
A -> G (IN REF. 1).
FG -> SE (IN REF. 1).
KL -> NV (IN REF. 1).
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27.1%; Pred. No. 0.87;
ive 14; Mismatches
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ProDom; PD000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
                                          Kelly C.D., Carter N.D., Jeffery S., "Characterisation of cDNA clones for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF037072; AAB925581; -.
EMBL; AB030829; BAB08111.1; -.
HSSP, P00918; LILM.
InterPro; IPR001148; Carb_anhydrase.
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MEDLINE-89166882; Pubmed-2852973;
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                                                                                                                                                                               Biosci. Rep. 8:401-406(1988).
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Best Local Similarity 27.18
Matches 29; Conservative
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118
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223
259 AA;
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Conservative
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318
880
1006
1097
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           1ULD; 01-APR-97
1ULP; 01-APR-97
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                                                                                                                                                                                       SM00409; IG;
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64
212
329
918
1008
831
882
1101
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Best Local Simi
Matches 32;
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P33998;
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ACT_SITE
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coutinho J.B., Moser B., Kilburn D.G., Warren R.A.J., Miller R.C. Jr.; "Nucleotide sequence of the endoglucanase C gene (cenc) of Cellulomonas fimi, its high-level expression in Escherichia coli, and characterization of its products."; Mol. Microbiol. 5:1221-1233(1991).
                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 1-64 FROM N.A., AND SEQUENCE OF 625-641.
MEDLINE-90103465; PubMed-2604391;
MOSER B., Glikes N.R., Kilburn D.G., Warren R.A.J., Miller R.C. Jr.;
MOSER B., Glikes of Rearacterization of endoglucanase C of Cellulomonas
"Purification and characterization of endoglucanase C of Cellulomonas
fimi, cloning of the gene, and analysis of in vivo transcripts of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miller R.C. Jr., "The binding of Cellulomonas fimi endoglucanase C (CenC) to cellulose and Sephadex is mediated by the N-terminal repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linkages in cellulose.
SIMILARITY: BELONGS TO CELLULASE FAMILY E (FAMILY 9 OF GLYCOSYL HYDROLASES).
SIMILARITY: CONTAINS 2 CELLULOSE-BINDING DOMAIN (CBD) REMOTELY RELATED TO BACTERIAL-TYPE CBD'S.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE DOMAINS.
              16-OCT-2001 (Rel. 40, Last annotation update)
Endoglucanase C precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase C)
                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97035265; PubMed-8880921; Bateman A., Eddy S.R., Chothia C.; Members of the immunoglobulin superfamily in bacteria."; protein Sci. 5:1939-1942(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coutinho J.B., Gilkes N.R., Warren R.A.J., Kilburn D.G., Miller R.C. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                       Appl. Environ. Microbiol. 55:2480-2487(1989).
[3]
CELLULOSE-BINDING DOMAINS.
01-MAR-1992 (Rel. 21, Last sequence update)
                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 33-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X57858; CAA40993.1; -.
EMBL; M29707; AAA23087.1; ALT_TERM.
EMBL; M29708; AAA23088.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .. Microbiol. 6:1243-1252(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4]
IDENTIFICATION OF IG-LIKE DOMAINS.
                                                                                                                                                                      STRAIN=ATCC 484;
MEDLINE=92065819; PubMed=1956299;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1375311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [5]
STRUCTURE BY NMR OF 33-184
                                                                            Cellulomonas fimi.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92269585;
                                                                                                                          NCBI_TaxID=1708;
                                               (Cellulase C)
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Mikuni O., Ito K., Mofatt J., Matsumura K., McCaughan K., Nobukuni T., Tate W., Nakamura Y.; "Identification of the prfc gene, which encodes peptide-chain-release factor 3 of Escherichia coli.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 RALFRAGTAPLVAFLDRTDKLVPLGQEHTL------GDFDGNLEDALGRILAEE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 RTAFEQGSAPLTG-----EPATREYAFTSNLTFPPDGDAPGQVAFHLGKAGAYE 315
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MEDLINE-94286535; PubMed-8016077;
Grentzmann G., Brechemler-Baey D., Heurgue V., Mora L.,
Buckingham R.H.;
"Localization and characterization of the gene encoding release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                              PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; FALSE_NEG.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat; Immunoglobulin domain; 30-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1101;
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CELLULOSE-BINDING 2.
CATALYTIC.
IG-LIKE DOMAIN 1.
IG-LIKE DOMAIN 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last sequence update)
01-MRA-2002 (Rel. 41, Last annotation update)
Peptide chain release factor 3 (RF-3).
PREC OR TOS OR MIAD OR B4375 OR 25976 OR ECS5333.
Escherichia coli, and
Escherichia coli o157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ENDOGLUCANASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%; Score 78.5; DI 27.4%; Pred. No. 4.9;
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InterPro; IPR003305; CBD_6.
InterPro; IPR001701; Glyco_hydro_9.
InterPro; IPR003599; Ig.
InterPro; IPR004197; celD_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94286525; PubMed-8016068;
                                                                                                                                                  Pfam; PF02018; CBD_6; 2.
Pfam; PF00292; CeID_N; 1.
Pfam; PF00759; Glyco_hydro_9; 1.
Pfam; PF00047; 19; 1.
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EMBL; AP002569; BAB38756.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21156231; PubMed-11258796; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCOP SIGNALS.";
J. Biol. Chem. 270:10595-10600(1995).
-!- FUNCTION: INCREASES THE FORMATION OF RIBOSOMAL TERMINATION
COMPLEXES AND STINULATES ACTIVITIES OF RF-1 AND RF-2. IT BINDS
GUANINE NUCLEOTIDES AND HAS STRONG PREFERENCE FOR UGA STOP CODONS.
IT MAY INTERACT DIRECTLY WITH THE RIBOSOME. THE STIMULATION OF RF-1 AND RF-2 IS SIGNIFICANTLY REDUCED BY GTP AND GDP, BUT NOT BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Osmo-expression and fast two-step purification of Escherichia coli translation termination factor RF-3.";
Eur. J. Biochem. 234:732-736(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21074935; PubMed=11206551;
Berna N.T., Plunkett G. III. Butland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                  "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mortensen K.K., Hansen H.F., Grentzmann G., Buckingham R.H., Sperling-Petersen H.U.;
                                                                                         SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                            Proc. Natl. Acad. Sci. U.S.A. 91:5848-5852(1994).
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95256223; PubMed=7737996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96163454; PubMed=8575429;
factor RF3 in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-0157:H7 / RIMD 0509952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRFC SUBFAMILY.
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SEQUENCE OF 1-18.
                                                                                                                                                                                                                                     Blattner F.R.;
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RANKER RA

EMBL, D17724; BAA04578.1; -. EMBL, Z26313; CAA01223.1; -. EMBL; U14003; AAA97271.1; -. EMBL; AE005608; AAC77328.1; -. EMBL; AE005668; AAC59555.1; -.

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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
ATPI OR DR0695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 YLYQSGKGHTIQEVRIVKGLNNP--DLDAAVGEDLAQQLRD-ELELVKGASNEFDKELFL 246
                                                                                                                                                                                                                                                                                                                                                                                                                               ::|: : | |:|| || : | || || 1837 LTFMNKLDRDIRDPMELLDEVENELKI -----GCAPITWPIGCGKLFKGVYHLYKDET 189
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=R1, MEDLINE=20036896; PubMed=10567266; MEDLINE=20036896; Particle Description J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----REL-LLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGA----DRALFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     !- SÜBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                48;
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                                                                                                                                                                                                                                                                                                                  11.1%; Score 78; DB 1; Length 528; 26.8%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                              18; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG----
                                                                                                                                                                                                                                 V -> L (IN REF. 2)
3EE94DE2B4C6B1C6 CRC64;
EcoGene; EG12114; prfC.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU.
Pfam; PF00009; GTP_EFTU_D2.
Pfam; PF03144; GTP_EFTU_D2.
PROSTTE; PF00301; EFACTOR_CTP; 1.
Protein blosynthesis; GTP-binding; Complete proteome.
                                                                                                                                                                    GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 AGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
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91
144
314 CT
314 V
59443 MW;
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Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                 314 3
528 AA;
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CONFLICT
SEQUENCE
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NP_BIND
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Length 259;

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Query Match
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                                                                                                                                                                                                                                                                                                  75 PAPAPLPAQSEWETVVEGAAQPVS----HLAKRRQELQSDLEVDRTYGDAVRALAR--- 126
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                           PGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVG-ADRALFRAGTA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                               InterPro; IPR003490; V_ATPase_sub_a.
Pfam; PF01496; V_ATPase_sub_a; 1.
Hydrolase; Hydrogen lon transport; Transmembrane; Complete proteome.
SEQUENCE 690 Aa; 75223 MW; 30D7785EFF388EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  studies.";
Jacohem. Genet. 27:17-30(1989).
-!- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse carbonic anhydrase III: nucleotide sequence and expression
                                                                                                                                                                          Length 690;
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                                                                                                                                                                          i; DB 1;
                                                                                                                                                                                                                                                                                                                                               93 PLVAFLDRTDK--LVP--LGQEHTLGDFDGNLEDALG 125
                                                                                                                                                                                                                                                                                                                                                                          ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
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                                                                                                                                                                      11.1%; Score 78; DB 30.9%; Pred. No. 3.1; tive 14; Mismatches
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ProDom; P0000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001148; Carb_anhydrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89227981; PubMed=2496681;
Tweedle S., Edwards Y.;
EMBL; AE001926; AAF10273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29397 MW;
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SWISS-2DPAGE; P16015; MOUSE.
MGD; MGI:88270; Car3.
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A43641; A43641.
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93
95
118
259 AA;
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Best Local Similarity
Matches 30; Conserv
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SEQUENCE FROM N.A.
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-I- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN PRESENCE OF ATP. HYDROLYZES TWO ATPS FOR EACH PEPTIDE BOND CLEAVED IN THE PROTEIN SUBSTRATE (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: HYDROLYSES Of large proteins such as globin, casein and denaturated serium albumin, in presence of ATP.

-I- SUBDINIT: HOMOTERRAMER (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI6; ALSO KNOWN AS THE LON FAMILY OF ATP-DEPENDENT PROTEASES.
                                                                                                                                                                                     86 PYRLRO-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPRYNTFGEALKQPDG 138
                                                                  Gaps
                                                                                                                         24 PYAIRMTFHLPGDAPVTWA----FGRELLLDGLNSPSGDGDVHIGP-----TEPEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels
                                                                                                                                                                                                                                                                                        : | | | ::| :: |: |: | 139 IAVVGILLKIGREKGEFQ-----ILLDALDKIKTKGKEAPFTHFD 178
                                                                                                                                                                                                                                                  71 · LGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFD 117
11.0%; Score 77.5; DB 1; 27.1%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-dependent protease La (EC 3.4.21.53)
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InterPro; IPR003393; AAA.
InterPro; IPR003393; AAA_subfam.
InterPro; IPR003111; LON.
InterPro; IPR001311; LON.
Pfam; PF00004; AAA; 1.
Pfam; PF01309; LON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                               29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LON OR AQ_242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LON_AQUAE
O66605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aeolicus
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Score 77; DB 1; Length 795; Pred. No. 4.7;

10.9%; 27.7%;

Best Local Similarity

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 5
                                 -!- SUBUNTT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING BOTH VEGETATIVE GROWTH AND
 30; Gaps
                     ------ALFRAGTA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE LON FAMILY OF ATP-DEPENDENT PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93322334; PubMed-8331082;
Gill R.E., Karlok M., Benton D.;
"Myxococcus xanthus encodes an ATP-dependent protease which is
required for developmental gene transcription and intercellular
                                                                                                                                                                                                                                                                                                                          for the development of
34; Indels
                                                                                                                                                                                                                           Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                     Tojo N., Inouye S., Komano T.; "The lonD gene is homologous to the lon gene encoding an
                                                              93 PLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGRILAEEQN 133
                                                                                    431 NPVIMLDEIDKLAI-----SFQGDPAAALLEVLDPEQN 463
                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
ATP-dependent protease La 2 (EC 3.4.21.53).
                                                                                                                                        826 AA
 Mismatches
                     PSGDGDVHIGPTEPEGLGDVHIRLQVGADR -----
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1-9.
                                                                                                                                                                                                                                                                                                                          protease and is essential
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                Bacteriol. 175:4545-4549(1993).
                                                                                                                                                                                                                                                                                 STRAIN=DZF1;
MEDLINE=93322335; PubMed=8331083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR003593; AAA.
InterPro: IPR003959; AAA_subfam.
InterPro: IPR003111; LON.
InterPro: IPR001984; Lon_endopep.
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D13204; BAA02491.1; -. EMBL; L19301; AAA72018.1; -.
 Conservative
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00004; AAA; 1.
Pfam; PF02190; LON; 1.
                                                                                                                                                                                                                                                                                                                                   Myxococcus xanthus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A36895; A36895
MEROPS; S16.003; -.
                                                                                                                                                                                                                  Myxococcus xanthus
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENT.
                                                                                                                                                                                                                                                 NCBI_TaxID=34;
                                                                                                                                                                                                                                                                                                                          ATP-dependent
                                                                                                                                      LON2_MYXXA
P36774;
01-JUN-1994 (
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28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 LVGPPGVGKTSLGQSVAKATGRKFVRLSLGGVRDEAEIRGHRRTYVGALPGRFIQSMKKA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: Periplasmic (Probable).
-:- INDUCTION: BY (GLCNAC)2.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL.
HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           52 LNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADR--------ALFRA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   periplasmic chitodextrinase.,;
J. Biol. Chem. 271:33414-33424(1996).
-!-FUNCTION: HYDROLYSES CHITIN OLIGOSACCHARIDES; (GLCNAC)4 TO (GLCNAC)2 AND (GLCNAC)5.6 TO (GLCNAC)2 AND (GLCNAC)3. INACTIVE TOWARDS CHITIN, GLUCOSAMINE OLIGOSACCHARIDES, GLYCOPROTEINS AND GLYCOPEPTIDES CONTAINING (GLCNAC)2. HAS OPTIWUM ACTIVITY AT PH 6.5-7.0 AND AT TEMPERATURE OF 35-37 DEGREES CELSIUS.
-!- CAPALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-acetyl-D-glucosamine polymers of chitin.
-!- EXZYME REGULATION: INHIBITED BY (GLCNAC)4, (GLCNAC)5, (GLCNAC)6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 furnissii. Molecular cloning, isolation, and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keyhani N.O., Roseman S.; "The chitin catabolic cascade in the marine bacterium Vibrio
SMART; SM00464; LON; 1.
PROSITE; PS01046; LON_SER; 1.
Hydrolase; Serine protease; ATP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                     10.9%; Score 77; DB 1; Length 826; 26.9%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                36; Indels
                                                                                                                                               ATP (POTENTIAL).
BY SIMILARITY.
: F6765E0D91C948D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 GTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLEDALGRILAEEQN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 GTKNPVMMLDEIDKLG-----ADFRGDPSAALLEVLDPEQN 471
                                                                                                                         GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chitodextrinase precursor (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1046 AA
                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 31-51.
MEDLINE-97125982; PubMed=8969204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR003510; Chitin_bind3.
InterPro; IPR001579; Chitinase_2.
InterPro; IPR00123; Glyco_hydro_18.
Pfam; PF00704; Glyco_hydro_18; 3.
SMART; SM00495; ChtBD3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND PNP-(GLCNAC)3.
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                                                                                                                                                                                                                                                                                                                                                                28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                             275
385
701
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701 7
826 AA;
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Best Local Similarity
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                                                                                                                      261
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P96156;
15-JUL-1999 (
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                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERAIN=CV. COLUMBIA;
Saria R., Lyzaik A., MacKenzie S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- SUBCELLULAR BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE LON
                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lon protease homolog 2, mitochondrial precursor (EC 3.4.21.-).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                       320 VAFSLPAWKTLPAGDTYELDMVYYLPISGPANYSVNINGVDYAFKFEQPDLPLADLSSGN 979
                                                                                                                                                                  19; Gaps
                                                                                                                                                                                                  9 LSFRIPVELRYEVGDPYAIRMTFHLPGDAP------VTWAFGREL-----LLDGL 52
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                                                                                                                          Query Match
10.7%; Score 75.5; DB 1; Length 1046;
Best Local Similarity 30.5%; Pred. No. 9.2;
Matches 25; Conservative 8; Mismatches 30; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01046; LON_SER; 1.
Hydrolase; Serine protease; ATP-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.5%; Score 74; DB 1; Length 941;
Best Local Similarity 31.4%; Pred. No. 11;
Matches 33; Conservative 8; Mismatches 34; Indels
                                                      CHITODEXTRINASE.

W; 40680F1642D55A1F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LON PROTEASE HOMOLOG 2. ATP (POTENTIAL).
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
Hydrolase; Glycosidase; Signal; Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                        941 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY OF ATP-DEPENDENT PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U88087; AAB48000.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR00359; AAA.
InterPro; IPR003111; LON.
InterPro; IPR001949; Lon_endopep.
Pfam; PF00004; AAA; 1.
Pfam; PF02190; LON; LON.
                                                                       SEQUENCE 1046 AA; 112380 MW;
                                                                                                                                                                                                                                                                                              980 GGGTGGGTTEP---GDV 998
                                                                                                                                                                                                                                                                         53 NSPSGDGDVHIGPTEPEGLGDV 74
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SMART; SM00382; AAA; 1.
SMART; SM00464; LON; 1.
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842
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941 AA;
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Search completed: July 18, 2002, 14:31:53 Job time: 942 sec

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brachydanio cyprinus ca

09e600 turkey herp 092y75 rhizobium m 09c621 arabidopsis 09v1j1 drosophila 093nx7 streptomyce

O26636 methanother O04954 arabidopsis

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Shinichi K., Ensign J.; "Cloning and characterization of a gene involved in sporulation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces griseus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Kawamoto S., Ensign J.C.;
"Cloning and characterization of a gene involved in regulation of
sporulation and cell division of Streptomyces griseus.";
Nippon Hosenkin Gakkaishi 9:136-151(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=B2682;
Kawamoto S., Ensign J.C.;
"Isolation of mutants of Streptomyces griseus that sporulate in
nutrient rich media.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97286526; PubMed-9141673;
Kawamoto S., Watanabe H., Hesketh A., Ensign J.C., Ochi K.;
"Expression analysis of a ssgA gene product associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell.division of Streptomyces griseus.";
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Q90YA0
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Q90Y99
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Q93NX7
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                                  PRELIMINARY;
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NCBI_TaxID=1911;
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P95753;
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P95753
  A PROPERTY OF A 
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                                                                                                                             July 18, 2002, 14:15:11; Search time 140.15 Seconds (without alignments) 166.638 Million cell updates/sec
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Q93jf9 streptomyce
Q9byg6 homo sapien
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streptomyce
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                                                                                                                                                                                                                                                  1 MSFLVSEELSFRIPVELRYE.......FDGNLEDALGRILAEEQNAG 135
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Q93JF9
Q9BYG6
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_phage:*
sp_plant:*
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sp_archeap:*
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Maximum DB seq length: 200000000
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sp_virus:*
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81
81
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Result 8 ö

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61 VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                Created)
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MEDLINE-97000351; PubMed-8843436;
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nes 105; Conservative
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          NCBI_TaxID=121022;
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Best Local S:
Matches 105;
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                                                                                              Gaps
                                                                                                                  1 MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 60
                                                                                                                                2 MSFLVSEELSFRIPVELRYEVGDPYAIRWIFHLPGDAPVTWAFGRELLLDGLNSPSGDGD 61
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van Wezel G.P., Rousseau C., Kraal B.;

van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces netropsis ssgA gene.";

Submitted (OCT-1898) to the EMBL/GenBank/DDBJ databases.

EMBL; AF195772: AAGS4813.1; -.

SEQUENCE 145 AA; 15838 MW; 92AC0F30DF3D2620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Streptoverticillium netropsis (Streptoverticillium flavopersicus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycesaceaxistreptomyces.
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                                                                    Length 136;
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Pred. No. 5.6e-52;
7; Mismatches 12; Indels
sporulation and cell division in Streptomyces griseus."; Microbiology 143:1077-1086(1997). EMBL; D50051; BAA21558.1; -. SEQUENCE 136 AA, 14783 MW; C6A28A7823AD7C8B CRC64;
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces goldeniensis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                  14783 MW; C6A28A7823AD7C8B CRC64;
                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                     100.0%; Score 704; DB 2; 100.0%; Pred. No. 1.2e-61;
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                                                                                            0; Mismatches
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(TrEMBLrel, 16, L
(TrEMBLrel, 18, L
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85.9%;
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(TrEMBLrel. 16, I
(TrEMBLrel. 16, I
                                                                                Best Local Similarity 100.
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Matches 116; Conserv
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SEQUENCE FROM N.A.

van Wezel G.P., Rousseau C., Kraal B.;

van Mezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces goldeniensis ssgA gene.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF195770; AAG28481.1; -,

SEQUENCE 135 AA; 14843 MW; 32006CC86BDE4ED6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinsch H.M., Denapaite D., Eichner A., Cullum J., Kinsch H.M., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

MOI. Microbiol. 21:77-96(1996).

EMBL: AL096823; CAB46964.1; -. SEQUENCE 136 AA; 14920 MW; 4867CIFIEOBECC88 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bacteria, Firmloutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                    Length 135;
                                                                                                                                                                                                                                                                Query Match 79.0%; Score 556; DB 2; Length 13 Best Local Similarity 78.5%; Pred. No. 4.2e-47; Matches 106; Conservative 12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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77.8%; Pred. No. 4e-46;
Live 12; Mismatches
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VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                                                                                                                                                                                                                                                                               Gaps
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBL_TaxID=1888;
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                                                                                                                                                                                                                                                                              Length 135;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                            van Wezel G.P., Rousseau C., Kraal B.; van Wezel G.P., Rousseau C., Kraal B.; "Cloning and sequencing of the Streptomyces albus ssgA gubmitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF19571; AAG28482.1; -
SEQUENCE 135 AA; 14735 MW; OFCBF4BDB2BA201B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                          Created)
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                                                                                                                                                                                                                                                                            65.9%; Score 464; DB 2;
65.9%; Pred. No. 4.5e-38;
ive 18; Mismatches 28;
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                                                                                                         01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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121 DDALNRSLAEEQSAG 135
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                                                                                         PRELIMINARY;
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Seeger K.J., Harris D
Submitted (JAN-2000)
                          121 EDALGRILAEEQNAG
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SCL2.31.
                                                                                                                                                         Streptomyces albus
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SEQUENCE FROM N.A.
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Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinsali H., Hopwood D.A.; Rinsali H., Hopwood D.A.; Ast of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL, AL137778; CAB70943.1; SEQUENCE 159 AA; 17472 MW; BA41013F940D7315 CRC64;
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"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL096852; CAB51005.1;
SEQUENCE 142 AA; 15364 MW; 857862390AA51CCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                              Length 159;
                                                                                                                                                                                                                       35.4%; Score 249; DB 2; Length 15: 43.1%; Pred. No. 7.1e-17; indels
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to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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MEDLINE-97000351; PubMed-8843436;
MEDLINE=97000351; PubMed=8843436;
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Best Local Similarity 37.77
Matches 49; Conservative
                                                                                                                                                                                                                                              Query Match 35.49
Best Local Similarity 43.19
Matches 56; Conservative
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SCE19A.24.
Streptomyces coelicolor.
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Submitted (JUL-1999)
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149 DQELSHILAE 158
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NCBL_TaxID=1902;
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SECURIO 2);
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed Benapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical methe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
BMBL: A1391041; CAO1575:1; -..
SEQUENCE 156 AA; 17188 MW; 7181972EE7F33FB0 CRC64;
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Rinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical methe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049863; CAB42928.1;
EMBL; AL049863; L5741 WW; E24AA52C00AF40F1 CRC64;
                                                                                                                                                        Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                      STRAIN=A3(2);
Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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34.7%; Pred. No. 3.6e-07;
tive 14; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 DVHIRLQVGADRALFRAGTAPLVAFLDRTDKLVPLGQE 110
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Streptomyces coelicolor.
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Oliver K., Harris D.;
Submitted (MAY-1999) t
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Best Local Similarity
Matches 34; Conserv
                      SEQUENCE FROM N.A.
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77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLG---- 131
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, ALG49587; CAB40672.1;
EMBL, ALG49587; CAB40672.1;
SEQUENCE 138 AA: 15261 MW; F531BA295144ABA5 CRC64;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Last annotation update)
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ilarity 31.3%; Pred. No. 3.7e-11;
Conservative 19; Mismatches 46;
                                                                                                                                                                            138 AA
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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                          PRELIMINARY;
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                                    120 LEDALGRILA 129
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132 IDDGLAELLA 141
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SEQUENCE FROM N.A.
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C24H11.6.
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                                                                                              Halobacterium
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EMBL: AAI132674; CAB59654.1; -.
Hypothetical protein.
SEQUENCE 126 AA: 13742 MW; D54A8574D28B4D69 CRC64;
                                                                                                                                                                                  70 GLGDVHIRLQVGAD-----RALFRAGTAPLVAFLDRTDKLVPLGQEHTLGDFDGNLE 121
                                                                                                  Gaps
                                                                           RIPV -- ELRYEVGDPYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPE 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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0.025;
~hes 30; Indels
                                     51; Indels
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Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Last annotation update)
                  3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                    126 AA
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                                     Mismatches
                  Pred. No.
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31.0%; Fre-
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MEDLINE-97000351; PubMed-8843436;
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                                     40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
                  Best Local Similarity
                                                                                                                                                                                                                                         122 DALGRILAE 130
                                                                                                                                                                                                                                                                             133 DFLAELTAE 141
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01-MAR-2001 (
01-JUN-2001 (
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Q9HSI1
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MEDLINE-2050483; PubMed-11016950;

MEDLINE-2050483; PubMed-11016950;

Ng W.V., Kennedy S.P., Mahairas G.G., Thorsson V., Sbrogna J.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swarzell S., Weil D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,

"Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 IGPTEPEGLGDVHIRLQVGADRA---LFRAGTAPLV-------AFLDRTDKLVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AAAT------ADRARSLLARRHTAPKTRHWCGAIADRVREAVADRGPAVPP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 FRIPVELRYEVGD-----PYAIRMTFHLPGDAPVTWAFGRELLLDGLNSPSGD-GDVH 62
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
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                                                                       Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.0%; Score 84.5; DB 17; Best Local Similarity 26.6%; Pred. No. 4.7; Matches 41; Conservative 11; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 LGQEHT-----LGDF-----DGNLED 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 VGDDHVADLAYYVVRDLVGDAELTIPIRDPNLED 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR000619; Guanylate_kin.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
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InterPro; IPR000223; Peptidase_S26A.
Pfam; PF00461; Peptidase_S26; 1.
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MEDLINE-99069613; Pubmed-9851916;
II SECRETION SYSTEM PROTEIN. OR VNG0218G.
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Science 282:2012-2018(1998).
EMBL; 281475; CAB03913.1; -.
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Search completed: July 18, 2002, 14:30:54
Job time: 943 sec
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STRAIN=CV. COLUMBIA;

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

A. Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,

Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,

Bowman C.L., White O., Nierman W.C., Fraser C.M.;

"Arabidopsis thaliana chromosome III BAC F7018 genomic sequence.";

REMBL; AC011437; AAF04911.1; -...

REMBL; AC011437; AAF04911.1; -...

RESP: P53041; 1A17.

RESP: P5
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                                                                                                                                                                                                                                                                                                                                                          58 DGDVHIGP----TEPEGLGDVHIRLQVGADRALFRAGTAPL-----VAFLDRTDKLVPLG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                               20; Gaps
                                                                                                                                                                                                                                                                                                               22 GDPYAIRMTFHL--PGDAPVTWAFGRELLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQ 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 VGADRALFRAGTAPLVAFLDRTDKLVPLGQEHT-----LGDFDGNLEDALGRILA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : : : : | : | 108 IWPPE---RAGWISDHWFWDKTQKLLKWADRMTQLQDMINEMAGLMTNAIGVLQA 159
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                                                                                                                                                                              Length 261;
                                                                                                                                                                                                                                               47; Indels
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PRINTS; PR00727; LEADERPTASE.
PROSITE; PS00761; SPASE_I_3; 1.
SEQUENCE 261 AA; 28732 MW; E13FFA7E14CC1FA2 CRC64;
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456 Aa; 49259 MW; BABCB372E8A0A531 CRC64;
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Last annotation update)
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                                                                                                                                                                       11.9%; Score 84; DB 5;
28.7%; Pred. No. 2.1;
tive 15; Mismatches 47
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PROSITE; PS50297; ANK_REP_REGION; 1.
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Best Local Similarity 25.0%
Matches 35; Conservative
                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 33; Conserv
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SEQUENCE 4
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62 HIGPTEPEGLGDVHIRLQVGAD-----RALFRAGTAPLVAFLDRTDKLVPLGQEHTLGD 115
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                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical methe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL59G162; CAC44582.1;
SEQUENCE 402 AA, 41429 MW; 06572345E802539A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PUTATIVE BLDA-REGULATED NUCLEOTIDE BINDING PROTEIN.
402 AA.
                                                         Created)
  PRT;
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MEDLINE-97000351; PubMed-8843436;
PRELIMINARY;
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د
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                                                                                                                                                                                             Streptomyces coelicolor.
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Submitted (JUL-2001)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
                                                      01-DEC-2001
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LUITEN RUDOLF GIJSBERTUS MARIA (NL); WEZEL GILLES PHILIPPUS
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AL036264 Streptomy
AE005712 Caulobact
AL035206 Streptomy
AL390975 Streptomy
AL390975 Streptomy
AL138852 Streptomy
AL138852 Streptomy
AL138852 Streptomy
AL358862 Streptomy
AL358862 Streptomy
                               AL096623 Streptomy
AX007222 Sequence
AF195770 Streptomy
AX007218 Sequence
AX007216 Sequence
D50051 Streptomyce
                                                                                                                                                               AX007224 Sequence
AF195772 Streptomy
AM28303 S.albus bet
AL096852 Streptomy
AL049587 Streptomy
AL049587 Streptomy
AX089419 Sequence
AX089416 Sequence
AX08946 Pseudomon
AL121596 Streptomy
Confination (8 of
AL040537513 Streptomy
Confination (8 of
AL040535 Streptomy
Confination (7 of
AL040535 Streptomy
Confination (7 of
AR0404279 Oryza sat
AL079355 Streptomy
Confination (7 of
AR0404279 Oryza sat
Confination (7 of
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AF143772 Wycobacte
U10405 Streptomyce
AC074105 Oryza sat
AY033407 Wyxococcu
AL096839 Streptomy
AY037870 Oryza sat
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Streptomyces albus G.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 407)
1 (hases 1 to 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF357202 Streptomy
AP002484 Oryza sat
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1. .407
/organism="Streptomyces albus /db_xref="taxon:1962"
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AF357202
AP002484
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OSJN00060
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LMFLCHR32_06
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Sequence 5 from Patent WO0000613.
AX007220
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SC9B5
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AF210249
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AE004546
SC5F8
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AX007222
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AX007218
AX007216
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AX089419
AX089416
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AX007220
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alignments)
Million cell updates/sec
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                                                                                                                                             July 18, 2002, 11:21:43; Search time 4085.76 Seconds
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                      (without a 2084.582 N
                                                                                                                                                                                                                                                                                                                                                                                      1797656 seqs, 10463268293 residues
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RELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTD
RGLSGSERAHADDSHLDDDLNRSLAEEQSAG"
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                                                                                                                    to Streptomyces griseus SsgA; possible cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCT 08-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Streptomycineae; Streptomycescaes: Streptomyces. 1 (bases I to 1544)
Kadenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 TGGGTCTTCGGGCGTGAACTGCTGGTCGAGGGAGTCCTGGACGCCGCGGGGGACGCGAC
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                                                                                                                                                                                                                                                                                                                                                         Length 566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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/db_xref-"taxon:1888"
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Streptomyces coelicolor A3(2)
                                                                                                                                      division protein"
                                                                                                                  /note="similar
                                                                                                                                                       /codon_start=1
                                                            /gene="ssgA"
26. .433
                               /gene="ssgA"
16. .20
                                                                                                 /gene="ssqA"
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ORIGIN
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                                                                                                                                  /protein_id="cac07386.1"
/db_xref="G1:995087"
/db_xref="G1:995087"
/ftanslation="MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
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/ftanslation="MSFLVSEELAFRIPVELRYETVDPYAVRTTLOYGSEQALFRVGKAPLLAFLDRTD
QGLSIGSERAHADPALMNSTABEQSAG"
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Submitted (18-OCT-1999) Biochemistry, University of Leiden, PO
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
1. .566
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I (bases I to 566)
Van Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces albus ssgA gene (npublished
2 (bases I to 566)
van Wezel, G.P.
                                                                                                                                                                                                                                                                                                                                                           1 atgagetteetegteteegaggagetegeetteegeateeeggtggagetgeggg
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Streptomyces albus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                            Length 407;

    >>405
    /gene="ssgA"
    /note="strain ATCC of Streptomyces albus G"

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Pred. No. 1.9e-36;
Mismatches 0;
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                                                                               /codon_start=1
/transl_table=11
/product="SsgA"
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ilarity 100.0%;
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AUTHORS
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JOURNAL
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Surding)

Surding)

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Kroph et al., Nuclet Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Int(291-bin)/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon gity, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid Q11 Cosmid Q11 lies between H24 and D78 on the Asel-Q genomic restriction fragment.
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/gene="SCQ11.01c"
complement(1. 289)
/gene="SCQ11.01c"
/gene="SCQ11.01c"
/note="SCQ11.01c"
/not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 15441)
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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/protein_id="CAB46956.1"
/db_xref="G1:5457268"
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1. .15441
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                                                                                                                                                                                                                                      Seeger, K. and Harris, D.
                                                                                                                                                                         (bases 1 to 15441)
                                                                                                                                                                                                                                                                                       Unpublished
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97000351
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gamma-synthase//yese, len: 392 as; previously sequenced as SW:CYSA_STRCO (EMBL:U37580), cysA, S.coellcolor putative cystathionine gamma-lyase (392 as). Similar to many e.g. SW:EMECL_PSEPU (EMBL:088554), mdeA, Pseudomonas putida methionine gamma-lyase (398 as), fasta scores; opt: 608 ascores: 653.6 E(): 4.5e-99; 36.9% identity in 404 as overlap. Highly similar to TR:03568 (EMBL:X9193) Streptomyces antibioticus hypothetical protein found as overlap). Contains Pfam match to PF01053 cys_Met_Meta_PP, Cys/Met_metabolism PLP-dependent enzyme
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RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAFFGLEDDSTLRTLHLAGPPEFTA
REALPALGETGEDGQAFALASFSGNBEETLEGLAGHHDLALGTTRRGALHATPL
CDEVHYLVATPHWARRAGVEDVRDTDASALKHYPVWEYHESLPFVGRWASVFDARPA
SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
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/db_xref="G1:5457270"
/translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     helix-turn-helix motif at aa 17-38 (Score 1659, +4.84 SD). Contains Pfam match to PRO0126 HH_1, Bacterial regulatory helix-turn-helix protein, lysR family and PS00044 Bacterial regulatory proteins, lysR family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and PS00868 Cys/Met metabolism enzymes pyridoxal-phosphate attachment site"
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/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative lysR-family transcriptional regulator"
/protein_id="CAB46957.1"
/db_xref="G1:5457269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="PS00044 Bacterial regulatory proteins, lysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(360. .1265)
/gene="SC011.02c"
/gene="SC011.02c"
/note="SC011.02c"
/note="
                                                      complement(1. .4279)
/note="sequence corresponding to EMBL:U37580 from 1 to
                                                                                                                                                                                                                                                                                  /note="overlap with Streptomyces coelicolor cosmid H24 (EMBL-AL049826) from 41528 to 41625" (complement(350, .1265) /gene="SCQ11.02c"
DDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTGTLAMPHTARAHEWILRAADDWN*

Complement (831. .1256)

/gene="8CQ11.02c"

/note="Match to PF00126 HTH_1, Bacterial regulatory
helix-turn-helix protein, lysR family Score 145.96"

/gene="SCQ11.02c"

/gene="SCQ11.02c"
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/gene="SC011.03c"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="abaB"
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/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFG
RELLIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPLGGERSLADPALLDEALDRILAEEQNAG"
135 c 145 q 171 +
                                                                                                                                                                                                                             filamentous microorganisms
Patent: WO 0006613-A 7 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
   PAT 06-SEP-2000
                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reducing branching and enhancing fragmentation in culturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GTCCACATCGCGCCCGCCGACCCGGAGACGTTCGGCGAGGTCCTGATCCGCCTGCAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ssgA"
/note="strain ATCC of Streptomyces goldeniensis"
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                                                                                              Streptomyces goldeniensis.
Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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     linear
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/organism="Streptomyces goldeniensis"
/db_xref="taxon:121022"
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Pred. No. 1.7e-18;
0; Mismatches 102;
     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="SsgA"
/protein_id="CAC07387.1"
/db_xref="G1:9995089"
   407 bp
Patent WO0000613
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1/transl_table=11
                                                         GI:9995088
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ilarity 74.9%;
Conservative
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Best Local Similarity
Matches 305; Conserv
                       7
                                                         AX007222.1
                         Sequence
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AUTHORS
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SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLM
IETPENPGLDVCDVRRLVBAAHAGGALVAVDNTLATPLGQRPLELGADPSVASGTKQL
TGHGDVLLGYVAGRDAGAMAAVRRWRTVGAIPGEMBAMLAHRSIATLQLRVDRQDST
ALKYAEALRTRPETIGLRYPGLIPDPSHKNASQQMLRYGCVVSFTLESRARADFFLDA
LRLVBGATSFGGVRSTAERRGRWGGDAVPEGFIRLSVGAEDPDDLVADLLRALDETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine-phosphatase (164 aa). Contains Pfam mi
to PF01451 LMWPc, Low molecular weight phosphotyrosine
protein phosphatase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complement(2693. .3187)
/gene="SCQ11.04c"
/note="SCQ11.04c, ptpA, low molecular weight
protein-tyrosine-phosphatase, len: 164 aa; previously
sequenced as Sw.PPPA_STRCO (EMBL.U37580), ptpA,
S.coelicolor low molecular weight
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                                                                                                           complement(1533. .2624)
/gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
complement(2031. .2075)
/gene="SCQ11.03c"
/note="SCQ11.03c"
/note="PSQ086 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
/gene="SCQ11.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 248.6; DB 1;
Pred. No. 1.6e-19;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine-phosphatase"/protein_id="CAB46959.1"
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/trans1_table=11
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75.78;
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Matches 308; Conserv
                                                                                                               misc_feature
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AUTHORS
TITLE
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VERSION
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                                                                              KEYWORDS
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                                                                                                                                                                                                                                                                                                                                   /transl_table=11
/product="SsgA"
/protein_id="AaG28481.1"
/db_xref="G1:11066159"
/db_xref="G1:11066159"
/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLFFHLPGDAPVTWAFG
RELLIDGAPRECGGOWHIAPADPEFRGEVLTRLQVGSDQAMFRVGTAPLVAFLDRTD
XIVPLGGERSLADFDALLDEALDDEALLDEADDFILEEQNAG"
115 c 145 g 77 t
                                                                                                                                                                                                                                                                                                         /note="similar to Streptomyces griseus SsgA; possible cell
division protein"
/codon_start=1
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 BCT 01-NOV-2000
                                                                                                                                                                                   Box
                                                                 Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescaes; Streptomyces.
1 (bases 1 to 408)
van Wezel, G. P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces goldeniensis ssgA gene Unpublished
2 (bases 1 to 408)
van Wezel, G. P.
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Submitted (18-OCT-1999) Biochemistry, University of Leiden,
9502, Leiden 2300 RA, Netherlands
1. .408
     Streptomyces goldeniensis SsgA (ssgA) gene, complete cds AF195770
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/db_xref="ATCC:21386"
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Pred. No. 1.7e-18;
0; Mismatches 102;
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                                                      goldeniensis.
goldeniensis
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Matches 305; Conservative
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filamentous microorganisms
Patent: WO 0000613-A 3 06-7AN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL OKGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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139 c 142 g 66 t
  PAT 06-SEP-2000
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Pred. No. 5.9e-18;
0; Mismatches 105; Indels
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Actinomycetales; Streptomycineae; Stre
1 (bases 1 to 407)
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AX007218 407 bp
Sequence 3 from Patent W00000613.
AX007218
AX007218.1 GI:9995084
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/gene="ssgA"
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                                    BCT 19-MAY-1999
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Shinichi, K. and Ensign, J.
Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus
Unpublished (1995)
S (base) to 1513)
Shinichi, K.
                                                                                                                                                                                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2,
Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996)
                                                                                                                                                                                                      1 (sites)
Kawamoto,S. and Ensign,J.C.
Cloning and characterization of a gene involved in regulation of
sporulation and cell division of Streptomyces griseus
Actinomycetol. 9, 136-151 (1995)
                                                                                                                                                                                                                                                                                             (sites)
Kawamoto,S. and Ensign,J.C.
Isolation of mutants of Streptomyces griseus that sporulate in nutrient rich media
Actinomycetol. 9, 124-135 (1995)
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Kawamoto,S., Watanabe,H., Hesketh,A., Ensign,J.C. and Ochi,K.

Expression analysis of the ssgA gene product, associated with sporulation and cell division in Streptomyces griseus Microbiology (Reading, England) 143 (Pt 4), 1077-1086 (1997)
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                                                                                                                           Streptomyces griseus (strain:B2682) DNA.
Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/strain="B2682"
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ESCOST. GI:1772323
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/codon_start=1
/transl_table=11
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducting branching and enhancing fragmentation in culturing filamentous microorganisms of patent: WO 0000613-A 1 06-JAN-2000;
(NL), NL DEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS VAN (NL)
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                                      06-SEP-2000
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                                                                                                                                                Streptomyces griseus
Bacteria; Actinobacteria; Actinobacteridae;
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/note="strain ATTC of Streptomyces griseus"
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Pred. No. 5.7e-18;
0; Mismatches 105; Indels
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AX007216
AX007216.1 GI:9995082
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Streptomyces netropsis SsgA (ssgA) gene, complete cds.
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/db_xref="G1:11066163"
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Submitted (18-OCT-1999) Biochemistry, University of Leiden, PO
9502, Leiden 2300 RA, Netherlands
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/db_xref="taxon:55404"
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Pred. No. 2.2e-16;
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/product="SsgA"
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/note="similar
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tgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcggggcgacggac 180
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                                                                                      gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc 240
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Reducing branching and enhancing fragmentation in culturing filamentcus microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTU (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHTIL VAN (NL)
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/db_xref="G1:153339"
/translation="MHPSTSRPSRTLLITATAGAALAAATLVPGTAHASSGGRGHGSG
/translation="MHPSTSRPSRTLLITATAGAALAAATLVPGTAHASSGGRCHGSG
LDRNDERFLAGLERASGARLGVYAYDTGSGRTVAYRABELFPMCSVFXTLSSAAVLRD
LDRNDEELSRRILYTODDVEQADGAGPETGROUNLANAQLIYVEELCRVSITASDNCAA
NIMLRELGGPAAVTRFVRSLGDRVTRLDRWEPELNSAEPGRVTDTTSPRAITRTYGRL
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PGRAPIVLTVLTAKTEQDAARDDGLVADAARVLAETLG"
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Dehottay,P., Dusant,J., De Meester,F., Joris,B., Van Beeumen,J., Erpicum,T., Ferre,J.,M. and Ghuysen,J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G Beta lactamase precursor
Eur. J. Biochem. 166, 345-350 (1987)
  TGGGCGTTCGGCCGGGAGCTGCTCGACGGGATCAACCGCCCGAGCGGCGACGGCGAC
                                                                                                                                       gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc 240
                                                                                                                                                                                                                                                                                                 accgaccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctc 360
                                                                                                                                                                                                                                                                                                                                      331 ACGGACAAGTCGGTGCCGCTCGGTCAGGAACAGACTCTGGGTGACTTCGAGGACAGCCTG 390
                                                                                                                                                                              GTCCACATCGCCCCGGACCGACCCCGAGGGCCTGTCGGACGTCTCCATCCGGCTCCAGGTG
                                                                                                                                                                                                                       ggctccgagcaggcgctcttccgcgtcggcaaggcgccgctgctcgccttcctcgaccgc
                                                           tgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcgggggacgcgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                               gacgacgctctgaaccgcagcctcgccgaggagcagagcgccggctg 407
                                                                                                                                                                                                                                                                                                                                                                                                        391 GAGGCCGCGTCGCCAAGATCCTCGCCGAGGAGCAGAACGCCGGCTG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-lactamase.
Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TMLACBG 1410 bp DNA albus beta-lactamase gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1410,
/organism="Streptomyces albus"
/strain="G"
/db_xref="taxon:1888"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="inverted repeat"
540 c 496 g 1:
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243. .1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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AUTHORS
                                                         121
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                                                                                                                                                                              211
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KEYWORDS
SOURCE
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Length 1410;

DB 1;

33.4%; Score 135.8;

Query Match

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The moore significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FremmePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
iun/cgi-bin/frammeplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 29-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetyltransferase; acyltransferase; adenine
phosphoribosiltransferase; DNA helicase; DNA polymerase III;
elongation factor; endodeoxyribonuclease; GTP pyrophosphokinase;
membrane protein; membrane transferase; protein-export membrane
protein; regulator; secreted protein; sugar transferase;
threonine-tRNA synthetase; transport system inner membrane protein.
Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (28-JAN-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescae; Streptomycescae; Streptomycescae; Streptomycescae; Kneptomycescae; Kneptomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is funded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CGGCTGACGTTCCACCTCCCCGGAGACGCCCCGGTCACCTGGGTCTTCGGGCGTGAACTG 120
                                                                                                                                                                                                                                                                                                                                                                                                         82 eggetgaegttecaceteceeggagaegeceeggteacetgggtettegggegtgaaetg 141
                                                                                                                                   81
             Gaps
                                                                                                                                                                                                        Streptomyces coelicolor sequencing at The Sanger Centre is fuby the BBSKC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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Cerdeno,A.M., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
                                                                                                                                          gagetegeetteegeateeeggtggagetgeggtaegagaeegtegateegtaegeggtg
      Indels
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      5.
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      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar of Tr. 033236 (EMBL:298209) Mycobacterium tuberculosis hypothetical 49.8 kD protein MTCY174.11, len: 650 as, fasta scores: opt: 843 z-score: 874.7 E(): 0, 45.9% identity in 1996 aa overlap. Contains possible coiled-coils region"
codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5\text{-}13\mathrm{bp} before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=3
/transl_table=11
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FAQLDAQREEARRIKERLVSFAREALSNSTDWGPTAARYRDLMSEWKAAGRRAGREEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWNRFRGAQDVFFAARSSVFAERDAEQSENLKLKEELVTEAEKLVPVTDLKSARAFR
SVNERWEAIGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGFTPRHARVPRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MDKLRSQVEQARAQGNDAKADKLARELEGRQALLDQALKGLHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="SCL2.03c, relA, GTP pyrophosphokinase, len: 847 aa;
                                                                                                                     IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   >328 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="previously sequenced region SW:SCAPTRELA EMBL:X87267 S.coelicolor apt & relA genes" complement(1229. .3772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein, len:
                                                                                                                                                                                                                                                                                                                            /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid L2"
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/gene="SCL2.02"
1010. .1150
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/note="SCL2.02, unknown, len: 46 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1229. .3772)
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                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                        upstream initiation codon.
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/transl_table=11
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                                                                                                                                                                                                                                                                                                      .38640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /partial
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                                                                                                                                                                                                                                             Cosmid L2.
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/gene="apt"//gene="apt"/gene="apt"/gene="apt"/gene="apt"/gene="gene="apt"/gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene="gene
                                      VUDK PAEGQPRPK PLPAERPONAP VVRAPAGOPARSGSSNRV PARLARLGVORANPYN PVLEPLLR IVRGNDPK LETSTLROL BRAYOVAERWHRGOKRK SGDPY TTHPLAYTT IL AELGMDPATLMAGLLHOTVEDTEYGLEDLRRDFGDVTLLVDGVTK LDKVKFGEAAQA ETVRKAVVAMAK DPBYVJ IKLADRLHWMRTMYKLKREKGEKGRKRARETLET YAPLAHRLG MYT IKWELEDLAFATLLI TAPLAHRLG MYT IKWELEDLAFATLLYPKMY DET VRLVAERAPKRDEYLAVYDEVQOLRAARIKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3273. .7460)
/note="previously sequenced region SW:SCSECAPT EMBL:X85969
S.coellcolor secb, secf & apt genes"
complement(3778. .3781)
                                                                                                                                                                                                                                                                                                           VTGRPKHYYSVYQKMIVRGRDFAEIYDLVGIRVLVDTVRDCYAALGTVHARWNPVPGR
FRVI TAMPKFMYQSLHTTVIGPGGRPLQLIRFDHIRRAFGGIAARMYKYQEAVAG
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TPKGDVIALPAGATPVDFAIAHTEVGHRTIGARVNGRLVPLESTLDNGDLVBFFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRGRGRKRRANADPGVVVKGVEDVWVKLARCCTPVPGDPIJGFVTRGSGVSVHRSDCV
NVDSLSREPERLLEVEWAPPJOSSVFLVAIQVEALDRSRLLSDVTRVLSDQHVNILSAA
VQTSRDRVATSRFTFEMGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
complement (1256 . .1474)
/gene="rela"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAGPSRDWLGFVKSPRARNKIRAWFSKERRDEAIEOGKDAIVRAMRKQNLPIQRIL
TGDSLVTLAHEMRYSDISALYAAIGEGHVSAPNIVQKLVQALGGEEAATEEIDESVPP
/translation="MPDEAQPLTAAKPESASASAAKPAPSAPQAKNDTHGPIQHAPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF01842 ACT, ACT domain, score 63.10, E-value 6e-15"
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/note="pfam match to entry PF00156 Pribosyltran,
Phosphoribosyl transferase domain, score 150.30, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SCL2.05c, secF, protein-export membrane protein, len: 373 aa; identical to previously sequenced SW:SECF_STRC0 (EMBL:X85969) Streptomyces coelicolor protein-export membrane protein SecF, 373 aa and similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
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/note="previously sequenced region SW:SCAPTRELA EMBL:X87267 S.coelicolor apt & relA genes" complement(3956. 4453)
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/protein_id="CaB70916.1"
/db_xref="GI:6822210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2378. .2401)
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complement(4468, .4503)
complement(4501, .5622)
/gene="secF"
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/gene="secF"
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/transl_table=11
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(bases 1 to 35284)

Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                                                                                                                                        35150 GGTCTTCGCCCGCGACCTGCTCGCCGAAGGTCTCCACCGTCCCACCGGCACCGGCGACG 35209
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                                                                                                                                                                     ccgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacct 121
                                           Gaps
                                                                                2 tgagcttcctcgtctccgaggagctcgccttccgcatcccggtggagctgcggtacgaga 61
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by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                      gggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcgggggacggcgacg
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James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (16-JUL-1999) Streptomyces coelicolor sequencin
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DB 1; Length 38640; 0.00022;
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  Score 110;
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                       Pred. No.
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27.0%;
55.1%;
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                                         215; Conservative
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                     Similarity
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  Query Match
                     Best Local
Matches 21
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VERSION
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MEDLINE
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(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)

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correct initiation codon. Where possible we choose an initiation codon (att) ttp or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be the entire insert of the sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid E19A lies between and overlaps cosmids E6 and E56 on the AseI-E genomic restriction fragment.
                                                                                                                                          are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
Substantially the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Which specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4766-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //note="SCE194.01, hypothetical protein, partial CDS, len:
>31 aa; unknown function, similar to members of the alkyl
hydroperoxde reductase C/thiol-specific antioxidant
family e.g. TR.053226 (EMB:ALO21185), bcp, Mycobacterium
tuberculosis bacterioferritin comigratory protein (157
aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06,
/codon_start=2
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(243. .845).
/gene="SCE19A.02c"
/note="SCE19A.02c"
/note="SCE19A.02c"
200 az; unknown function, similar to many e.g.
SW:703Q_MYCTU (EMBL:273902) Mycobacterium tuberculosis
hypothetical protein (204 aa), fasts acores; opt: 633
z-score: 743.6 E(1): 0, 52.0% identity in 200 aa overlap.
Similar to SW:YGGV_ECOLI (EMBL:028377), yggv, Escherichia
CDS are numbered using the following system eg SC787.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                  The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140. .226
/note="tRNA Leu anticodon TAG, Cove score 69.78"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Streptomyces coelicolor A3(2)"
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/protein_id="CAB50982.1"
/db_xref="GI:5531350"
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/protein_id="CAB50983.1"
/db_xref="G1:5531351"
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/db_xref="taxon:100226"
/clone="cosmid E19A"
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complement(243, .845)
/gene="SCE19A.02c"
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1. .35284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label-SCE19A.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCE19A.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label-SCE19A.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aa overlap)
                                                                                   strand)
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/translation="MASKAEKIVAGLGGIDNIDEIEGCITRLRTEVNDPALVNEAALK
AAGAHGVVKNGTAIOVVIGTDADPIAAEIEDWM"
complement(2385. 2489)
/gene="SCE194.05c"
/note="Pfam match to entry PF00367 PTS_EIIE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL391041.1 GI:9716211
amino acid transport integral membran protein; branched amino acid
binding secreted protein; branched amino acid transport system
ATP-binding protein; branched amino acid transport system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04 - AUG - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integral membrane protein; ion transport integral membrane protein; bylysaccharide blosynthesis protein; requlator; requlatory protein; secreted amidase; secreted peptidase, secreted protein; sigma factor; transcriptional regulator; transcriptional regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae, Streptomycetaceae; Streptomyces. 1 (bases 1 to 32704)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                      /note="SCE19A.06, possible PTS transmembrane component, len: 431 aa; similar to many PTS (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10202 CGGACGATCCTACGCCGTGCACATCACCTTCCACATCGACTCCGGCCACCCGGTGCACT 20261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20142 TCAGGCTCGTCCTGTCGCCCGAGAGCGGCATTCCGGTGCCGGCCCGGCTCGGCTACCACA 20201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00367 PTS_EIIB,
EIIB, score 43.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ccgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgcccggtcacct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 tccgggtctgcccggtggggcagacggccaccaggggaggtgcacatcacctccaggtcg 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 tgagcttcctcgtctccgaggagctcgccttccgcatcccggtggagctgcggtacgaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20262 GGACGTTCGCCCGCGACCTTCTGGTGGAGGCGTTCCGGCCGTCCGGGCACGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 ccgaccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 gggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcggggggacgcgacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 getecgageagegetetteegegteggeaaggegeegetgetegeetteetegaeegea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCT
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 109.6; DB 1
Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32704 bp DNA coelicolor cosmid 8A11.
                                                                                                                                                                                            phosphotransferase system,
     /protein_id="CAB50986.1"
/db_xref="GI:5531354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                           2660. 3955
/gene="SCE19A.06"
2660. 3955
/gene="SCE19A.06"
/note="SCE19A.06, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%;
56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces
AL391041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20502 CCGA 20505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 acga 365
                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
SC8A11
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1454. .2191)
/gene="SCE19A.04c"
/note="SCE19A.04c" rph, probable ribonuclease PH, len: 245
aa; highly similar to many e.g. SW:RNPH_ECOLI
(EMBL:X00781), rph, Escherichia coli ribonuclease PH (238
aa), fasta scores; opt: 916 z-score: 1116.8 E(): 0, 60.8$
identity in 240 aa overlap. Contains Pfam match to entry
PF01138 RNBASe_PH; 3' exoribonuclease family and PS01277
Ribonuclease PH signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown function, similar to parts of many sugar permeases e.g. TR:P96159 (EMB:U65013), malx, Vibrio furnissii PTS (phosphoenolpyruvate-dependent sugar phosphotransferase system) permease for glucose (523 aa), fasta scores; opt: 217 z-score: 287.9 E(): 1.1e-08, 48.1% identity in 77 aa overlap. Contains Pfam match to entry PF00367 PTS_EIIB,
TGVTFAENALLKAHALAEATCLPAVADDSGLCVDVLNGAPGIFSARMAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGQLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTABEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="maasrhrrlrrtytavatvatlaltagliffgcdavdkrlrtyaalabsvelgogavenaddptqweeslnsidknldrigdqtdntdvnkavddlgkav
Dnvrtsvengdetpdlspvtdaageltkvctp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEGVPRWRKGSGEGWVTAEYAMLPRATNTRGDRESVKGRIGGFTHEISKLIGRSLRAV
TOYRALGEWIYVLDCOVLQADGGTFRTAAITGRYVALADAVARAGGRKLIKANRKFLTG
TVSAVSOTVOTPLLLLRYEEDVRADTDMNVVCTGDGRFVEVQGTAEARPFARDELN
TLLDLATAGCTELAELQRKALDATLER"
                                                                                                                                                                                   /note="SCE19A.03c, possible secreted protein, len: 134 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative ribonuclease PH"

protein_id="CABSO981."

/db_xref="G131353"

/translation="MSRIDGRTPQQLRPVTIERGWSKHAEGSVLVSFGDTKVLCNASV
                                                                                                                                                                                                               unknown function, probable CDS suggested by GC frameplot, positional base preference and amino acid composition. Contains probable N-terminal signal sequence and appropriately positioned PS000013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exoribonuclease family, score 266.70, E-value 3.1e-76" complement(1805. .1843) /gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1201. .1233)
/gene="SCE19A.03c"
/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site" complement(1454. .2191)
/gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SCE19A.05c, hypothetical protein, len: 77 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1511. .2185)
/gene="SCE19A.04c"
/note="Pfam match to entry PF01138 RNase_PH, 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS01277 Ribonuclease PH signature"
complement(2268. .2501)
/gene="SCE19A.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative secreted protein"
/protein_id="CAB50984.1"
/db_xref="G1:5531352"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCE19A.05c"
/note="ccm1"
                                                                                  complement(892. .1296)
/gene="SCE19A.03c"
                                                                                                                                       complement(892. .1296)
/gene="SCE19A.03c"
                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/transl_table=11
/label=SCE19A.05c
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                    lipoprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="rph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=rph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                    CDS
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TITLE

COMMENT

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/transla_tantrative regulator"
/product="putative regulator"
/product="putative regulator"
/product="cac01575.1"
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PDHPLLYTIRRAPEGAPPYTWINGRDLHHEGLRTTSGLGDVQWADTPTDRETAWLQV
NAHGDTAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
complement(3297. .7058)
/gene="SC8A11.04"
/opto="SC8A11.04"
/note="SC8A11.04"
/no
                                                                                                                                                                         YTRATVADRLSTHRALAETLEGSPGRRLVHLAAATLGPDDELAGQLERFADDAQKRGQ
LAAAVPALRQAGELVHDPRRQTGLLVRAAELASEINDRVQAQILLNRADLAEPGPTER
ARLMLVSDKAAFEPDEPQRRIQDMIDAAAGAFDVGSTSVAENLLWRAAARCFFQDGDA
                                                                                                                                                                                                                                                                                                      RVRAQAAAELDRWKPDPDAPHVLTVRAYTEPYRRGTDLIARLEKLRPDREDGRLLHYL
GSGSMAIGDVGRATRYLAQAASVWRSQGRLGLLARSLAGSWBRIKLIGDLAQAREBSAAE
GIALAETGWIVWLGLKATGALTAVLRGERBAARRYRELRAHSLFPVWPFASVWAO
QVEGILALFDSRAVAZVAALARAFDKTDPHYHSTSRWLLVPDLVDAAAAAGRNEGARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIVELPELADRLPSEMMIVARTYSTAVLAPDDTAEDCYDSALSALPDTWPLARARLHL
VOHRRLERRRYRNYDARKPLRLARDEFDRVGAQPWADMAREQLRAAGESDGRRRPSKGE
SLTVQERQIABLASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
LGDDQPTSGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="SCBAll.03, possible regulator, len: 156 aa; similar to TR:0952F7 (EMBL:AL096852) Streptomyces coelicolor putative regulator SCE19A.24, 142 aa; fasta scores: 0pt: 272 z-score: 355.0 E(): 3.4e-12; 36.9% identity in 130 aa
                                                 /translation-"IGAARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
VRAFILORAAGNPLALVELPRAAGGISPPLDDLPLTORLETAFASRTDSLTRECRTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MASAAATAGTAGALPVMSGQAHADTRGLPSLWDVDRSVVNPENA
YTVTVDQVRAEVAQLMGATEEEFTRPRSAGRLRARPAPRRACRGW"
                                                                                                                                 LVLAAEPTAPLNQLLDVASRLAGSEVTVYALQEAVDAGLVVLTGRTPEFRHPLMRSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2093. .2176
/gene="SC8A11.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteases, subtilase family, aspartic acid active site, PS00137 Serine proteases, subtilase family, histidine active site and PS00138 Serine proteases, subtilase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family, score 49.10, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
product="hypothetical protein SC8A11.02c"
/protein_id="CAC01574.1"
/db_xref="GI:9716213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2184. .2453)
/gene="SC8A11.02c"
complement(2184. .2453)
/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2787. .3257
/gene="SC8A11.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2042. .2239
/gene="SC8A11.01"
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/gene="SC8A11.03"
2787. .3257
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Kroph et al., Nucleic Acids Research, 22(22):478-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nin.go.jp/

in/Cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon gig, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most thoman initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                  Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="SCBAIL.01, possible transcriptional regulator (fragment), len: >750 aa; similar to TR:095124 (EMBL:AL10947) Streptomyces coelicolor probable transcriptional regulator SCJ21.13, 919 aa; fasta scores: opt: 818 z-score: 913.7 E(): 0; 32.6% identity in 775 aa overlap. Contains Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR family and match to Prosite entry PS00622 Bacterial regulatory proteins, luxR family signature. Also contains a possible helix turn helix motif at residues 699. 720 (+3.25 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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/product="putative transcriptional regulator (fragment)"
/protein_id="CAC01573.1"
                                                                                                                                                                                                                                                                                                                                                                                          Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrellGeanger.ac.uk Cosnids supplied by Prof. David A. Hopwood, 131 John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                             3 (bases 1 to 32704)
Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptomyces coelicolor A3(2)"
    Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                 Saunders, D.C. and Harris, D.
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/gene="SC8A11.01"</pre>
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                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                  ALTVGAVNGPCKGVDQLADFSSRGPRVGDNAVKPDLTAPGVGVLAARSRTAPEGEGAY
OSLGTSGATTARTPHVAGAALLAAEHPPWTGQRLEALVGTTATGTQRESPDGSGSRVDV
AAAVRSTLLASGDAFRQAHVEYTPGGTVRRDVTYTNSGPAPVALDLALSPAELPEGLF
TLSEAOVTVPAHGTASVGVTTHLDAAEDNGAYATRLVASGADGAVLARTPVGVNKEGR
RATLALTARTBLUSTULKUSPRTTAFKYSVDASGRIDLILSESPTSYWMNSA
VPGTGGTHTLGFARTAPRYTLILDABENTAPKYYSVDASGRIDLILSLESPTSYWMNSA
VPGTGGTHTLGFARTAPRYTLADBATTAFTRANFFLELLILSTESPTSYWNSA
NTGLFPFMDSYVAEXWRYDSLWYTPTPEVRTGSYTFATRWRQIQPPLTFSAGSQTFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCT 05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQHPRLLSDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGE
LLGEDVNERIVWVGGLSPGPRPYRLVLEGSRNLPDRPYSTRTRTVWDFTSATTDPTRL
TPLPLVQLDYAVAVDLSGRAHRRTELTVTASHLEGAAGAGAIRTATVEVSYDDGATWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABC transporter; amino acid permease; BCCT family; carboxypeptidase; D-amino acid oxidase; dadh, dimethylarginine dimethylaminohydrolase; dehydrogenase; efflux protein; endonuclease; enoyl CoA hydratase; IPP isomerase; metallopeptidase;
                                                                                                                                                                                                                                         GPTRVLTLITGDRVTVTGEDGAETVLSVTDPHGRSGGAHVMTVGSDTYVYPDAAVPYL
GSGALDERLFNVTELLEDGYDDARADELPLIVTYTDTAARSLGARTPEGARRTRALSS
                                                                                                                                                                                                                                                                                                                             LSDTTAQIGAPDVWSGGNTGECVGVAVLDTGVDAGHPDFAGRIAATASFVPDQDVTDR
NGHCTHVASTVAGTGAASGGVEKGVAPGASLHIGKVLDNSGSGQDSWVLAGMEMAVRD
QHAKIVSMSLGDSPTDGTDPLSEAVNWLSAETGALFVVAAGNSGPEAYTVGTPAAADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTVQSRSPQLPEGTRAYRAVWAGDGSATEFRCAEVRDRVAVVRRSDTVAPTDQAAAAE
KAGARQLLILNDGYGKFDPWADLPEAAPLPVASLGTDDSARLLARFRGAGTTTLRVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPVPRYAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSQGRAVEYRQDISLLGQ
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                                                                                                                                                                                                          /translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVPPAPPTAPA
                                                                                                                                                                                                                                                                                                 IRGAAISAEHSRAADFWTSLTGTGDAAAGGSAARSATSGGRLAGGIAKVWLDGKVRAT
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/gene="SCBA11.04c"
/note="Pfam match to entry PF02225 PA, PA domain, score
19.00, E-value 0.058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2894 CGTTCCGGCGGAGTTCCGTTACGATCCCGACCACCCCCTCCTCGTCACGATCCGCTTCGC 2953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3014 GCGCACCACGAGCGGCCTGGGGGACGTCCAGGTGTGGGCCGACACCCCCACACGGGGA 3073
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family, serine active site. Also contains possible N-terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTALRKSADGWTARLDAPGRARYASLRTTAKDTEGNGVGQTLIRAFGLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2954 CCCCGAGGGCGCCCCACCGGTCACCTGGCATGTCGGCCGTGACCTGCTGCACGAGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggaggtgcacatcaccetecaggteggetecgageaggegetetteegegteggeaagge
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                                                                                                                   /product="putative secreted peptidase"
/protein_id="CAC01576.1"
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                                                                                          /transl_table=11
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52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.0
Best Local Similarity 52.1
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SC5F2A
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codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colnay, Norwich, Norfolk NR4 7UH, UK On May 10, 2000 this sequence version replaced gi:4584464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
oxidoreductase; racemase; regulator; thiolase; transferase.
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescales; Streptomycineae; Streptomycescales; Streptomycescales; Streptomycineae; Streptomycescales; Kinashi, M. Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
Ast of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /jote="SC5F2A.01c, ddah, dimethylarginine
dimethylaminohydrolase, len: 258 as; hydrolyses
asymmetrically methylated arginine with preference
dimethylated arginine over monomethylated arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 37245)
Bentley,S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission

    37245
/organism="Streptomyces coelicolor A3(2)"

    105
/note="Nominal overlap with cosmid 4C6"
complement(83. .859)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Oliver, K. and Harris, D.
Unpublished
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/gene="SC5F2A.02c"
/gene="Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MPSKKALVRRPSPRLAEGLVTHVEREKVDHGLALEGWDAYVEAL
SAGNGWELTEVDPADDCCPDSVPYEDAVVVFRNYALITREGAESRRAETAGVEEAVARLG
CSVMWYWEPGTLDGGDVLKTGDTTYVGRGGRTNAAGYQQLRAAFEPLGARVVAVPVSK
VLHLKSAVTALPDGTVIGHIPLTDVPSLEPRRLAVPEBSGAHVVLLGGSRLLAMAASAP
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TIAVESRRQLNETFTWFVRNRLPRYERPHADALEGLTPAIVVDQRPVGGHSRSTVGTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDIHSVLRVLFSRHGTPGAGGATAYSFNDPSGMCPGCDGLGRRYQPDWDRILDPARSL
ADGAVREPPEAGTWGGQTYUNTEELDTGKPVGDFTAARRAFLMRGRPGSKYTVSGSG
GTWSTEYSGLADRFERLIYTKRDLSGBSTRDLVRGFLVBARCPDCGGARLNAAALAS
RIDGHSIADCSRWQTTDLIAVLRGIDDPARLPVAGAVAALERVBAAGLGSLSLDRET
ATLSGGEGQRLKTVRHLGSSLTGMTYIFDEPSVGLHPRDVGRLGDLLLRLRDKGNTVL
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VRAPTGELWVKGAERHNLREVTVAFPTGVLTAVTGVAGSGKSTLVAELTGAHPDAVVV
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ALLDRLVDAGNTVVVVEHNLDVVAHADRVIDLGPDGGRDGGRVIFEGTPRELLAARGS
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                                        NG.NG-dimethylarginine dimethylaminohydrolase from Homo sapions (285 aa) fasta scores; opt: 323, z-score: 384.7, E(): 4.1e-14, (35.7% identity in 272 aa overlap)." /codon_starte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1090. .1803)
/gene="SC5F2A.02c"
/note="Pfam match to entry PF00005 ABC_tran, ABC
transporter, score 101.40, E-value 1.7e-26."
/gene="SC5F2A.02c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
/gene="SC5F2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Journal of the match to entry PF00005 ABC_tran, ABC transporter, score 35.60, E-value 4e-08." complement(3118. 3141)
/gene="SC52A,02c" //oce="PS00017_ATP/GTP-binding site motif A (P-loop)."
(experimental). Similar to TR:D1038106 (EMBL:AB001915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (P-loop). Also contains possible membrane spanning hydrophobic regions."
                                                                                                                                                                                                                                                                                                       /product="dimethylarginine dimethylaminohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTAELLADLGHEPVLVDIGEFEKLEGCVTCLSVRLRELYD"
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/protein__d=CAB40669.1"
/db_xref="G1:4584466"
/db_xref="SPTREMBL:09X7M5"
                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB40668.1"
/db_xref="GI:4584465"
/db_xref="SWISS-PROT:Q9X7M4"
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/gene="SC5F2A.03c"
complement(3245. .4879)
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/note="sc5F2A.03c"
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/gene="SC5F2A.02c"
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                                                                                                                                                                                                                 /transl_table=11
/label-ddah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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CDS

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AGDVREEHFETVGDDWDVEERALATLGELGLDHIGLDRTVGEVSGGESVLLRLAALLL
RENDVLLLDEPTNNLJVYARRELYAAFSWPCWAVVSHDRELLDRVDJADLRAGSV
TWYGGNLTAYEBEALAVYOEGAARSWPCWARS
TWYGGNLTAYEBAAVAYCGAARSWPCWARS
TKREPRAVWKLRARTAQGSAGKYRIMHEEKLAGAKERLDDAVEAVRDDDEIRVDLPYT
TKREPRAVWKLTRALELAYGARVAGGLIHGPRRIALLGRAGKTTLLTRALELAYAGELAPV
AGEATAHVELRELAYGARVAGGLIYAARVARFAPGATINNRTRALLARFLFRGARADO
OAATLSGGERFRAALMABPAPQLLMLDBPTNNLDMASVROLTGALBAYEGALLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:09X7M6"
/translation="MSTSPTSLTCTSLSFAWPDGTEVFDGLDVAFGPGRTGLVGLNGA
GKSTLLKLIAGRLTPADGTVRVAGQVGYLPQNVTLDTALRVDEALGIDGRRAALHAIE
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TR:054381 (EMBL:X79146) from the lincomycin-production gene cluster of Streptomyces lincolnensis 78-11 (578 as) fasts ascores; opt: 1624, 2-score: 1696.3, E(): 0, (50.3% identity in 541 as overlap). Contains two Pfam matches to entry PF00005 ABC_tran, ABC_transporter, two Prosite matches to PS00017 AFP/GFP-binding site motif A (P-loop) and Prosite match to PS00211 ABC transporters family signature. Also contains a possible coiled-coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF00005 ABC_tran, ABC transporter, score 122.30, E-value 9e-33" complement(3743. .3766) /gene="SC5F2A.03c" /note="PS00017" rapporter pS00017" rapporter pS000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rungplement(4703...447)
/gene="SC5F2A.03c"
/note="PS00211 ABC transporters family signature."
complement(4739...4762)
/gene="SC5F2A.03c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6178
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Pred. No. 1.8;
0; Mismatches 161; Indels 18;
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/db_xref="GI:4584467"
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/gene="SC5F2A.03c"
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/transl_table=11
/label=SC5F2A.03c
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/gene="SC5F2A.04"
4942. .5850
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Best Local Similarity 53.9%;
Matches 209; Conservative (
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Db 6006 CCAGGCCGCCGCCGCGGTGGTGCGTCGGTCTCGAGCACCTCCAGCTGGACCTGGACCA 5947

Search completed: July 18, 2002, 11:22:05 Job time: 13735 sec

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mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 3004; bioinsecticide; receptor agonist; antagonist; biomass; ds.
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AAQ79400
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ABI99191
AAV82889
AAA95012
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ABI99189
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AAA95038
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AAA95036
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ABI99192
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ABI99190
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AAQ79405
AAQ79404
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1..405
/*tag= a
/label= SsgA_protein
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ABI99194
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AAA95037
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mat_peptide
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                       July 18, 2002, 11:36:11; Search time
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Listing first 45 summaries
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AAZ49730
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                                                                                                                           The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entitumour sents. antimigraine agents, hebbicides, antibarasiic agents, runinant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ssgA: liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 21386; blownsecticide; receptor agent; antagonist; blomass; ds.
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                                                                                   microorganisms used to improve their liquid culturing properties
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                                                                         Reducing branching and enhancing fragmentation in filamentous
                                                                                                                                                                                                                                                                     Length 407;
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                                                                                                                                                                                                                                     Sequence 407 BP; 57 A; 150 C; 139 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                    ; Score 407; DB 21;
; Pred. No. 2.8e-61;
0; Mismatches 0;
WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces goldeniensis ssgA gene.
                                                                                                     Disclosure; Fig 5; 60pp; English.
                      Luiten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 407; Conservative 0;
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(NEWE-) NEDERLANDSE ORG
                     'n
                      Kraal
                                         2000-147269/13
                                                    P-PSDB; AAY44650
                     /an Wezel GP,
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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antiblotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, erryme inhibitors, antimigraine agents, herbicides, antiparasitic agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
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SsgA_protein
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                                             Location/Qualifiers 1..405
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goldeniensis
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/label= 8
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Matches 305; Conserv
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tgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgat 180

gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc

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                                                                                                                                                                                                                                                                                                                                         mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesteroleamic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agents; antagonist; biomass; ds.
                                                                                                                                                                                                                                                                                                                   liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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                                                                                                                                                                                                                                                              Streptomyces griseus ssgA gene-2.
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                                                                                              AAZ49728 standard; DNA; 407 BP
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                                                                                                                                                                                                        (first entry)
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P-PSDB; AAY44649.
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mat_peptide
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparaslite agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesteroleamic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agent; antagonist; blomass; ds.
                                                                                                   accgaccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctc 360
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                                  241 ggctccgagcaggcgctcttccgcgtcggcaaggcgccgctgctcgccttcctcgaccgc
                                                  181 gtgcacatcggcccgaccgagcccgagggcttcggagatgtccacatccggctccaggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolite;
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                                                                                                                                                                    filamentous bacteria; secondary
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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Length 407; Indels

Score 239; DB 21; Pred. No. 1.2e-32; Mismatches 105;

58.7%; 74.2%;

0;

Conservative

Similarity

Query Match Best Local Simi Matches 302;

61 accgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacc 120 gleggegatecgtatgecatecggatgaegttecaeetteeeggegatgeeeetgtgaee 120 tgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcggggcgacggcgac 180

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P-PSDB; AAY44652
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                                                                                                                                                                                                                                                                                                                                                                                                                             ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agonist; antagonist; blomass; ds.
                                                                                                            ggcgcggaccgtgcgctgttccggggcggggacggcaccgctggtggcgttcctcgaccgg 330
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                                              Gaps
                                                                         1 atgagetteetegteteegaggagetegeètteegeateeeggtggagetgeggtaegag 60
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                           Length 438;
                                             Indels
                                                                                                                                                                                                                                                                                          gacgacgctctgaaccgcagcctcgccgaggagcagagcgccggctg 407
                                                                                                                                                                                                                                                                                                    72 T; 0 other;
                          Score 239; DB 21;
Pred. No. 1.2e-32;
0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WETENSCHAPPELIJK ONDERZO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
A; 145 C; 153
                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces netropsis ssgA gene.
                                                                                                                                                                                                                                                                                                                                                         BP.
                          58.7%;
illarity 74.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                        AAZ49731 standard; DNA; 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98EP-0202148
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(NEWE-) NEDERLANDSE ORG W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kraal B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces netropsis.
89
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                           Query Match
Best Local Similarity
Matches 302; Conserv
BP;
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Sequence 438
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The present sequence is a DNA (ATCC 23940) encoding S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and blomass.
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transgenic plant; insect resistance;
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 224.6; DB 21; Length
Pred. No. 3.3e-30;
0; Mismatches 114; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 407 BP; 63 A; 151 C; 131 G; 62 T; 0 other;
                                                                                                           Disclosure; Fig 5; 60pp; English.
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macrolide; insecticidal; ds.
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Best Local Similarity 72.0%;
Matches 293; Conservative (
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Saccharopolyspora spinosa.

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Pred. No. 0.00012;
0; Mismatches 75; Indels 0
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                                                                                                                                                                                              Salas JA;
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Best Local Similarity 61.1%;
Matches 118; Conservative
99DE-1057268
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                                                                                                                                                                                           Eberz G, Moehrle V,
                                                                                                                                                                                                                                                           WPI; 2001-267102/28.
                                                                                                                             (FARB ) BAYER AG.
29-NOV-1999;
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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in blosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the blosynthesis of adding forosamine or trimethylthamnose to a spinosyn or polyketide adding forosamine or trimethylthamnose to a spinosyn or polyketide adding forosamine or trimethylthamnose to a spinosyn or polyketide adding forosamine or trimethylthamnose to a spinosy or polyketide adding trimethylthamnose to a spinosy or polyketide adding trouchinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of (II), their precursors or derivatives, including production of (II), their precursors or markers for sequencing of the Sacharopolyspora spinosa genome. (II) are markers for sequencing of the Sacharopolyspora spinosa genome. (II) are also useful for identifying approduce of a spinosa spinosa sequence represents a genomic DNA fragment (I) may produce (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding requines for proteins involved in forosamine, trimethylrhamnose and polyketide synthase biosynthesis.
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                                                                                                                                                                                                                                                    Velten R,
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ID AAT68715 standard; DNA; 15872 BP.
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                                     DE19957268-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces venezuelae vep ORP1 (AAT68715) comprises the polyketide synthase (PKS) gene cluster encoding a polyene of 12 carbons (see also AAM19629-30 and AAM00918). It contains 5 PKS modules, with a 5 loading module and 3 'end domain. Each of the sequenced modules includes a keto-ACP, an acyltransferase, a dehydratase, a keto-reductase and an acyl carrier protein domain. The gene cluster was cloned using a heterologus hybridisation strategy from a genomic DNA library. A novel expression cassette encoding the first module from the vep gene cluster and module 7 from the Streptomyces tylp gene cluster has polyhydroxyalkanoate (PHA) monomer synthase activity and can be used for PHA prodn. in host (esp. insect) cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cttcgggcgtgaactgctggtcgagggagtcctggacgccgcggggcgacgtccg 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression cassettes for production of polyhydroxyalkanoate(s) provide wide range of biodegradable polymers for medical or
                                                             synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15872 BP; 2093 A; 6313 C; 5503 G; 1963 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                      Polyketide synthase; polyhydroxyalkanoate monomer syn
polyhydroxybutyrate; biodegradable polymer; vep gene;
Streptomyces venezuelae polyketide synthase vep ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60.8; DB 18;
Pred. No. 0.017;
0; Mismatches 202;
                                                                                                                                                                                                                                           Location/Qualifiers
20..13912
/*tag= a
14056..14136
/*tag= b
14148..15827
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xue Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 54; Fig 23; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.9%;
ilarity 47.4%;
Conservative C
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                                                                                                                          metabolic engineering; ss.
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                                                                                                                                                                                        Streptomyces venezuelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MINU ) UNIV MINNESOTA
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Best Local Similarity
Matches 182; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-1997
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                                                                                                                                                                                                                                                     Key
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comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AAY77199)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "vep ORF 1 amino acid sequence #2 (AAY77178)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "vep ORF 1 amino acid sequence #1 (AAY7717)"
                                                                                     The invention relates to an isolated and purified nucleic acid segment
246 cgagcaggcgctcttccgcgtcggcaaggcgccgctgctcgccttcctcgaccgcaccga 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
                                                                                                                                                                                                                                                                                                                                                                                              Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromyc;
neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase;
biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma,
chronic obstructive pulmonary disease; respiratory inflammation;
hypercholesterolaemia; crop protection agent; ds.
                                 1615 gegeetegeegteetgtteageggeeaagggtgeecaaegtaegggeatggggeatggagtt
                                                                   306 ccagggettgtcgetcggcagcgagcgggcacacgccgaettcgacagccacetcgacga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "vep ORF 1 amino acid sequence #3
14167..15827
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Figure 23; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                venezuelae vep ORF 1, SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY77177, AAY77178, AAY77199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
20..13912
                                                                                                                                                        Streptomyces venezuelae ATCC15439
                                                                                                                                      cgctctgaaccgcagcctcgccga 389
                                                                                                                                                                                                                                                            AAZ87283 standard; DNA; 15872 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14056..14151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-160679/14
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                                                                                                                                                                                                                                                                                                                              05-JUN-2000
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                                                                                                                                                                                                                                          AAZ87283
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proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as blopolymers, e.g., in packaging or blomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary conclusers as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including anti-pathogens, or as crop protection agents (e.g., unit-inqu resistant pheumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., tungicides or insecticides) via expression of polyketides in plants. The present sequence represents a Streptomyces venezuelae ATCC 18439 DNA sequence, designated vep ORF 1 in the specification, which actually contains 3 open reading frames, which encode proteins AAY77177-Y77178 and AAY7719.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15872 BP; 2088 A; 6304 C; 5513 G; 1967 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60.8; DB 21;
Pred. No. 0.017;
0; Mismatches 202;
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14.9%;
Best Local Similarity 47.4%;
Matches 182; Conservative
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Location/Qualifiers

Key

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polynucleotides and polypeptides can also be used to confer
calicheamicin resistance to a subject, e.g. by using gene therapy.
Human bone marrow cells can be transformed with calc gene and
returned to the patient allowing the patient to tolerate calicheamicin
treatment and be able to receive higher doses of calicheamicin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a CalH protein of Micromonospora echinospora. The protein is TDP-6-deoxy-D-glycerol-1-threo-4-hexulose 4-transaminase. The gene is present on the nonchromoprotein enediyne biosynthetic gene cluster. The calicheamicin gene cluster can be genetically manipulated to produce calicheamicin analogues. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 tacgcggtgcggctgacgttccacctccccggagacgccccggtcacctgggtcttcggg 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 taccoggtggacctcaaccggctgcgcgccgtcgtggaccgggccacggcgggatacgac 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 ccgctgggcacgcacggcaacgtctgcgtgtacagcaccggcgcgatcaagatcctgacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616 accygcaycygcygcttcytcytyccygacyacyacctytacyaccygctccygcty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 ggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctcgacgacgc
                                                                                                                                                                                                                                                                                                                                                          Novel Micromonospora echinospora gene cluster which codes for calicheamicin biosynthesis polypeptides, used for production of calicheamicin compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.5%; Score 59; DB 21; L. Best Local Similarity 52.2%; Pred. No. 0.048; Matches 156; Conservative 0; Mismatches 140;
                               /product= "CalH protein"
/transl_except= (pos: 1..3, aa:
                                                                                                                                                                                                                                 (SLOK ) SLOAN'KETTERING INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                  /*tag= a
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1..1155
                                                                                                                                                                                                                                                                                                      WPI; 2000-442652/38.
                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY93894
                                                                                     WO200037608-A2
                                                                                                                                                                                              07-DEC-1998;
                                                                                                                       29-JUN-2000
                                                                                                                                                                                                                                                                      Thorson J;
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us-09-749-185-4.rng

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The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 31-40. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce
Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB07580, AAB07581, AAB07582, AAB07583, AAB07584, AAB07585,
AAB07586, AAB07587, AAB07588, AAB07589.
                     BLM gene cluster; bleomycin gene cluster; polyketide metabolite; bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine; thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules -
                                                                                                                                   /transl_except= (pos: 1..3, aa: Met)
/note= "ORF31; encodes AAB07580"
925..9450
                                                                                                                                                                                                                                                                                                                                                                     transl_except= (pos: 1..3, aa: Met)
note= "ORF37; encodes AAB07586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          _except= (pos: 1..3, aa: Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "ORF40; encodes AAB07589"
/note= "no termination codon given"
                                                                                                                                                                        /*tag= b
/note= "ORF32; encodes AAB07581"
9447..10802
                                                                                                                                                                                                                                                        note= "ORF34; encodes AAB07583"
11888..12640
/*tag= e
                                                                                                                                                                                                          /*tag- c
//note-"ORF33; encodes AAB07582"
//0864..11877
/*tag- d
                                                                                                                                                                                                                                                                                                                                 "ORF36; encodes AAB07585"
                                                                                                                                                                                                                                                                                             note- "ORF35; encodes AAB07584
                                                                                                                                                                                                                                                                                                                                                                                                                     "ORF38; encodes AAB07587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen M,
                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 'note= "ORF36
                                                                                                                                                                                                                                                                                                                                                                                              14743.,16479
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17646..18659
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05-FEB-1999; 99US-0118848.
05-JAN-2000; 2000US-0477962.
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                                                                        Streptomyces verticillus.
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/note=
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branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiazolidne, thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel; glutamate; hippocampus; rat; pcDNA1; NMDA receptor; antagonist; ds.
                                                                                                                                                                                                                                                                                                                                                                            5484
                                                                                                                                                                                                                                                                                                            5485 gacggcgctgatgcgcgtggcggtggcccggctggcggacgacgatcacgtgctggtg 5544
                                                                                                                                                                                                                                                      5305 gagacgetgeggaeggegttegtegageggaeggggtgeeeeaecaggtggteteggeg 5364
                                                                                                                                                                                                                            43 giggagotigoggiacgagaccgicgatccgiacgcggigoggctgacgitccaccicccc 102
                                                                                                                                                                                                                                                                                   103 ggagacgcccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac 162
                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                          223 cacatcaccetecaggteggetecgageagegetetteegegteggeaaggegeetg
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/product= C-terminal 946 a.a of NMDAR2C receptor
                                                                                                                                                                  Length 18660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 18660 BP; 2365 A; 7239 C; 6510 G; 2546 T; 0 other;
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                                                                                                                                                                 14.3%; Score 58.4; DB 21; Length 50.0%; Pred. No. 0.043; ive 0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NMDAR2 receptor subunit clone NMDA26 gene.
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189..3025
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                                                                                                                                                                                                Matches 146; Conservative
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                                                                                                                                                                                Best Local Similarity
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P-PSDB; AAR66060.
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                                                                                                                                                                  Query Match
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The nucleotide sequence of the novel N-methyl-D-aspartate (NMDA)

receptor 2C (NMDAR2C) gene clone NWDA26. This clone covers bases 1-3025

of the complete NMDAR2C gene (AAQ79372), thus lacks the 3' 1043 bases.

CT he NMDA receptor contains two subunits and lacks the 3' 1043 bases.

CT he NMDA receptor forms the subunits 2A (AAQ79375), 2B (AAQ79377), 2C

and 2D (AAQ79378). The receptor forms part of a family of NMDA receptors

WICH have cation-selective channels and bind glutamate and NMDA. The

NMDAR2C gene was obtained by amplifying cDNA derived from human brain

tissues with primers corresponding to sequences in the rat NMDAR2A

receptor DNA and using the resultant fragments as probes to screen a cDNA

receptor DNA and using the resultant fragments as probes to screen a cDNA

cecptor DNA and using the resultant fragments as probes to screen a cDNA

cecptor DNA and using the resultant fragments as probes to screen a cDNA

cecptor DNA and screen thought to be splice variants of each other.

MAD31 (AAQ79402). The clones are thought to be splice variants of each other.

Based on the sequence of the 4 clones, a series of variants (AAQ79403-7)

of the NMDAR2 creeptor were constructed. The expression of the genes

allows the reconstruction of the NMDA receptor. The complete receptor can

be used to identify compounds which bind or are antagonistic to the human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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    used as probes in the identification and isolation of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3025 BP; 526 A; 1017 C; 926 G; 556 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   918 ggtctggtggggcccggccacgtgtggctggtgcccaacctggcgctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56.2; DB 15;
Pred. No. 0.13;
); Mismatches 183;
                   nucleic acids encoding related receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NMDAR2 receptor subunit clone NMDA22.
                                                                Claim 11; Page 99-104; 156pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMDA. The NMDAR2C gene was obtained by amplifying cDNA derived from human brain tissues with primers corresponding to sequences in the rat NMDAR2A receptor DNA and using the resultant fragments as probes to screen a cDNA library derived from human hippocampal RNA. 4 basic clones were isolated: NMDA21 (AAQ79399), NMDA22 (AAQ79400), MMDA24 (AAQ79401) and NMDA26 (AAQ79402). The clones are thought to be splice variants of each other Based on the sequence of the 4 clones, a series of variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AAQ79403-7) of the NMDAR2C receptor were constructed. The expression of the genes allows the reconstruction of the NMDA receptor. The complete receptor can be used to identify compounds which bind or are antagonistic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 ggagacgccccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 geettegeegteateaceageetgeaceegggeeaegegetetteetggagggegtgege 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
            /product= NMDA22 variant NMDAR2C
1034..1045
/*tag= b
//note= "11 bp insertion found in this clone"
1604..1605
/*tag= c
//note= "15 bp deletion of NMDAR2C sequence between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 gtgtccctggagcagcagctgcaggtgctgttcaaggtgctggaagagtacgactggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 gtggagetgeggtaegagaeegtegateegtaegeggtgeggetgaegtteeaeeteeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gccgcgggcgacggcgacgtccgggtctgcccggtggggcagacggccaccagggaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 gecgtegecgaegecagecacgtgagttggeggetgetggaegtggteaegetggaaetg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA encoding a human N-methyl-D-aspartate receptor subunit - used as probes in the identification and isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids encoding related receptor subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.2; DB 15;
Pred. No. 0.12;
0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                             Lu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 99-104; 156pp; English.
                                                                                                                                                             these bases"
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47.6%;
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Best Local Similarity 47.6
Matches 166; Conservative
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                             Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-341863/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR66058.
                                        misc_feature
                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                          20-APR-1993;
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                                                                                                                                                                                                                                           27-OCT-1994
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Sequence 3698 BP; 612 A; 1283 C; 1159 G; 644 T; 0 other;
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                                                                            166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human N-methyl-D-aspartate (NMDA) receptor subunit (NMDAR). The nucleic acid sequence does not contain the 366 5'-most nucleotides, has an additional 11 nucleotides between nucleotides 1300 and 1301, nor the 15 nucleotides at positions 1960-1974, nor the 1061 3' nucleotides, as set forth in AAV82889. The CDNA sequence is derived from clone NMDA22. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective ion channels. In addition to being useful for the production of NMDA receptor subunit proteins, the nucleic acids are also useful as probes to identify and isolate nucleic acids encoding related receptor subunits. Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutamate receptors can be assembled from several NMDA receptor subunit proteins of one type (homomeric) or from combinations of subunit proteins of different types (heteromeric). The present invention also comprises methods for using such receptor subunits to identify and characterise compounds which affect the function of such receptors, e.g. agonists, and anagonists and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are functional as NMDA receptor subunits.
 tttgtggcctactgctcgcgcgaggaggccgaggtgctcttcgccgaggcggcgcaggcc 551
                                                                                                                                                                                                                                                                                                                                                     NMDA-activated cation-selective ion channel; glutamate receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding N-methyl-D-aspartate receptor subunit - useful for the assembly of functional glutamate receptor subunits
                                            gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg 391
                                                                                                                         Human N-methyl-D-aspartate receptor subunit clone NMDA22
                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= NMDA_receptor_subunit
/note= "no termination codon"
                                                                                                                                                                                                                                                                                                                                       N-methyl-D-aspartate receptor; NMDAR2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Columns 253-262; 203pp; English.
Location/Qualifiers
                                                                                                                                                                                                                 AAV82909 standard; cDNA; 3698 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0231193.
93US-0052449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                .3698
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AAV82909
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/transl_except= (pos:3681..3683,aa:Xaa)
/note= "this sequence contains a number of in-frame
stop codons, represented by Xaa in the protein sequence"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human N-methyl-D-aspartate receptor subunit NMDAR1A coding sequence #17.
                                                                43. giggagotigoggiacgagaccgicgatccgiacgcggigoggctgacgitccaccicccc 102
                                                                                                                                                                                                                                                              282
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                                                                                               252 gigicociggagoagoagoigoigoigoigoigoigoigoigoigoigaagagiaogaoigago 311
                                                                                                                                                                                                                              431
                                                                                                                                                                                                                                                                                             491
                                                                                                                                                                                                                                                                                                                                                            551
                                 Gaps
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glutamate receptor; drug screening; animal model; disease diagnosis;
genetic screening; ss.
                                                                                                                                 103 ggagacgccccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac
                                                                                                                                                               312 geettegeegteateaceageetgeaceegggeeacgegetetteetggagggegtgege
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                                                                                                                                                                                                                                                                                               432 gacccgggagggccgcgcgcgcacgcagcctgctgctgcgccagctcgacgcgccgtg
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Length 3698;
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552 ggtctggtggggcccggccacgtgtggtggctggtgcccaacctggcgctgg 600
                                 Indels
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(pos:1431..1433,aa:xaa)
(pos:1503..1508,aa:xaa)
(pos:1770..1772,aa:xaa)
(pos:2136..2138,aa:xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (pos: 2232. 2237, aa. xaa)
(pos: 2529. 2531, aa. xaa)
(pos: 244. 2546, aa. xaa)
(pos: 3027. 3029, aa. xaa)
(pos: 3456. 3458, aa. xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (pos:1266..1268, aa:Xaa)
(pos:1266..1268, aa:Xaa)
(pos:1314..1316, aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                              343 gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         912..914, aa: xaa;
                                0; Mismatches 183;
Score 56.2; DB Pred. No. 0.12;
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(pos:1041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product- "NMDAR1A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA95032 standard; cDNA; 3698 BP
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/transl_except=
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 13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                 Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                Novel DNA fragment encoding human N-methyl-D-aspartate receptor subunit for identifying mutations and for developing drugs against various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctcccc 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggagacgccccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggac 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gccgcgggcgacggcgacgtccgggtctgcccggtggggcagacggccaccagggaggtg 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 gaccegggagggccgcgcgcgcgcacgcagcctgctgcgccagctcgacgcccgtg 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.8%; Score 56.2; DB 21; Length 3698; Best Local Similarity 47.6%; Pred. No. 0.12; Matches 166; Conservative 0; Mismatches 183; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3698 BP; 612 A; 1283 C; 1159 G; 644 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; column 255-264; 205pp; English.
                                                                                           97US-0940086
                                                                                                                              94US-0231193
93US-0052449
                                                                                                                                                                                           (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                       WPI; 2000-578607/54.
                                                                                                                                                                                                                                    Daggett LP, Lu C;
                                                                                                                                                                                                                                                                                           P-PSDB; AAB26239
                                                                                                                                                                                                                                                                                                                                                                          disease states
                                                                                                                                20-APR-1994;
20-APR-1993;
                                                                                           29-SEP-1997;
                US6111091-A.
                                                     29-AUG-2000
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Search completed: July 18, 2002, 11:36:31 Job time: 11256 sec

QY Db

492 tttgtggcctactgctcgcggaggaggccgaggtgctcttcgccgaggcggcgcaggcc 551

THIS PREE BLANK USPION

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(without alignments)
603.847 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43,
Sequence 43,
Sequence 43,
Sequence 43,
Sequence 53,
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Sequence 49,
Sequence 49,
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Sequence 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5
Sequence 5
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4
Sequence 4
Sequence 4
                                                                                                                    atgagetteetegteteega......gaggageageggeetg
                                                        July 18, 2002, 11:24:51; Search time 165.56 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
version 4.5
- 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-105-537-1
US-08-403-852D-14
US-08-401-1818-14
US-09-231-818-14
US-08-231-193A-43
US-08-480-474-43
US-08-490-035A-43
US-08-490-035A-53
US-08-490-035A-53
US-08-490-035A-53
US-08-940-035A-53
US-08-940-035A-53
US-08-940-035A-49
US-08-940-035A-49
US-08-940-035A-49
US-08-940-035A-47
                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                   383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                      nucleic search, using sw model
                                                                                                                                                 Gapop 10.0 , Gapext 1.0
GenCore (c) 1993
                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*
                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                US-09-749-185-4
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                                                                                                                                       IDENTITY_NUC
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3698
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Match 1
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                                      nucleic
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Maximum DB
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Sequence 51, Appl
Sequence 51, Appl
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Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 1, Appl
Sequence 1, Appl
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Sequence 1, Appl
Sequence 2, Appl
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Sequence 2, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cttcctcgtctccgaggagctcgccttccgcatcccggtggagctgcggtacgagaccgt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggtctgcccggtggggcagacggccaccagggaggtgcacatcaccctccaggtcggctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 cgagcaggcgctcttccgcgtcggcaaggcgccgctgctcgccttcctcgaccgcaccga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1615 gegeetegeegteetgtteageggeeagggtgeeeaacgtaegggeatggagtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 ccagggcttgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctcgacga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15872;
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JULY, H.
APPLICANT: LAW, Y.
APPLICANT: ALW, Y.
APPLICANT: Shao, L.
TILE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEO ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60.8; DB 4;
Pred. No. 0.00059;
0; Mismatches 202;
            US-08-940-035A-5

US-08-21-193A-51

US-08-480-474-51

US-08-940-086A-51

US-08-940-035A-51

US-08-231-193A-45

US-08-231-193A-45

US-08-480-273A-45

US-08-480-273A-45

US-08-940-035A-45

US-08-940-035A-15

US-08-940-035A-15
US-08-940-086A-5
US-08-940-035A-5
US-08-231-193A-51
US-08-486-273A-51
                                                                                                                                                                                                 US-09-103-840A-1
US-09-130-114-2
US-08-804-227C-7
                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces venezuelae US-09-105-537-1
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nilarity 47.4%;
Conservative
4068
4077
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4092
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30001
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2219
4411529
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Best Local Similarity
Matches 182; Conserv
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APPLICANT: Sherman,
 SEQ ID NO 1
LENGTH: 15872
                                                                                                                                                                                                                                                                                                                     US-09-105-537-1
 TYPE: DNA
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Sequence Sequence

Sequence

Sequence 47

Sequence 47 Sequence 47 Sequence 47

Sequence

265

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APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                     86 tgacgitccacciccccggagacgccccggicaccigggicttcggggcgigaactgctgg 145
                          146 tegagggagteetggaegeegeggggggaeggegaegteegggeeggtegggeaga 205
                                                                                                         221 CCGTCGGCAGCCCCGTCGCCGCCCGCCCACGACGCCCTCGACGACCTCGTGGGCTTCT 280
                                                                                                                                                                                                                                                  266 teggeaaggegeegetgetegeetteetegaeegeaeegaeeaggettgtegeteggea 325
                                                                                                                                                                                                         281 TCGTCAACACCCTCGTCCTGCGCACCGACCTCCGGCGACCCCACCTTCCGCGAACTCG 340
                                                                                                                                                                                                                                                                                            341 TCGCACGCGTGCGGCAGTTCGACCTCGCCGCCTACACGCACCAGGACATGCCGTTCGAAA 400
                                                                                                                                                                    SEE: Finnegan, Henderson, Farabow, Garrett & Dunner: 1300 I Street, N.W., Suite 700 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B FILING DATE: 03-AUG-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03806.0054-01000
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-510-646B-14; Sequence 14, Application US/08510646B patent 0. 6077699; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 036
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nathalie
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Thibaut, Denis
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Blanche, Francis
Crouzet, Joel
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2IP: 20005-3315
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                           386 ccgaggagcag 396
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STREET: 13
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COUNTRY:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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STREET: 1300 I Street, N.W., Suite 700
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Pred. No. 0.0039;
0; Mismatches 159; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DGCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/FR 93/00923 FILING DATE: 25-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 92/11441 FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
                                                                                                                                              Sequence 14, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
                                       1735 cetectegaceggeeectegeega 1758
  366 cgctctgaaccgcagcctcgccga 389
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                                                                                                                                                                                                                                                       Joel
Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%;
                                                                                                                                                                                                                                   Blanche, Francis
                                                                                                                                                                                                                                                                                                                                          Zagorec, Monique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: Z0005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                  Thibaut, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 474 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-403-852D-14
                                                                                                                                                                                                                               APPLICANT: Blanche,
APPLICANT: Crouzet,
APPLICANT: Jacques,
                                                                                                                                                                                                                                                                                                Lacroix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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                                                                                                      RESULT 2
US-08-403-852D-14
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Best Local Simi
Matches 152;
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APPLICANT:
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STRANDEDNESS:
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US-08-231-193A-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                    tgacgttccacctccccggagacgccccggtcacctgggtcttcggggcgtgaactgctgg 145
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VENTION: Polypeptides Involved In The
VENTION: Blosynthesis Of Streptogramins, Nucleotide S
VENTION: Coding For These Polypeptides And Their Use
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                                                                                                                                                                                                                                                                                                                                                 Length 474;
                                                                                                                                                                                                                                                                                                                                              Score 56.6; DB 3; Length 4
Pred. No. 0.0039;
0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                           /product= "Partie du gene SnbD"
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Patent No. 6171846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
                                                                                                                                                                                                           ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zagorec, Monique
Debussche, Laurent
                TELEFAX: (202) 408-4400 INFORMATION FOR SEQ 1D NO: 14: SEGUENCE CHARACTERISTICS: LENGTH: 474 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacques, Nathalie
Lacroix, Patricia
(202) 408-4000
                                                                                                                                                                                                                                                                                                                                              13.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thibaut, Denis APPLICANT: Zagorec, Monique
                                                                                                                                                                                                                                                                                                                                              Query Match 13.99
Best Local Similarity 48.99
Matches 152; Conservative
                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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; OTHER INFORMATION:
US-08-510-646B-14
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CITY: Washington
                                                                                                                                                                                                                                           NAME/KEY: CDS
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                                                                                                                                                     HYPOTHETICAL:
ANTI-SENSE:
TELEPHONE:
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APPLICANT:
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Pred. No. 0.0039;
0; Mismatches 159; Indels
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                                                                                           PatentIn Release #1.0, Version #1.30
                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATORNEY/AGENT INFORMATION:
NAME: MGYERS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/POCKET NUMBER: 25,146
RELECOMMUNICATION:
                                                                                                                                      US/09/231,818
COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 48.9%;
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 474 base pairs
nucleic acid
EDNESS: double
                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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NO
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US-09-231-818-14
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Sequence 43, Application US/08486273A
Patent No. 595586
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA
TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
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                                                                              552' GGTCTGGTGGGGCCCGGCCACGTGTGCTGCCCAACCTGGCGCTGG 600
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                                              343 'gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-FOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: NS/08/486,273A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
CLASSIFICATION 1435
ATTORNEY AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9383B
TELECOMUNICATION INFORMATION:
TELECHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 3...3698
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Best Local Similarity 47.6%;
Matches' 166; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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ZIP: 92101-2926
COMPUTER READABLE FORM:
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LOCATION:
US-08-486-273A-43
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                                                                                         APPLICANT: Daggett, Lorrie P.
APPLICANT: Elis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-chun W.
APPLICANT: Lu, Chin-chun W.
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 cacatcacctccaggtcggctccgagcaggcgctcttccgcgtcggcaaggcgccgctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-LOUS/MS-LOUS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION STA
ATTONNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 31,779
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 31,779
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 30,000
REGISTRATION NUMBER: 30,
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47.6%; Pred. No. 0.0044;
tive 0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 43, Application US/08231193A Patent No. 5849895 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Coding Sequence LOCATION: 3...3698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 166; Conserv.
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: SUBUNITS, NUCLBIC ACIDS ENCODING SAME AND USES THEREFOR TITLE OF INVENTION: 63
CORRESPONDENCE 63
ADDRESSEE: Heller Ehrman White & MCAULIffe
                                                                                                                                      491
                                                                                                                                                                                      283 ctcgccttcctcgaccgcaccgaccagggcttgtcgctcggcaggggaggggcacacgcc 342
  163 gccgcggggcgacggcgacgtccgggtctgcccggtggggcagacggccaccagggaggtg 222
                                                                                                                                                                                                                                 551
                                                                                           223 cacatcaccetecaggteggetecgageaggegetetteegegteggeaaggegeegetg
                                                                                                                               432 GACCCGGGAGGCCGCGCGCGCCCACGCCTGCTGCCGCCAGCTCGACGCCCCGTG
                                             372 GCCGTCGCCGACGCCACGCACGTGAGTTGGCGGCTGCTGGACGTGGTCACGCTGGAACTG
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 29-SEPT-97
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Heller Ehrman White & McAuliffe : 4250 Executive Square, 7th Floor La Jolla
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9383C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 29-SEPT-97
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 43, Application US/08940086A
; Patent No. 6111091
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Daggett, Lorrie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: (619) 450-8400 TELEFAX: (619) 450-8499 INFORMATION FOR SEQ ID NO: 43:
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LENGTH: 3698 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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APPLICANY: Ellis, Steven B.
APPLICANY: Liaw, Chen W.
APPLICANY: Liaw, Chin-chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSE: Brown, Martin, Haller & McClain
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223 cacatcaccetecaggicggetecgageageagegetettecgegteggeaaggegeegetg 282
                                                                                        43 gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctccc 102
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                                           432 GACCCGGGAGGGCCGCGCGCGCGCACGCGCCTGCTGCGCCCAGCTCGACGCGCCCGTG 491
                                                                                                                            252 GTGTCCCTGGAGCAGCAGCTGCTGCTGTTCAAGGTGCTGGAAGAGTACGACTGGAGC 311
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Pred. No. 0.0044;
0; Mismatches 183; Indels 0
                                                                                                                                                                                 343 gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg 391
                                                                                                                                                                                                                            552 GETCTGGTGGGGCCCCGCCACGTGTGGCTGCCCAACCTGGCGCTGG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                             Sequence 43, Application US/08480474 Patent No. 6033865 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 636
TELECOMMUNICATION: TELEPHONE: 619-238-0999
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Best Local Similarity 47.6%;
Matches 166; Conservative
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ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 3698 base pairs
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STRANDEDNESS: single
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; LOCATION:
US-08-480-474-43
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Sequence 53, Application US/08231193A
Patent No. 5849895
GENERAL INFORMATION:
APPLICANT: Diaw, Chen W.
APPLICANT: Liaw, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 TITGIGGCCIACTGCTCGCGCGAGGAGGCCGAGGTGCTCTTCGCCGAGGCGGCGCAGGCC
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                                                                                                                                                                                                                                                                                                             Score 56.2; DB 4; Length 3 Pred. No. 0.0044; 0; Mismatches 183; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
CLASSIFICATION: 536
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STREET: 1660 Union Street
                                                                                                                                           NAME/KEY: Coding Sequence LOCATION: 3...3698
                                                                                                                                                                                                                                                                                                                Query Match 13.8%;
Best Local Similarity 47.6%;
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NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,7
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
   STRANDEDNESS: single
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                                                                    MOLECULE TYPE: CDNA
                                           linear
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US-08-940-035A-43
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US-08-231-193A-53
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Patent No. 6316611
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                            491
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                                                                                                                                                                        252 GTGTCCCTGGAGCAGCAGCTGCAGGTGCTGTTCAAGGTGCTGGAAGAGTACGACTGGAGC 311
                                           Gaps
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47.6%; Pred. No. 0.0044;
tive 0; Mismatches 183; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, 7th Floor CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-SEPT-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6362-9383E
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seidman, Stephanie REGISTRATION NUMBER: 33,
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SEQUENCE CHARACTERISTICS:
LENGTH: 3698 base pairs
                                       Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     619-238-0062
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MEDIUM TYPE: Floppy
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       Best Local Similarity
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ZIP: 92037
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TYPE: nu
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US-08-480-474-53
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Sequence 53 Application US/08486273A
Batent No. 5985586
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA
TITLE OF INVENTION: BUCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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Pred. No. 0.0044;
0; Mismatches 183; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Brown, Martin, Haller & McClain
1660 Union Street
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APPLICATION NUMBER: US/08/486,273A
FILING DATE: 06-JUN-1995
REFERENCE/DOCKET NUMBER: 6362-9383
             TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                          Query Match 13.8%;
Best Local Similarity 47.6%;
Matches 166; Conservative
                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 189..3833
US-08-231-193A-53
                                                                                                                                           STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
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Sequence 53, Application US/08480474
Patent No. 6033865
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING TITLE OF INVENTION: SAME AND USES THEREFOR NUMBER OF SEQUENCES: 54
COMMERS POWDENCE STOWN, Martin, Haller & McClain
STREET: 1660 Union Street
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Pred. No. 0.0044;
0; Mismatches 183;
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/231,193
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
                                                                                                                                                      NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 4002 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.8%;
Best Local Similarity 47.6%;
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), NAME/KEY: CDS
; LOCATION: 189..3833
US-08-486-273A-53
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MOLECULE TYPE: cDNA
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CITY: San Diego
STATE: CA
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COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             Floppy disk
                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
         La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    both
                                                                                            MEDIUM TYPE:
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                                                         92037
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US-08-940-086A-53
                                                                                                                                                  SOFTWARE:
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                                           COUNTRY:
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APPLICANT: Ells, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-chu W.
APPLICANT: Lu, Chin-chu W.
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIALS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/480,474
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56.2; DB 3;
Pred. No. 0.0044;
0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Heller Ehrman White & McAuliffe 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                      6362-9382B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/08940086A Patent No. 6111091 GENERAL INFORMATION:
                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0062
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             189..3833
                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                          both
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                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-08-480-474-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%; Score 56.2; DB 3; Length 4 47.6%; Pred. No. 0.0044; tive 0; Mismatches 183; Indels
Patentin Release #1.0, Version #1.25
              SOUTHWRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,086A
FILING DATE: 29-SEPT-97
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
ATTORNEY AGGNT INFORMATION:
NAME: Seldman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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US-08-940-035A-53
Sequence 53, Application US/08940035A
Patent No. 6316611
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 450-8499 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 4002 base palrs
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Best Local Similarity 47.6
Matches 166; Conservative
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APPLICANT: Daggett, Lorrie P.
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: HUMAN N-WETHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 gtggagctgcggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctcccc 102
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Pred. No. 0.0044;
0; Mismatches 183; Indels 0
                       343 gacttcgacagccacctcgacgacgctctgaaccgcagcctcgccgagg 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
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APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                             RESULT 15
18-00-231-193A-49
Sequence 49, Application US/08231193A
Patent No. 5849895
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NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/POCKET NUMBER: 6362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEPA: 619-238-0062
INFORMATION FOR SEO ID NO: 49: SEQUENCE CHARACTERISTICS:
LENGTH: 4017 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92101-2926
COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 47.69
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 92101-2926
                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dagget
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US-08-231-193A-49
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                                            APPLICANT: Liaw, Chen W.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
UNMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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Pred. No. 0.0044;
0; Mismatches 183; Indels 0
                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,035A
FILING DATE: 29-SEPT-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
                                                                                                                                                                              E: Heller Ehrman White & McAuliffe 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6362-9383E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
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NAME: Setionan, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362
FELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0099
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 4002 base pairs TYPE: nucleic acid STRANDENESS: both
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,779
Daggett, Lorrie P. Ellis, Steven B. Liaw, Chen W.
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Matches 166; Conservative
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; LOCATION: 189..3833
US-08-940-035A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                   STREET: 4250 EXCITY: La Jolla
                                                                                                                                                                                                                                                                                            92037
                                                                                                                                                                              ADDRESSEE:
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Search completed: July 18, 2002, 11:25:01 Job time: 10891 sec

AQ851215 LMAJFV1_ BG263173 WHE2337_ AQ848096 LMAJFV1_

Perfect score:

ou:

Scoring table: Sequence:

Searched:

Database

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- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp., the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                     BI726984 1031088H0
AL106054 Drosophil
BG366417 HVSME1000
AL066742 Drosophil
BE230578 99AS792 R
ALS049222 RANJFYL_1
BARS49292 LAMJFYL_1
BARS5934 HVSMEN001
AL50999 AL50999 AL50999 AL509103 AL509903 BF5837 HVSME1000
BF483973 WHE2306_G
BES5537 HVSME1000
BF483973 WHE2306_G
BES5537 HVSME1000
BF58537 HVSME1000
BF58537 HVSME1000
BF58537 HVSME1000
BF58537 HVSME1000
BF58537 HVSME1000
BF5859130 LG1_224_G
BG357931 OV2_31_C
AL066742 Drosophil
BG585950 WHE3443_C
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPC1-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope.

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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BI953854
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 BF266913 HV_CEa001
AG076818 Pan trog1
AG851336 LMA.FV1_1
BM325544 PTC1_34_C
BM325544 PTC1_45_H
BG809984 mgctC02xd
BE490147 WHE0366_A
                                                                                                                 (without alignments)
1139.217 Million cell updates/sec
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A0846145 LMAJFV1_1
B2496986 WHE0763_A
BE593775 WS1_102_A
AV938413 AV938413
ALSO8175 ALSO8175
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AL053013 Drosophil
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Lutter( 202-JUN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- who is www.genoscope.cns.fr)

- betermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="RPCI-98"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RRCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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NS / Beverley, SM
 Contact: Akopyants, NS /
WashU Leishmania Project
                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing: a resource for DNA microarrays and expression
and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSGSSGCSCCSCCSCSSSSSSSCSCCCCCCCCGCGMSMCSGCGGGSSCGGCCSGCCCSCCCCCSSCCCC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ846145
LMAJFV1_Im15c01.y1 Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm15c01 5' similar to contains element 212bp.2 leishmania repetitive element ; DNA
                                                                                                                                                                                                                                                                                                                                                  83 ggctgacgttccacctccccggagacgccccggtcacctgggtcttcgggcgtgaactgc 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tagtcgagggagtcctggacgccgcggggcgacggcgacgtccgggtctgcccggtggggc 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcagcgagcggggcacacgccgacttcgacagccacctcgacgacgctctgaaccgcagcc 382
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            gcgtcggcaaggcgccgctgctcgccttcctcgaccgcaccagggcttgtcgctcg
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Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
1 (bases 1 to 390)
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                                                                                                                                                                                                                                                       Length 935;
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Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
21192569
                                                                      1. .935
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/clone_lib="RPCI-98"
/clone="BACR14N09"
/note="end: T7"
                                                                                                                                                                                   250
                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                           Conservative 104; Mismatches 165;
                                                                                                                                                                                                                                                                        Pred. No. 0.88;
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                                                                                                                                                                                                                                                       15.8%; Score 64.2; 29.5%; Pred. No. 0.8
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/clone="LMAJFV1_Im15c01"
/clone="LMAJFV1_Im15c01"
/clone=lib="Leishmania major FV1 random genomic library"
/lab_host="TOP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline Phosphatase and ligated into pZero-2 vector's EcoRV site."

12 c 167 g 30 t
                                                                                                                                                                            DNA Sequencing by: Washington University Genome Sequencing Center If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain VI genome by shotgun sequencing' and the Washington University Genome Sequencing Center For information on obtaining clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgtcgatccgtacgcggtgcggctgacgttccacctccccggagacgccccggtcacctg 122
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WHE0763_A05_A092S Wheat heat stressed seedling cDNA library Triticum aestivum cDNA clone WHE0763_A05_A09, mRNA sequence. BE496986.1 GI:9695603
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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                                                                                                                                                         Ph.D.
                                                                                                                           Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%; Score 58.8; DB 12;
llarity 48.8%; Pred. No. 5.6;
Conservative 0; Mismatches 167;
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Location/Qualifiers
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/organism="Leishmania
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/cultivar="Chinese Spring"
/cultivar="Chinese Spring"
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                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae; Proideae; Triticeae; Triticea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 ggtcgagggagtcctggacgccgcgggcgacgcgacgtccgggtctgcccggtggggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 gacggccaccagggaggtgcacatcacctccaggtcggctccgagcaggcgctcttccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 GAAGGCCGGCGCCCGAGGTCCTCAATGGCCTCTTCCTAAGGTATGAGGCCCCCGAAGGAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 510555818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
gquality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58.8; DB 10;
Pred. No. 5.6;
0; Mismatches 202;
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Best Local Similarity 47.1%;
Matches 180; Conservative 0
                                                                                    Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
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                                   SOURCE
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COMMENT
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                                                                                                                                                                                                                                                                                               AUTHORS
KEYWORDS
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/ Gostantsm="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WSI)"
/clone_lib="Water-stressed 1 (WSI)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after-water was withheld; Vector: Lambda Zap; Site_l: XhoI;
water was withheld; Vector: Lambda Zap; Site_l: XhoI;
Site_l: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
a 168 c 225 g 128 t
                                                                                                                                                                                                                                      WS1_102_A08.gl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caccttccaggtcggtccgagcaggcgtttccgcgtcggcaggcgcgttgctgc 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 gcrerricegicaderegicegececederricadececedadecedecererregica 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gotgoggtacgagaccgtcgatccgtacgcggtgcggctgacgttccacctccccggaga 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  egococegicacotegggtcttcegggcgtgaactgctggtcgagggagtcctggacgccgc 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 gggcgacggcgacgtccgggtctgcccggtggggcagacggccaccaggggaggtgcacat 227
                          414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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355 - CGAGAAGGGGTCGTTCGAGGTGGACGCGATCGTGGGCGCGGACGGCGCTTCCCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An EST database from Sorghum: water-stressed plants Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-Plant 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.4%; Score 58.6; D 50.8%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 605)
Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is 20.
Seq primer: PolyTMix
High quality sequence start: 98
High quality sequence stop: 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                384 cgccgaggagcagagcggc 405
                                                                                                                                415 GCCCAAGGACATGGGCGCGGGC 436
                                                                                                                                                                                                                                                                                                                                                                       GI:9848848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 167; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       BE593775.1
                                                                                                                                                                                                                                                                                                                                                                                                                             sorghum.
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us-09-749-185-4.rst

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Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp. 3 others
                                                                                                                                                                                                                                              AL508175 623 bp mRNA linear EST 04-JAN-2001 AL508175 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY07P24V 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aichalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Unpublished (2000)
Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Corrensstr. 3, D-0646 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: 73 primer for 5'end.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
XhoI; mRNA was made from developing caryopsis (3.-15.DAP)
of spring barley variety 'Barke', a high quality malting
variety. Cloning sites: EcoRI (5'-end of CDNA) and XhoI
(3'-end of cDNA). NOTE: Due to a cloning artefact caused
by the kit, in most cases the EcoRI site is NOT present,
as well as the EcoRI adapter. Average insert size is 1 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib-"Hordeum vulgare Barke developing caryopsis (3.-15.DAP)" //issue_type="developing caryopsis (3.-15.DAP)" //lab_host="XLOLR"
59 GCTCTGCATGGNGTCCGAGTTCGACCTGCCGCTGGACCTCGTCGACAGAGGGTCACCAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GATGAAGATGATTTCGCCCTCCAACGTCGCCGTCGACATCGGCCGCACGCTCGCGCCGCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 CGAGTACATTGGCATGGTCAGGCGCGAGGTGCTCGACGACTTCCTCCGTACCTGGCGCGCAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gctcgccttccgcatcccggtggagctgcggtacgagaccgtcgatccgtacgcggtgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gotgacgttccacctccccggagacgccccggtcacctgggtcttcggggcgtgaactgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggtcgagggagtcctggacgccgcgggcgacgcggcgacgtccgggtctgcccggtggggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .623
/organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Barke"
/db_xref="taxon:4513"
/clone="HY07P24V"
                                                                                                                                                                                                                                                                                                                    AL508175
AL508175.1 GI:12034390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.9%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 623)
                                                                                                                                                                                                                                                                                                                                                                                      barley.
Hordeum vulgare
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                                                                                           402 cqqc 405
                                                                                                                                     374
                                                                                                                                     371 GGGC
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                                                                                                                                                                                                                                                                     DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
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                                                                                                                                                                                                         RESULT ALSO8175
                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
SOURCE
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                                            Dp
                                                                                                                                     ΩD
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                                                                                                                                                                                                                                         AV938413 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum AV938413
                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplanta; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, Pooldeae
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/clone_lib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
186 c 183 g 82 t
                                                   cggagacgccccggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctgga 161
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1 (bases 1 to 566)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
121 81-559-81-6856
Fax: 81-559-81-6855
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Pred. No. 6.4;
); Mismatches 191;
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                                                                                                                                         /db_xref="taxon:77009"
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Location/Qualifiers
1. .566
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14.3%;
Best Local Similarity 47.5%;
Matches 173; Conservative
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-ad sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cnbw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be located the cond at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                        B44 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACKIL116 of RPCI-98 library from Drosophila melanogaster (fruit AL056652
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324 cagcgagcggcacacgccgacttcgacagccacctcgacgacgctctgaaccgcagct 383
                                                                                                                                                             CAACGGCACGTACACGGTGCACTACAACCACTACGACAGCTCCAACGCAAGGTGGGCGG 358
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                                                            cgtcggcaaggcgccgctgctcgccttcctcgaccgcaccgaccagggcttgtcgctcgg
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/db_xref="taxon:7227"
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112 c 92 g
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/note="Vector: lambdaZAP; Site_1: ECOR1; Site_2: Xhol; /note="Vector: lambdaZAP; Site_1: ECOR1; Site_2: Xhol; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns triamed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified CDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (WING, YU, Frisch, Henry, Simmons, Oates, Rambo, Main).
                                                                                                                                                                                                                                                                                                                                                                                                   BE603206 53.2 bp mRNA linear EST 22-OCT-2001
HVSMEh0102H24f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0102H24f,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Hordeum vulgare 5-45 DAP spike EST library HvcDnA0009 ($ 10.0 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                         248
129 cgggcgtgaactgctggtcgagggagtcctggacgccgcggggcgacggcgacgtccgggt 188
                                   189 ctgcccggtgggggaggcaccagggaggtgcacatcacctccaggtcggctccga
                                                                                                                                          /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0102H24f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Total hq bases = 418
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 7
High quality sequence stop: 528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BE603206
BE603206.2 GI:13191055
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High quality sequence stop: (
Location/Qualifiers
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Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 473
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al Similarity 46.9%;
179; Conservative
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
1 (bases 1 to 761)
                                                                                                                                                                                                                                                                                                                              ;
0
                                                          http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 166 c 179 g 78 t l others
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Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla13) unpublished (2001)

On Nov 17, 2000 this sequence version replaced gi:11197908.
      or
and contains a minimum of 100 bases of phred value 20 above. For more details on library preparation and
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                                                                                                                                                                                                                                                                                                                                                                      24 gctcgccttccgcatcccggtggagctgcggtacgagaccgtcgatccgtacgcggtgcg
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100 Jordan Hall, Clemson, SC 29634, USA
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Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                 Score 57.2; DE Pred. No. 9.6;
                                            sequence analysis see
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46.98;
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/note="Vector: lambdaZAP; Site_1: ECOR1; Site_2: Xhol; /note="Vector: lambdaZAP; Site_1: ECOR1; Site_2: Xhol; C.I. 16155 (Mla13) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate A27 (AvrMla13) of Blumeria grammins f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson indivored.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/corders Also see Close TJ, wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 237 c 271 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
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                                                                                                                                                                                                                                                                                        /clone="HV_CEa0016G14f"
/clone_llb="Hordeum vulgare seedling green leaf EST
/lbrary HVCDNA0004 (Blumeria challenged)"
/tissue_type="seedling green leaf"
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Pred. No. 9.4;
0; Mismatches 203;
                                                                                                                                                                  /organism="Hordeum vulgare"
/cultivar="C116155 (Mla13)"
/db_xref="taxon:4513"
Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                                                                                                                                                                                       GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-071C05.R.
Pan troglodytes
                                                                                                                                                                                  GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC endwas generated during the R&D process and may have higher chance of
                                                                                                                                                                     AGU76818 1152 bp DNA linear GSS 03-NOV-200.
Pan troglodytes DNA, clone: PTB-071C05.R, genomic survey sequence.
AG076818
                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
79 gtgcggctgacgttccacctccccggagacgccccggtcacctgggtcttcgggcgtgaa 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fuliyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /scal_type="lymphoblast"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC 3
488 c 514 g 23 t 93 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.1%; Score 57.2; DB 12; Best Local Similarity 46.5%; Pred. No. 9.3; Matches 152; Conservative 0; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site 1 : SacI
Site 2 : SacI.
Location/Qualifiers
1 . 1152
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-071C05.R"
/sex="male"
                                                                                        530 GGCCAAAGATATGGCCGCGGGC 551
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                                                       384 cgccgaggagcagagcgccggc
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DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite;
If using this information please cite;
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu)
Seq primer: -40RP from Gibco
Class: shotgun
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I (bases I to 474)

Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L.,

Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A.,

Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, T., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M.,

Harvey, N., McCann, R., Tsagarelshvill, R., Willams, T., Jackson, Y.,

Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M.,

A survey of the Leishmania major Friedlin strain VI genome by
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                                                                                                         319 ctcggcagcgagcgcacacgccgacttcgacagccactcgacgcgctctgaaccgc 378
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                         Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Contact: Akopyants, NS / Beverley, SM
WashU Leishmania Project
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:6055984
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Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20. Three-prime sequences, which are obtained with PolyTMix or
T7 sequencing primer, are presented as the reverse complement.
High quality sequence stop: 469
POLYA-No.
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An EST database from Sorghum: plants infected with a compatible
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                6 cttcctcgtctccgaggagctcgccttccgcatcccggtggagctgcggtacgagaccgt 65
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/clone_lib="Pathogen infected compatible 1 (PIC1)"
/tissue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
Colletotrichum graminicola"
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   Length 474;
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Score 55.6; DB 12;
Pred. No. 17;
); Mismatches 154;
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Contact: Cordonnier-Pratt MM
Department of Botany
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.

(Dases 1 to 615)
Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C., Dean, R., Wing, R.,
Sudman, M. and Pratt, L.H.
An EST database from Sorghum: plants infected with a compatible
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PIC1_45_H11.b1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum
bicolor cDNA, mRNA sequence.
/note="Vector: pBluescript II SK(-) from Lambda Zap II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 ggtcacctgggtcttcgggcgtgaactgctggtcgagggagtcctggacgccgcggggga 173
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Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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Pred. No. 19;
0; Mismatches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 706 542 1860
Fax: 706 542 1805
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T7 sequencing primer, are presented as the reverse complement. Seq primer: JEN REV High quality sequence stop: 607 POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 TCTCGAGGTCAAGCAGCGGACGGTGTCGGACAAGGGGCAGTTCAGAGGCTACATCGGCCA 297
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                                                                                                                                                                                                                                                                                    /organism="Sorghum bicolor"/cultivar="BTx623"
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                      .615
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Search completed: July 18, 2002, 10:12:49 Job time: 9969 sec

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July 18, 2002, 14:15:01; Search time 130.38 Seconds (without alignments) 115.010 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                     747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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687
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Perfect score:
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| SIDSS/gcddata/geneseqp/geneseqp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	treptomyces albus	reptomyces golde	Streptomyces grise	reptomyces netro	abidopsis thalia	Arabidopsis thalia	pylori ORF 02qe	osophila melanog	elicobacter pylor	. epidermidis ope	Putative P. abyssi
SUMMARIES		AAY44650 St	0,	0,			AAG35779 Ar					AB96082 Pu
	a ID	21 A	21 A	21 A	21 A	21 A			22 A	~	22 P	22 P
	% Query Match Length DB	135	135	135	135	257					309	344
	% Query Match	100.0	70.0	67.5	64.9	11.4	11.4	11.1	11.1	11.0	10.9	10.8
	Score	687	481	464	446	78	78	76.5	16	75.5	75	74.5
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AAU56042 AAB48832 AAU30706 AAW34764 AAU57583 AAW78247	AAB15495 AAY 2167 AAB47047 AAB99599 AAW99599 AAW94763 AAW94765 AAB28377 AAG73991	AAW14287 AAY70071 AAY69622 AAW85025 AAW85013 AAW85013 AAW85994 AAY23960	AAX 67527 AAX 87407 AAR 05041 AAB 5334 AAB 02005 AAB 9308 AAB 4308
	22 20 20 20 20 20 20 20 20 20 20 20 20 2		
540 623 7478 790 717	773 1241 1241 1558 478 478 478 478 478	2555 2555 2755 1256 1256 1256	1248 3596 3647 231 1063 1134 623
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113 114 114 114	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	

T 1 650 AAY44650 standard; Protein; 135 AA AAY44650; 18-APR-2000 (first entry) Streptomyces albus G SsgA protein.
T 1 650 AAY44650; AAY44650; 18-APR-20i Streptomy

ALIGNMENTS

SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoctr; bioinsecticide; receptor agonist; antagonist; blomass.

Streptomyces albus G

WO200000613-A1 06-JAN-2000. 99WO-NL00395 25-JUN-1999;

98EP-0202148 26-JUN-1998; (UYLE-) RIJKSUNIV LEIDEN. (NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.

Luiten RGM; Van Wezel GP, Kraal B,

WPI; 2000-147269/13. N-PSDB; AAZ49729.

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25-JUN-1999;
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                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                           AAY44649;
                                                                                                                                                        Query Match
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Matches 9
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                                                   The present sequence is S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                         VRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                          1 MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antimigraine agent; ruminant growth promoter; biolnsecticide; receptor agonts; antagonist; blomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SsgA; liquid culture; filamentous bacteria; secondary metabolite;
Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                    Length 135;
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                                                                                                                                                                                                   100.0%; Score 687; DB 21; 100.0%; Pred. No. 4.1e-75;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces goldeniensis SsgA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                              AAY44651 standard; Protein; 135 AA.
                                Disclosure; Fig 5; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces goldeniensis.
                                                                                                                                                                                                                         Matches 135; Conservative
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                                                                                                                                                                                                            Similarity
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                                                                                                                                                                   Sequence
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                                                                                                                                                                                                    Query Match
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The present sequence is S. griseus SagA protein. SagA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous
                                  mycelium
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The present sequence is S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycel in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antiblotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, immunosuppressive antiparaine agents, bioinsecticides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SsgA. liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosupressive agent; mypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%; Score 481; DB 21; Length 135; 71.1%; Pred. No. 3.6e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
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N-PSDB; AAZ49727, AAZ49728.
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|dealdrilaeeqnag 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                          135 AA;
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99US-0134370
99US-0134768
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121 eaalgkilaeeqnag 135
                                                                                                                                                                                                                                                                                                                                                                                                                  termination sequence
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                                      135 AA;
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06-APR-1999;
08-APR-1999;
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30-APR-1999;
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05-MAY-1999;
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06-MAY-1999;
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bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents,
                                                                                                                                                                                                                          61 VRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SsgA; liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                     Length 135;
                                                                                                                                           Indels
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NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                   Score 464; DB 21;
Pred. No. 4.1e-48;
8; Mismatches 28;
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                                                                                                                                           18;
                                                                                                                    67.5%;
65.9%;
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edalgrilaeeqnag 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces netropsis
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                                                                                                                               Similarity
                                                                                   AA;
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Best Local Simi
Matches 89;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass
                                                                                                              Length 135;
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                                                                                                              64.9%; Score 446; DB 21; 63.0%; Pred. No. 6.2e-46; ive 20; Mismatches 30;
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99US-0128134
99US-01281714
99US-0139845.
99US-0130077
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99US-0130891.
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99US-0134218.
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                                                                                                                                Similarity 63.0 S5; Conservative
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90S - 0134941 90S - 0135124 90S - 0135233 90S - 013623 90S - 0136782 90S - 013722 90S - 0137528 90S - 0137504 90S - 0137604 90S - 0137604	990S-013451.9 990S-013451.9 990S-013452.9 990S-013454.9 990S-013455.9 990S-013456.9 990S-013456.9 990S-013458.9 990S-013459.9 990S-0139461.9 990S-0139461.9 990S-0139461.9 990S-0139461.9 990S-0139462.9 990S-0139462.9 990S-0139763.9 990S-014083.9 990S-014089.9 990S-014083.9 990S-014083.9 990S-014083.9 990S-014083.9 990S-014083.9 990S-014083.9 990S-014287.9	90S - 0142977 90S - 0143542 90S - 0144005 90S - 0144086 90S - 0144332 90S - 0144333 90S - 0144334 90S - 0144334 90S - 0144334 90S - 0144352 90S - 0146352 90S - 0145087 90S - 0145087
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9905 - 0136021
9905 - 0136392
9905 - 0137222
9905 - 0137228
9905 - 0137528
9905 - 0137724
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14 - JUN - 1999;
16 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                    50 ECVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGS 109
                                                                                                22; Gaps
                                                                                                                                      39 dgtsdsdsdpdppk-pegdtrrqellari-----amigtskvrltdflderseyltkfa 91
                                                                          Query Match 11.4%; Score 78; DB 21; Length 257; Best Local Similarity 29.7%; Pred. No. 0.53; Matches 30; Conservative 14; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 43757.
                                                                                                                                                                          110 ERAHADFD-----SHLDDALNRSL-----AEEQSAG 135
                                                                                                                                                                                                                                        AAG35779 standard; Protein; 258 AA
           990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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990x-012548
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26-0CT-1999;
26-0CT-1999;
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99US-0161361.
99US-0161920.
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28-OCT-1999;
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This sequence is a H. pylori cellular protein.

The protein may be used in a vaccine to prevent or treat H. pylori cellular protein.

The protein may be used in a vaccine to prevent or treat H. pylori for the cycle activators or inhibitors. The useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (APCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for one of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF
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                                                                                                                                                  EGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGS 109
                                                                                                               Gaps
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                                                                       ; DB 21; Length 258;
. 0.54;
tches 35; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H. pylori ORF 02gel0116_23866562_c3_146 cellular protein.
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                                                                                                                                                                                                                                                        93 eeanaefdkvgedamkdldeastrilenieskmqafeesag 133
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                                                                                              Best Local Similarity 29.7%; Pred. No. 0.54 Matches 30; Conservative 14; Mismatches
                                                                           11.4%; Score 78; 29.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                        AAW55684 standard; Protein; 632
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96US-0625811.
96US-0758731.
96US-0736905.
96US-0738859.
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28-OCT-1999;
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29-MAR-1996
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                           44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                               11;
                                                                                                                                    Length 632;
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                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 6642.
                                                                                                                                  DB 18;
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                                                                                                                                                                                                                                                    102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                       Score 76.5; D. Pred. No. 2.8;
                                                                                                                                                               15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         ABB59950 standard; Protein; 736 AA.
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                                                                                                                                  11.1%; 29.9%;
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                                                                                                Local Similarity
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                                                                                        632 AA;
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736 AA;

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                                                                                                         272 fttsngsvfriglgngve-vdpeeinvtfedvkgcdeakgelkevveflkspekfsnlgg 330
                                                                                                                                                                              331 klpkgvllvgppgtgktllarav---ageakvpffhaagpefdevlvgggarrvrdlfka 387
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                                     Gaps
                                                                     ---HLPG 35
                                                                                                                                          36 DAPVTWVF-----GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRV 89
                                     46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides for the identification and development of
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Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibiotics, comprise sequences of antisense nucleic acids
                                     Indels
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                                   62;
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DB 22;
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                                   24; Mismatches
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11.1%; Score 76; 23.3%; Pred. No.
                                                                     3 FLVSEELAFRIPVELRYETVDPYAVRLTF----
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2000US-253625P.
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2001US-269308P.
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                Best Local Similarity 23.39
Matches 40; Conservative
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27-NOV-2000;
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16-FEB-2001;
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Yamamoto RT,
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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                           AAB96082;
                                                                                                                            Query Match
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                                                                                                                                          Best Local
Matches 2
                                                                                                                                                                                                                                    . 65
                                                                                                                                                                                                                                                                                                                    AAB96082
     888888888
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                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                             ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the september of vectors on taining them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides may also be used to assay for other inhibitors of their The polypeptides may also be used to assay for other inhibitors of their creatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA AAH55090 represent oligonucleotide sequences from the present invention. AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                     4;
                                                                                                                                                                                                              44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                   11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

    S. epidermidis open reading frame protein sequence SEQ ID NO:1608.

    a wide variety of organisms. The present sequence represents an
                                                                                                                                         Length 632;
               essential prokaryotic cellular proliferation protein.
Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic
format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                   Indels
                                                                                                                                         DB 22;
                                                                                                                                                                  42;
                                                                                                                                                                                                                                                 102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                 Score 75.5; DB
Pred. No. 3.6;
5; Mismatches
                                                                     ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                             AAG82257 standard; Protein; 309
                                                                                                                                                                  15;
                                                                                                                                       11.08; 29.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-2000; 2000WO-US30782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                       Best Local Similarity
                                                                                                632 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH53107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200134809-A2.
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                                                                                                                                                                  29;
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                                                                                                                                                                                                                                                                                                                                                                        AAG82257;
                                                                                                 Sequence
                                                                                                                                       Query Match
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                                                                                                                                                                  Matches
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                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: This patent is in the same patent family as WO200055062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                   FRIPVELRYETVD--PYAVR----LIFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVC 64
                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide sequences isolated from Pyrococcus abyssi encode
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                                                                             Length 309;
                                                                                                                              37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative P. abyssi ATPase subunit of ABC transporter #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forterre P, Thierry JC, Prieur D, Dietrich J, 1
Querellou J, Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                          10.9%; Score 75; DB 22; 28.1%; Pred. No. 1.6; Live 13; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 74.5; Di
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Pages 705-706; 1657pp; French.
                                                                                                                                                                                                                                                                                                                                                134 nvginptrsgildivkqmggnielsnvsk 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                           PVGQTATRE - - VHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB96082 standard; Protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; 27.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins useful in industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                 Conservative
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Best Local Similarity
                                                                                                        Similarity
309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 AA;
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us-09-749-185-5.rag

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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by a canes. The groteins and diagnosis of medical conditions caused by pertosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and diagnostic agents for determining P. acnes in the antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; udeltis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                            SFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGV----LDAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
  35; Gaps
                                                                                                                 G------DGDVRVC------PVGQTATREVHITLQVGSEQ-----ALFRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhatia A;
  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #16938.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitcham JL, Wany
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID No 17237; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW, Persing DH, Mitcham J
L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                                                                                                                                                                 AAU56042 standard; Protein; 540 AA.
                                                                                                                                                                                           91 KAPLLAFLDRT---DQGLSLGSE 110
                                                                                                                                                                                                                                  309 gitlkafitrsslielgisegre 331
18;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2002 (first entry)
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200181581-A2.
39;
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  Matches
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                             211 qiyystadgvderddvelptdahthmswafskpgvykavfaa----tlstpqgnasfga 265
                                                                                                                                                                                                                                                                       74 VHITLQVGSEQALFRVGKAPLLAFLDRT--DQGLSLGSERAHADFDSHLDDALNRSLAEE 131
                                                                                                                                                                                                16 ELRYETVDPYAVRLTFHLPGDA--PVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTATRE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid molecule encoding polypeptide having pyranose oxidase activity used to design oligonucleotide probes to identify a clone DNA encoding the polypeptide from different genera or species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyranose oxidase, expression construct, recombinant production, monosaccharide oxidation; 2-keto derivative; hydrogen peroxide production.
                                                                                                                                                               24;
                                                                                                                          10.8%; Score 74; DB 22; Length 540; 25.8%; Pred. No. 4.5;
                                                                                                                                                               51; Indels
                                                                                                                                                               17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB48832 standard; Protein; 622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trametes hirsuta pyranose oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                               32; Conservative
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                                                                                                                                              Similarity
                                                                          540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trametes hirsuta.
                                                                                                                                                                                                                                                                                                                                           132 QSAG 135
                                                                                                                                                                                                                                                                                                                                                                              311 tggg 314
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                                                                           Sequence
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416 AA;
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            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS9510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
(fungi or bacteria). The present sequence represents pyranose oxidase from the fungus Trametes hirsuta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                              26 AVRLTFHL-----PGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQ 79
                                                                                                                                                                                                                                                                                                                                                                       22 akratahslpplpgpgdlp-----pgmnveydvalvgsg-----pigctyarel---ve 67
                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                             Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 VGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAH-ADFDSHLDDALN 125
                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                             DB 22;
                                                                                                                                                                                Query Match 10.8%; Score /4; LL L. Best Local Similarity 26.2%; Pred. No. 5.4; Matches 28; Conservative 17; Mismatches
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26-JAN-2001; 2001US-0770160
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                                                                                                 622 AA;
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                                                                                                                                                             133. pv11teaplnpkanrekmtgilcfetfntpghvp--wpiqavls1xs1waqp1givmdsg 190
                                                                                                                                                                                                                                         || || || : : || :| || :: |
191.dgvthtvpilrgattllhailrlg------pgla-rdltdylmkiltergys-ft 237
                                                                                                                                                                                                              58 DGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovalicin; fumagillin; type 2 methionine aminopeptidase; inhibitor;
MetAP2; angiogenesis; tumour; diabetic retinopathy; arteriosclerosis;
inflammatory disease; immune reaction; autoimmune disease; allergy;
                                                      Gaps
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                                                   31;
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methionine amino-peptidase, useful for treating or diagnosing
diseases involving abnormal angiogenesis or immune reactions
  Length 416;
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                                                      40;
  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat type 2 methionine aminopeptidase (MetAP2).
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Pred. No. 5.7;
0; Mismatches
Score 73.5; D
Pred. No. 3.6;
                                                      18; Mismatches
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illarity 28.8%;
Conservative 2
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inflammatory disease; immune
tissue graft rejection; rat.
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Db 242 lgyddi----ckidfgthisgriidcaftvtfnpkydillkavkdatntgikcagidvrl 297
Qy 64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
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Search completed: July 18, 2002, 14:15:02 Job time: 10332 sec

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; ORGANISM: Coriolus Versicolor
US-09-305-381-2
TYPE: PRT
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/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-040-774-2
US-09-040-774-2
US-09-093-448-1
US-08-093-448-1
US-08-01-532-2
US-08-01-1582D-14
US-09-005-532-2
US-08-06-76B-9
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US-08-465-965-17
US-08-465-965-17
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US-08-465-966-17
US-08-468-884-8
US-08-127-499A-8
US-08-127-499A-8
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US-09-320-878-3
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                                                                                                                                                                  hits satisfying chosen parameters:
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                                                                                                                                                  231628 seqs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext
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28 65.5 9.5 989 4 US-09-199-637A-273 Sequence 273, Appl 29 65 9.5 184 2 US-08-199-637B-12 Sequence 10, Appl 31 64.5 9.4 416 2 US-08-993-22B-12 Sequence 12, Appl 32 64.5 9.4 411 6 2 US-09-188-7 Sequence 302, Appl 32 64.5 9.4 416 2 US-09-188-7 Sequence 302, Appl 33 64.5 9.4 466 2 US-08-995-138-7 Sequence 2, Appl 33 64.5 9.4 106.4 US-08-080-044-2 Sequence 2, Appl 35 64 9.3 1064 2 US-08-092-2 Sequence 2, Appl 36 64 9.3 1064 2 US-09-093-289-5 Sequence 2, Appl 39 64 9.3 1082 1 US-08-357-598-5 Sequence 2, Appl 39 64 9.3 1082 1 US-08-357-598-5 Sequence 5, Appl 39 64 9.3 1082 1 US-08-357-598-10 Sequence 5, Appl 41 64 9.3 1082 2 US-09-003-289-5 Sequence 5, Appl 41 64 9.3 1082 2 US-09-003-289-10 Sequence 10, Appl 42 64 9.3 1082 5 PCT-US95-16435-10 Sequence 10, Appl 44 63.5 9.2 992 1 US-08-127-493A-1 Sequence 1, Appl 44 63.5 9.2 105-08-093-453B-3 Sequence 3, Appl 14 63.5 9.2 105-08-093-453B-3 Sequence 3, Appl 14 63.5 9.2 105-08-093-453B-3 Sequence 3, Appl 1
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ALIGNMENTS

us-09-749-185-5.rai

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Sequence 1, Application US/09093448A
Patent No. 6207704
GENERAL INFORMATION:
APPLICANT: Liu, Jun O.
APPLICANT: Su, Zhuang
TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
FILE REFERENCE: 0492611-0346
    103 LSDDAEYECQVGRSEMGPELVSPRVI-LSILVPPKLLLLTPEAGTMVTWVAGQEYVVNCV 161
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                                                                                                                                                                                      Sequence 3, Application US/09040799
Patent No. 585820
GENERAL INFORMATION:
APPLICANT: CHANG, YIE-HWA
TITLE OF INVENTION: CLONE OF A NUCLEOTIDE SEQUENCE ENCODING
TITLE OF INVENTION: A PROTEIN HAVING TWO FUNCTIONS
NUMBER OF SEQUENCES: 5
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CURRENT APPLICATION DATA:
BLILCATION NUMBER: US/09/040,799
FILING DATE: 18-MAR-1998
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                                                                         162 SGDAKPAPDITILLSGQTIS-DISANVNEGSQQKLFTV 198
                                             53 L-DAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRV
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                                                                                                                                                                                                                                                                                                                                                          :: HOWELL & HAFERKAMP, L.C. 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-MAR-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R
REGISTRATION NUMBER: 35,197
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 314-727-6092 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 28.88
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL &
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                                                                                                                                                                                                                                                                                                                                             25; Gaps
                                                                                                                                                                                                                                                                                                                 17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG-----DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- GDAPVTWVFGRELLVEGV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1241;
                                                                                                                                                                                                                                                                                                                                                                                                                          298 CDVGE-AIQEVMESYEVEIDGKTYQV--KPI----RNLNGHSIGPYRIHA 340
                                                                                                                                                                                                                                   Score 72.5; DB 4; Length 478;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive, Suite 3200
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,774 FILING DATE: 18 MAR 1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
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                                                                                                                                                                                                                  10.6%; Scor. 28.8%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tryggvason, Karl
APPLICANT: Kestila, Marjo
APPLICANT: Lenkkeri, Ulla
APPLICANT: Mannikko, Minna
TILE OF INVENTION: Nephrin Gene and Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
CURRENT APPLICATION NUMBER: US/09/093,448A CURRENT FILING DATE: 1998-06-08 NUMBER OF SEQ ID NOS: 4 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VSEELAFRIPV --- ELRYETVDPYAVRLTFHLP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09040774 Patent No. 6207811 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGIETRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 97,84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1241 amino acids
                                                                                                                            ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-093-448-2
                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.8%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.68
Matches 28; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                       LENGTH: 478
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/915,214 FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-915-214-2; Sequence 2, Application US/08915214; Patent No. 5814457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                IBM PC compatible
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TELECOMMUNICATION:
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Haile, Lisa A.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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STATE: CA
COUNTRY:
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Patent No. 6207704
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jun O.
APPLICANT: Su, Zhuang
TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 0492611-0346
CURRENT PELLOM NUMBER: US/09/093,448A
CURRENT FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 4
SOUTHWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                             25; Gaps
                                                                                                                                                                                                                                                                                                        17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG------DVRV 63
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                                                                                                                                                                                                                        Query Match 10.3%; Score 70.5; DB 4; Length 478; Best Local Similarity 28.8%; Pred. No. 2.3; Matches 32; Conservative 19; Mismatches 35; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                        64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.3%; Score 70.5; DB 4; Length 478; Best Local Similarity 28.8%; Pred. No. 2.3; Matches 32; Conservative 19; Mismatches 35; Indels 29
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Patent NO. 5712097
GENERAL INFORMATION:
APPLICANT: Rein, Scott E.
APPLICANT: Hahn, Stephan A.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: La Jolla
CURRENT APPLICATION NUMBER: US/09/093,448A CURRENT FILING DATE: 1998-06-08 NUMBER OF SEO ID NOS: 4 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-093-448-3
                                                                                                                                       ; ORGANISM: Mus musculus US-09-093-448-1
                                                                                                   LENGTH: 478
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US-09-093-448-3
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US-08-588-821-2
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STATE:
                                                                                SEQ ID NO 1
                                                                                                                        TYPE: PRT
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25; Gaps
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APPLICANT: Hahn, Stephan A.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAPPLICATION DATA:
APPLICATION NUMBER: US/08/588,821
FILING DATE: 19-JAN-1996
CLASSIFICATION: 435
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PatentIn Release #1.0, Version #1.30
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/079001
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-509
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
TYPE: protein
US-08-588-821-2
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SER: 07265/079001
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Sequence 9, Application US/09096776B Patent No. 6270994; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22-AUG-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: REA, TEFESSA SCANCE,
REGISTRATION NUMBER: 30,427
REFRENCE/DOCKET NUMBER: 0249
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 836-66:
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552 amino acids
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                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria STATE: Virginia COUNTRY: U.S.A. ZIP: 22313-1404
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Best Local Similarity
Matches 30; Conserv
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TOPOLOGY: lir
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US-08-701-582D-14
                                                                                                                                            RESULT 10
US-08-701-582D-14
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                                                                                                                                                                                                                                                                                           5 VSEELAFRIPV------ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.1%; Score 69.5; DB 2; Length 552; Best Local Similarity 30.9%; Pred. No. 3.7; Matches 30; Conservative 15; Mismatches 27; Indels 2
                                                                                                                                                                                                     DB 2; Length 552;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Kern, Scott E.
APPLICANT: Heahn, Scephan A.
TITLE OF INVENTION: NOVEL TUMOR SUPPRESSOR GENE, DPC4
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STRRET: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/005,532
                                                                                                                                                                                                                                                                                                                                                                  356 PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 385
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                                                                                                                                                                                                 Query Match
10.1%; Score 69.5; DE
Best Local Similarity 30.9%; Pred. No. 3.7;
Matches 30; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,821
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/079001
TELECCOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09005532
Patent No. 5955292
               TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619/678-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                , MOLECULE TYPE: protein US-08-915-214-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-005-532-2
                                                                                        amino acid
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 TELEPHONE:
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                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-005-532-2
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Gaps
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                                                                                                                                                              Sequence 14, Application US/08701582D

Patent No. 6017755

GENERAL INFORMATION:
APPLICANT: WRANA, Jeffrey
APPLICANT: ATTISANO, Liliana
APPLICANT: SCHERER, Stephen W.
TITLE OF INVENTION: MADR2 TUMOUR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIONE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,582D
FILING DATE: 22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                             356 PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 385
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55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
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APPLICANT: Kawabata, Masahiro
TITLE OF INVENTION: SMAD6 AND USES THEREOF
FILE REFERENCE: L0461/7038
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5 VSEELAFRIPV------ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54

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3;

Gaps

22;

37; Indels

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47 LLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLD----
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tronanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                 100 RTDQGLSLGSERAHADFDSHLDDALNRSLAEEQSAG 135
                                                                                                                                                                              600-1-097CIP1DIV2
  Best Local Similarity 28.1%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,572

FILING DATE: 23-MAY-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: PCT/US92/03725

FILING DATE: 04-MAY-1992

CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,965
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08465965
Patent No. 5968512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07/695,613
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U//o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jackson, David
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackenser STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE:
US-08-465-965-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                              25; Gaps
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                                                                                                                                                                                                                                                                                                                                                                    Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tuomanen, Elaine
APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIAN
COMPUTER: TBM PC COMPATIAN
COMPUTER: TBM PC COMPATIAN
COMPUTER: PATENTING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/348,353
FILING DATE: 30-NOV-1994
CLASSIFFCATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Jackson, David
RESISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                               ; Score 69.5; DB 4;
; Pred. No. 3.7;
15; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
PRIOR APPLICATION NUMBER: US,09/096,776B

PRIOR FILING DATE: 1998-06-12

PRIOR FILING DATE: 1997-06-13

PRIOR FILING DATE: 1997-06-13

PRIOR FILING DATE: 1997-07-18

PRIOR FILING DATE: 1997-07-18

PRIOR FILING DATE: 1997-11-18

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 9

LENGTHRE: PATENTIN VERSION 3.0

SEQ ID NO 9

LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08348353 Patent No. 5932217 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                 10.1%;
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                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-096-776B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Best Local Similarity
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US-08-348-353-17
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US-08-348-353-17
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Gaps
                              22;
    DB 2; Length 1248;
                              37; Indels
                              10; Mismatches
    10.0%; Score 69; 28.1%; Pred. No.
                            Conservative
Query Match
Best Local Similarity
Matches: 27; Conserv
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Length 1248;

10.0%; Score 69; DB 2;

Query Match

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Houston
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ZIP: 77210
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                                                                                                                                    RESULT 15
US-08-726-214-2
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                                                                                                                                                                                                                                                                                                                                                                                              CITY:
STATE:
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                    47 LLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLD-
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson, David
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-097CIPIDIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                    132 RAQQKLELGSVKSDGGLQAAAGGAL--SLAAAEVAG 165
                                                                         100 RTDQGLSLGSERAHADFDSHLDDALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 10.0%; Score 69; DB 3
Best Local Similarity 28.1%; Pred. No. 14;
Matches 27; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRENT AFFLICATION NUMBER: US/08/465,966
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/247,572
FILING DATE: 23-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCI/US92/03725
FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
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APPLICATION NUMBER: 07/695,613
ELLING DATE: 03-MAY-1991
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              Sequence 17, Application US/08465966 Patent No. 6015560 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                       APPLICANT: Tuomanen, Elair
APPLICANT: Masure, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-465-966-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-08-465-966-17
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47 LLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLD---

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 RVCPVGQTATREVHITLQVGSEQALFR----VGKAPLLAFL--DRTD----QGLSLGSE 110
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Indels
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Tang, Wel-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/726,214 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                      100 RTDQGLSLGSERAHADFDSHLDDALNRSLAEEQSAG 135
                                                                                                   132 RAQQKLELGSVKSDGGLQAAAGGAL--SLAAAEVAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%; Score 68.5; Di
25.6%; Pred. No. 14;
:1ve 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: Concurrently Herewith CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: July 18, 2002, 14:16:07
Job time: 9697 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     ; Sequence 2, Application US/08726214; Patent No. 6107076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1134 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.0%
Best Local Similarity 25.6%
Matches, 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  NÚMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, Whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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US-08-726-214-2
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July 18, 2002, 14:17:33 ; Search time 73.98 Seconds (without alignments) 175.345 Million cell updates/sec
                                                                                                                                                                                                 US-09-749-185-5
687
1 MSFLVSEELAFRIPVELRXE......FDSHLDDALNRSLABEQSAG 135
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                             283138 seqs, 96089334 residues
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. pir1:* pir2:* pir3:* PIR_71:* Database

SUMMARIES

COLUMNICO		T37179 probable requiator	probable	probable	probable	S68694 hexokinase (EC 2.7	hypothetica			T47267 cell cycle protein	H69789 probable alcohol o					hypothetical			2,3-			precorrin-3B			T36503 hypothetical prote		4250	cell divis	A46702 methionvl aminopep
	В							2 T3													_								
	7	136						862																					
æ	Query Match	72.5	29.2	22.6	17.0	13.2	11.9	11.5	11.4	11.4	11.4	11.2	11.1	11.1	11.0	11.0	11.0	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.6	•	10.6	•	10.6
	Score	498	203	155	117	90.5	82	79	78.5	78.5	78	77	76.5	76.5	75.5	75.5	75.5	74.5		74.5	74.5	74	^	73.5	73	73	73	7	72.5
	Result No.	-1	7	æ	4	5	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28

conserved hypothet	succinoglycan bios	hypothetical prote	probable dihydroxy	nephrin - human	quinone oxidoreduc	probable glycosylt	hypothetical prote	hypothetical prote	methyltransferase	probable methyltra	methionyl aminopep	2,3-dihydroxybenzo	diol dehydratase-r	conserved hypothet	hypothetical prote
AE0332	A96232	AD3054	E64752	T37190	G83766	AI0767	B83360	C84321	AE2776	C97556	DPHUM2	SYECEB	AD1219	G96034	A96710
7	7	7	~	7	7	7	7	7	7	7	+		7	7	7
921	797	797	655	1241	322	406	514	283	303	321	478	536	909	640	296
9.	5.5	.0.5	10.4	10.4	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.2
10	Ä														
72.5 10			71.5	71.5	71	71	71	70.5	.70.5	70.5	70.5	. 70.5	70.5	70.5	70

ALIGNMENTS

RESULT T37179

283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Ribeager, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.C.; Kajandream, M.A. Ribeager, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.C.; Kajandream, M.A. Reference number: 221598 A; Cross-references: EMBL:ALO96823; PIDN:CAB46964.1; GSPDB:GN00070; SCOEDB:SCOII.09 A; Residues: 1-136 csEE A; Cross-references: EMBL:ALO96823; PIDN:CAB46964.1; GSPDB:GN00070; SCOEDB:SCOII.09 A; Experimental source: strain A3(2) A; Cross-references: EMBL:ALO96823; PIDN:CAB46964.1; GSPDB:GN00070; SCOEDB:SCOII.09 A; Experimental source: strain A3(2) A; Gene: ssqA; SCOEDB:SCOII.09 A; Experimental source: strain A3(2) A; Gene: ssqA; SCOEDB:SCOII.09 A; Experimental source: strain A3(2) A; Gene: ssqA; SCOEDB:SCOII.09 A; Marches 102; Conservative 9; Maimatches 24; Indels 0; Gaps 0; Asches: 102; Conservative 9; Maimatches 24; Indels 0; Gaps 0; Asches: 102; Conservative 9; Maimatches 24; Indels 0; Gaps 0; Asches: 102; Conservative 9; Maimatches 24; Indels 0; Gaps 0; Aschession: 11
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1.142 <see> A;Cross-references: EMBL:AL096852; PIDN:CAB51005.1; GSPDB:GN00070; SCOEDB:SCE19A.24 A;Experimental source: strain A3(2) C;Genetics:</see>
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3;

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A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
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31.3%;
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27.0%;
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Best Local Similarity 31.3%
....has 36; Conservative
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-484 <SK2>
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         C;Genetics:
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R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, April 1999
A; Reference number: Z21573
A; Accession: T35247
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T35247
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T35247
A; Status: DNA
A; References: EMBL: AL049587; pIDN: CAB40672.1; GSPDB: GN00070; SCOEDB: SC5F2A.05c
C; Genetics: A; Genetics: Strain A3(2)
C; Genetics: A; Genetics: Genetics: A; Genetics: Genetics: A; Genetics: Genetics: A; Genetic
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A;Cross-references: EMBL:AL049863; PIDN:CAB42928.1; GSPDB:GN00070; SCOEDB:SC5H1.03
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: OS-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Accession: T35319
R;Oliver, K; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, Submitted to the EMBL Data Library, May 1999
A;Reference number: Z21575
A;Accession: T35319
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                             LVEGVLDAAGDGDVRVCPVGQTAT-REVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLS 106
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A;Gene: SCOEDB:SCE19A.24
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                Length 142;
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                                                                                                                                                                                            Indels
                                                                                                                          Query Match 29.5%; Score 203; DB 2; Lr
Best Local Similarity 37.3%; Pred. No. 1.7e-13;
Matches 47; Conservative 16; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
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1 Similarity 31.2%; Pred. No. 1.3e-08;
44; Conservative 16; Mismatches 63.
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Matches 44; Conserv
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137 AELLAR 142
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hexokinase (EC 2.7.1.1) 1 - fission yeast (Schizosaccharomyces pombe)
N.Alternate names: protein SPAC24H6.04
C.Specias: Schizosaccharomyces pombe
C.Specias: Schizosaccharomyces pombe
C.Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Accession: $68694; T38360; $62406
R.Petit, T.: Blazquez, M.A.; Gancedo, C.
FEBS Lett. 378, 185-189, 1996
A:Title: Schizosaccharomyces pombe possesses an unusual and a conventional hexokinase
A:Reference number: $68693; MUID:96140736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: EMBL:254142; NID:9984697; PIDN:CAA90848.1; PID:9984701; GSPDB:GNO A.Experimental source: strain 972h-; cosmid c24H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-484 <PRIS-
A; Residues: 1-484 <PRIS-
A; Cross-references: EMBL: X92894; NID:91160507; PIDN:CAA63487.1; PID:91160508
A; Cross-references: EMBL: X92894; NID:91160507; PIDN:CAA63487.1; PID:91160508
R; Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
Submitted to the EMBL Data Library, September 1995
A; Reference number: 221788
A; Accession: T38360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A83271
hypothetical protein PA2984 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83271
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                                                                                                                                          10 AFRIPV - - ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVG 67
                                                                                                                                                                                                               19 ADRFPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRPES 78
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                                                                                                                                                                                                                                                                                                                         68 QTATREVHITLQVGS-----EQALFRVGKAPLLAFLDRTDQGLSLGSERAHAD 115
                                                                        10;
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Length 142;
; Score 117; DB 2; Length 142; Pred. No. 0.00011; 15; Mismatches 54; Indels
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A;Molecule type: DNA
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C;Superfamily: hexokinase; hexokinase homology
C;Keywords: ATP; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;40-466/Domain: hexokinase homology <HXK>
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Conservative
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 SLAEEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 DLTPEE 185
                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Biadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Mature 406, 959-964, 2000.
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathols, R;Reference number: A82950; MUID:20437337
                                                                                                                                                               A;Residues: 1-741 cSTO>
A;Cross-references: GB:AE004724; GB:AE004091; NID:g9949083; PIDN:AAG06372.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;011ver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1999
A;Reference number: 221573
A;Accession: 136380
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-862 <OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL049628; PIDN:CAB40869.1; GSPDB:GN00070; SCOEDB:SCE94.20
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable large ATP-binding protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHLDDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QFLSRFREHTGADVQEFLATS 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GRAEVRVLDVGQGLAVLVRTREHVLLYDS 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 LRYETVDPYAVR-----LIFHLPGDAPVTWVFGREL-----LVEGVLDAAGDG-DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 AVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQ-----TATREVHITLQV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thiamin monophosphate kinase [imported] – Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 GSEQALFRVGK---APLLAFLD-RTDQGLSLGSERAHADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 GARGGAFDMGERVVVPVLRSLDLRRLDGLLL----SHADND 558
                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 79; DB 2
Pred. No. 6.7;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Query Match 11.9%; Score 82; DB Best Local Similarity 32.7%; Pred. No. 2.8; Matches 33; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DSTAARVVHTAVSVGSEAAL
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ilarity 31.7%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 39; Conserv
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                                                                                                                                   A; Accession: A83271
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                A; Gene: PA2984
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A.Reference number: AB1807; MUID:21595285; PMID:11759840
A.Accession: AE2438
A.Molecule type: DNA
A.Residues: 1-332 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Helicobacter felis
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
C;Accession: 147267
R;Bayle, D:; Wangler, S.; Weitzenegger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.
J; Bayle, D:; Wangler, S.; Weitzenegger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.
J; Batteriol. 180, 317-329, 1998
A;Title: Properties of the P-type ATPases encoded by the copAP operons of Helicobacte
A;Reference number: 224437; MUID:98101471
A;Accession: T47267
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
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A;Cross-references: EMBL:AJ001932; NID:g2660538; PIDN:CAA05102.1; PID:g2660540
A;Experimental source: strain ATCC 49179
                                                                                                                                                                                                                                                                              A; Cross-references: GB:BA000019; PIDN:BAB76760.1; PID:917134199; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SHAGLELLLDPKIGK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82; PLGITIALALPGDLSVSWV---ERLYQGITECLQKYHTPIVGGDVVRSPITTLSITAFGQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 VH-----ITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHLDDALNR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 PYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAG-----DGDVRVCPV---GQTATRE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
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                                                                                                                                                                                                                                                                                                         A.Experimental source: strain PCC 7120
C.Genetics: alx561
C.Superfamily: conserved hypothetical protein MJ0640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 DQGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 78.5; DB 25.4%; Pred. No. 2.5;
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llarity 29.9%; Pred. No. 5.3;
Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 VHPNRIIRRSTAQVGDAIAITGVHGA-
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22;

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ATP-dependent zinc metallopeptidase - Helicobacter pylori (strain J99)
C; Species: Helicobacter pylori
A; Vartacy: strain J99
A; Vartacy: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jan-2000
C; Accession: D71941
E; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-291 <COL>
A;Residues: 1-291 <COL>
A;Cross-references: GB:281451; GB:AL123456; NID:93261662; PIDN:CAB03770.1; PID:916661 A;Experimental source: strain H37Rv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-632 <ARN>
A; Cross-references: GB: AE001471; GB: AE001439; NID: g4154880; PIDN: AAD05932.1; PID: g415
A; Experimental source: strain J99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Accession: H70678
R; Cole, S; T: Brosch, R: Parkhill, J: Garnler, T:; Churcher, C.; Harris, D.; Go, S; T: Brosch, R:; Deviln, K:; Feltwell, T:; Gentles, S:; Hamin, N.; Holrn; Connor, R.; Boavies, R.; Deviln, R.; Feltwell, T:; Gentles, S.; Hamin, N.; Holrn Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Rteference number: A; Reference number: A; Reference number: H70670; MUID: 98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 REVH-----ITLQVG-----SEQALFRVGKAPLLAFLDRTDQGLSLGSER 111
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                                                                                                                                                                                                     30 TFHLPGDAPVTWVFGRELLVE--GVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
H70678
hypothetical protein Rv2426c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                      88' R-----VG---KAPLLAFLDRTDQGLSLGSERAHADFDSHLDDALNRSLAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 291;
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                                                                                                                            Indels
                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                DB 2;
                                    11.2%; Score //, 29.5%; Pred. No. 8.3; +ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 76.5; DE; Pred. No. 3.4; 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Gene: Rv2426c
C;Superfamily: hypothetical protein MTH1814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.6%;
Matches 36; Conservative 1
                                                                                                                                Conservative
                                                Query Match
Best Local Similarity
Matches 33; Conservat
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Broulle, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Charter 390, 249-256, 1997
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A; Authors: Foulager, D.; Fritz, C.; Fullta, M.; Fullta, V.; Funa, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laullo, M.F. Koetter, P.; Koningstein, G.; Krogh, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portectall, A.; Authors: Lauder, J.; Berker, B.; Rose, M.; Sadie, Y.; Sato, T.; Sanlon, A; Authors: Schleich, S.; Schroeter, B.; Rose, M.; Sadie, Y.; Sato, T.; Sanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Tognoni, A.; Tosako, Y.; Sanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sadiguchi, J.; Sekowska, A.; Sanlon, A; Authors: Schleich, A.; Yamamoto, H.; Yamane, K.; Yasta, K.; Yoshida, K.; Authors: Schleich, A.; Yamano, K.; Yasta, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumsteh, E.; Yoshikawa, H.; Danchin, A.; Danchin, A.; Mapet, A.; Yamano, K.; Yasta, K.; Yoshida, K.; Atthors: Yoshikawa, H.F.; Zumsteh, E.; Yoshikawa, H.; Danchin, A.; Atthors: Yoshikawa, H.F.; Zumsteh, E.; Yoshikawa, H.; Danchin, A.; Atthors: Yoshikawa, H.S.; Zumsteh, E.; Yoshikawa, H.; Danchin, A.; Accession: H69789
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Rosidues: 1-346 cKun>
A; Roperimental source: strain 168
C; Genetics:
A; Roperimental source: strain 168
C; Genetics:
A; Roperimental source: strain 168
C; Roywords: metalloprotein; NAD: Ordeductass: 210c
C; Roywords: metalloprotein; NAD: Ordeductass: 210c
C; Roywords: metalloprotein; NAD: Ordeductass: 210c
F; 22-334/Domain: long-dapalaha-beta NAD nucleotlde-binding clud
F; 171-200/Region: beta-alpha-beta NAD nucleotlde-binding clud
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A58842; MUID:21396508; PMID:11481431
A;Accession: F96037
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-693 < KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49966.1; PID:g15141454; GSPDB:GN00167
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C;Specdes: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F96037
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R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
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A;Title: The composite genome of the legume symbiont Sinorhizoblum meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 1;
Pred. No. 2.9;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 DAAGDGD---VRVCPVGQTATREV 74
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Match 11.4%; Local Similarity 39.3%; les 33; Conservative 6

Query Match

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A;Gene: agpA; SMb21647

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Gaps

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Search completed: July 18, 2002, 14:17:35
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C; Genetics:
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C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession: F97414
R; Godoner, B.: Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
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                                     A;Gene: ftsH_2
C;Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain homd
F;184-395/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AGR_C_807 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AB2632
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C;Genetics:
A;Gene: AGK_C_807
A;Map position: circular chromosome
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 GKTLLAKAV -- - AGEAHVPFFSMGGSSFIEMFVGLGASRVRDLFETAKKQAPSIIFIDEI 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 GVLDIAADGSLRTDKDFISVYTDGSKLIEGLELRSLASPGQLDIVFEAGVTTAHAVTD 91
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Pred. No. 3.6;
6; Mismatches
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Best Local Similarity 31.2%;
Matches 30; Conservative
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A;Molecule type: DNA
A;Residues: 1-248 <KUR>
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Residues: 1-248 <KUR>
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C; Genetics:
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51; GVLDAAGDGDVR-----VCPVGQTATR--EVHITLQVGSEQALFRVGKAPLLAFLD 99
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                                                                                                                                                 19;
                                                                                                 DB 2; Length 248;
                                                                                                                                                 Indels
                                                                                               Score 75.5; DB 2; I
Pred. No. 3.6;
6; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                     92_TETDESVILGMPATDATFEFHLDMALRQTGDALNDS 127
                                                                                                                                                                                                                                                                                                     100 -RTDQGLSLGSERAHADFDSHLD-----DALNRS 127
A;Gene: Atu0453
A;Map position: circular chromosome
                                                                                               Query Match 11.0%;
Best Local Similarity 31.2%;
Matches 30; Conservative
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Gaps

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GenCore version 4.5
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- protein search, using sw model OM protein July 18, 2002, 14:31:53; Search time 45.63 Seconds Run on:

(without alignments)
114.555 Million cell updates/sec

US-09-749-185-5 687

1 MSFLVSEELAFRIPVELRYE......FDSHLDDALNRSLAEEQSAG 135 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0.
Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Q09756 schizosacch	032617 helicobacte		Q9zm66 helicobacte		-			P77596 escherichia	P89684 barley mild		_	P10378 escherichia	· P97471 mus musculu	Q13485 homo sapien	Q9gkq9 sus scrofa	070437 rattus norv	Q9plj6 c riboflavi	P12255 bordetella	P16767 human cytom	P23439 bos taurus		-	P46508 schistosoma	P40713 escherichia				P46550 caenorhabdi	Q14624 h inter-alp	-	P19725 rubella vir	P96889 mycobacteri
SUMMARIES	ID	HXK1_SCHPO	FTSH_HELFE	AGPA_RHIME	FTSH_HELPJ	FTSH_HELPY	FTSH_MYCGE	FTSH_MYCPN	AMP2_RAT	YAGF_ECOLI	POL2_BAMMN	AMP2_HUMAN	AMP2_MOUSE	ENTE_ECOLI	SMA4_MOUSE	SMA4_HUMAN	SMA4_PIG	SMA4_RAT	RIBD_CHLMU	FHAB_BORPE	UL36_HCMVA	CNRB_BOVIN	CYA1_BOVIN	SCRK_KLEPN	YME1_SCHMA	SCRK_ECOLI	HMCT_BOMMO	AROA_STAAU	GABD_RHISN	TCPZ_CAEEL	ITH4_HUMAN	GLMS_MYCLE		YW84_MYCTU
	DB	-	-	П	Н	Н	7	-	Н	-	Н	Н	-	-	-	П	-	-	Н	Н	-	П	-		-	-	7	Н	Η	Н	-	-	-	-
	° Query Match Length	484	638	693	632	632	702	709	478	655	891	478	478	536	551	552	552	552	371	3591	476	853	1134	307	662	305	3133	430	491	539	930	624	1063	143
d	Query Match	13.2	11.4	11.2	11.1	11.0	10.6	10.6	10.6	10.4	10.3	10.3	10.3	10.3	10.3	10.1	10.1	10.1			10.0	10.0		6.6			9.7					9.5	9.5	9.5
	Score	90.5	78.5	77	76.5	ഗ	73			71.5	71	70.5	70.5	70.5	.70.5	69.5	69.5	69.5	69	69	68.5	68.5	68.5	68	68	66.5	66.5	99	99		99	65.5	65.5	65
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Length 484;

Score 90.5; DB 1; Pred. No. 0.11;

13.2%; 27.0%;

Query Match Best Local Similarity

P20324 bacteriopha		Q9y4w6 homo sapien						-	_	P80668 escherichia
VCAP_BPT3	PTLB_LACLA	AF32_HUMAN	YEC4_EBV	CH60_THEBR	GP60_BPSP1	RPOD_HALMA	YMEH_CAEEL	YSCB_YEREN	NOLF_RHIME	FEAB_ECOLI
-		Н	Н	Н	Н	Н	Н	-	Н	П
310	568	797	289	540	73	259	9/9	137	367	499
o o rv	, Q	9.5	9.4	9.4	9.3	9.3	9.3	9.5	9.5	9.5
65	92	65	64.5	64.5	64	64	64	63.5	63.5	63.5
34	300	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HAS LOW AFFINITY FOR GLUCOSE AND SOME OF ITS ANALOGS.
-!- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
-!- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

PEDILINE—56140736; Pubmed=8549830;
Petit T., Blazquez M.A., Gancedo C.;
"Schizzosaccharomyces pombe possesses an unusual and a conventional hexokinase: biochemical and molecular characterization of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Kinase; Glycolysis; ATP-binding; Multigene family.
BINDING 115 115 APP (BY SIMILARITY).
DOMAIN 154 180 GLUCOSE-BINDING (POTENTIAL).
SEQUENCE 484 AA, 53597 WW, 165500F19E6BBB0F CRC64;
                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
HXK1.0R SPAC24H6.04.
                                    484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X92894; CAA63487.1; -.
EMBL: 254142; CAA90848.1; -.
HSSP, P19367; 1HKC.
InterPrc; IPR001312; Hexokinase.
Pfam; PF00349; hexokinase; 1.
PRINTS; PR00475; HEXOKINASE.
ProDom; PD001109; HEXOKINASE.
PROSITE; PS00378; HEXOKINASE; 1.
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 378:185-189(1996).
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                              HXK1_SCHPO
Q09756;
                                                                                                                                                                                                                                                                                                                                                                    hexokinases.
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Query Match
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 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; 1.
Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
                                                                                                           | ::||| | : || GGT-NLRVCAVEVQGNGKFDITQSKYRLPQELKVGTREALFDYIADCIKKFVEEVHPGKS 150
                                                                                           AGDGDVRVCPVGQTATREVHIT---------DVGSEQALFRVGKAPLLAFLDRT----D 102
                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN-ATCC 49179;
STRAIN-ATCC 49179;
Bayle D., Wangler S., Weitzenegger T., Volz J., Steinhilber W.,
Przybylski M., Sachs G., Schafer K.P., Melchers K.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
   29; Gaps
                                ELAFRIPVELRYETVDPYAVRLTFHL---PGDAPV--TWVFGRELLVEG-----VLDA 55
                                                         EEQFTIPTELLHRVTDRFVSELYKGLTTNPGDVPMVPTWIIGTP----DGNEHGSYLALDL 91
                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
CAA4818021A243A0 CRC64;
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1 COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-1 SUBCELLULAR LOCATION: Integral membrane protein.
-1 SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC.
METALLORPOTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. PERIPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
 55;
                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Cell division protein ftsH homolog (EC 3.4.24.-).
                                                                                                                                                                                                                                                                638 AA.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000642; Peptidase_M41.
                                                                                                                                                                                                                                                                PRT;
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Pfam; PF01434; Peptidase_M41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ001932; CAA05102.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA.
InterPro; IPR003959; AAA_subfam.
 19;
                                                                                                                                                                           QNLEIGFTFSYPCVQRSINDA 171
                                                                                                                                                      QGLSLGSERAHADFDSHLDDA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70245 MW;
 Conservative
                                                                                                                                                                                                                                                                STANDARD;
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638
223
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638 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=214;
                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter.
38;
                                                                                                                                                                                                                                                                FTSH_HELFE
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DOMAIN
NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Periplasmic. SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                            221 GKTLLAKAV---AGEASVPFFSMGGSSFIEMFVGLGASRVRDLFDIAKKEAPSIIFIDEI 277
                                                                        44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-219568; PubMed-11481431;
MEDINE-2195508; PubMed-11481431;
MEDINE-2195508; PubMed-11481431;
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A., The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing endosymbiont Sinorhizoblum mellioti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
-i- FUNCTION: PROBABLY INVOLVED IN AN ALPHA-GALACTOSIDES INTAKE TRANSPORT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERIPLASMIC ALPHA-GALACTOSIDE BINDING
                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Periplasmic alpha-galactoside binding protein precursor.
AGPA OR RB1567 OR SMB21647.
Rhizoblum meliloti (Sinorhizoblum meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group;
Rhizobiaceae; Sinorhizoblum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAINE-1021;
MEDLINE-99009011; PubMed-9791127;
Gage D.J., Long S.R.;
"Alpha-galactoside uptake in Rhizobium meliloti: isolation and characterization of appA, a gene encoding a periplasmic binding protein required for melibiose and raffinose utilization.";
J. Bacteriol. 180:5739-5748(1998).
                                     11;
 Length 638;
                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E -> K (IN REF. 1).
76F9B95708C2DF9F CRC64;
 DB 1;
                                                                                                                                                102 DQGLSLGSERAHADFDSHLDD----ALNRSLAEEQSAG 135
                                                                                                                                                                    278 D---AIGKSRAAGGMISGNDEREQTLNQLLAEMDGFG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF119834; AAD26274.1; -.
EMBL; AL603647; CAC49966.1; -.
InterPro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 2.
PF00496; SBP_BACTERIAL_5; FALSE_NEG.
Sugar transport; Transport; Periplasmic; Sign
                                                                                                                                                                                                                                                                             693 AA
                                    16; Mismatches
11.4%; Score 78.5; 29.9%; Pred. No. 2.4
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                                    Conservative
                                                                                                                                                                                                                                                                             STANDARD;
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693
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                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                     29;
                                                                                                                                                                                                                                                                         AGPA_RHIME
Q9X4Y1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-1021
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                    Best Local
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                                    Matches
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us-09-749-185-5.rsp

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FTSH_HELPY
         SEQUENCE
                                            Query Match
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                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Hydrolase; Metalloprotease;
                                                                  MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
                                                   30 TFHLPGDAPVTWVFGRELLVE--GVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT 2INC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                            Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
ATP (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY).
                                                                                                R-----VG---KAPLLAFLDRTDQGLSLGSERAHADFDSHLDDALNRSLAE 130
                                                                                                             Length 693;
                              39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-C77-2001 (Rel. 40, Last annotation update)
Cell division protein ftsH homolog (EC 3.4.24.-).
        DB 1;
                                                                                                                                                                                632 AA.
       s; Score 77; DB
s; Pred. No. 3.8;
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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InterPro; IPR003593; AAA.
InterPro; IPR003950; AAA_sub.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR000642; Peptidase_M41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
       11.2%;
29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; 1.
Cell division; ATP-binding;
                              Conservative
                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METALLOPROTEASE).
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                  Similarity
                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=85963;
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138
210
434
435
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                              33;
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NP_BIND
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SEQUENCE FROM N.A.
STRAIN-26695 / ATCC 700392;
MEDLINE-9734467; PubMed-9252185;
MEDLINE-9734467; PubMed-9252185;
Tomb.J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Goccayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Friji C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                  215.GKTLLAKAV---AGEAHVPFFSMGGSSFIEMFYGLGASRVRDLFETAKKQAPSIIFIDEI 271
                                                                                                                                                                                                                                                             44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                Gaps
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J. Biol. Chem. 271:446-457(1996).
-!- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melchers K., Weitzenegger T., Buhmann A., Steinhilber W., Sachs G., Schafer K.P.; "Cloning and membrane topology of a P type ArPase from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIANE=97386403; PubMed=9244252;
Beier D., Spohn G., Rappuoli R., Scarlato V.;
Hidentification and characterization of an operon of Helicobacter pylori that is involved in motility and stress adaptation.",
J. Bacteriol. 179:4676-4683(1997).
                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequencing, expression, and genetic characterization of the Helicobacter pylori fish gene encoding a protein homologous to members of a novel putative ATPase family."; J. Bacteriol. 178:6151-6157(1996).
ZINC (CATALYTIC) (BY SIMILARITY).
2FB67B43C51559FB CRC64;
                                                                                                                                DB 1; Length 632;
                                                                                                                                                                                             42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P71408: 007679; Q4268; 01-NOV-1997 (Rel. 35, Created) (01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) (Cell division protein ftsH homolog (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                          102 DQGLSLGSERAHADFDSHLDD----ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 76.5; DE
29.9%; Pred. No. 3.8;
Live 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     632 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-NOTC 11639 / UA802;
MEDIINE-97047972; PubMed-8892813;
Ge Z., Taylor D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96132941; PubMed=8550601;
                              69765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 324-632 FROM N.A.
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
438 4
632 AA;
                                                                                                                                                              Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=210;
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Created)

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Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
       01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cell division protein fisH homolog (EC 3.4.24..).
                                                                       Mycoplasmataceae; Mycoplasma
 01-FEB-1996 (Rel.
                                                                                  NCBI_TaxID-2097;
                                         FTSH OR MG457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                  InterPro; IPR003593; AAA_sub.
InterPro; IPR003596; AAA_sub.
InterPro; IPR003595; AAA_subfam.
InterPro; IPR000642; Peptidase_M41.
Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
PROSTE; PS00674; AAA; 1.
Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease; Zinc; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 GRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK--APLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
G -> P (IN REF. 1).
V -> MI (IN REF. 1).
L -> F (IN REF. 2).
H -> D (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 75.5; DB 1; Length 632; 29.9%; Pred. No. 4.8; tive 15; Mismatches 42; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQ -> FE (IN REF. 1).
RQ -> KL (IN REF. 1).
R -> K (IN REF. 1).
I -> M (IN REF. 2).
A -> G (IN REF. 2).
S -> Y (IN REF. 2).
V -> F (IN REF. 2).
K -> E (IN REF. 1).
V -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1D0674163FFC206D CRC64;
(BY SIMILARITY).
COFACTOR: BINDS 1 ZINC IÔN (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAI MEMDIANE PIOTEIN.
SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC
                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 D----AIGKSRAAGGVVSGNDEREQTLNQLLAEMDGFG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 DOGLSLGSERAHADFDSHLDD---ALNRSLAEEQSAG 135
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                        EMBL, U59452; AAC44563.1; -. EMBL, U97567; AAB60317.1; -. EMBL, AE000614; AAB08115.1; -. EMBL, U59625; AAB05472.1; -.
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4430
4430
455
455
616
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                                                     METALLOPROTEASE).
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616
632 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 29; Conserv
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3354
401
401
449
455
499
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TRANSMEM
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METAL
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NP_BIND
METAL
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9
InterPro; IPR003969; AAA_sub.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR000642; Peptidase_M41.
Pfam; PF00404; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
SMART; SM00082; AAA; 1.
Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 GRELLVEGVLDAAGDGDVRVCPVGQ-TATREVHITLQVGSEQA--LFRVGK--APLLAFL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
ATP (POTENTIAL).
SINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INC (CATALYTIC) (BY SIMILARITY). ADB26C68CD780535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 73; DB 1; Length 702; 30.9%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 DRTDQGLSLGSERAHADFDSH--LDDALNRSLAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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76729 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003593; AAA.
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45
179
702
278
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                                                                                                                                                                                                                                                                                                METALLOPROTEASE).
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494
497
702 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; M41.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc; Complete
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702 AA.

PRT;

STANDARD;

FTSH_MYCGE P47695;

FTSH_MYCGE RESULT A D Ŋ

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Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
Zinc; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
D07585386C8B4C94 CRC64;
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                                                                                                                                                                                                                                                                                                   Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY STATLARITY).
-!- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41 (ZINC METALLOPROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cell division protein fish homolog (EC 3.4.24.-).
FTSH OR MPN671 OR MP171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.6%; Score 73; DB 1;
30.9%; Pred. No. 9.8;
ive 17; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
ZINC (CATALYTIC
330 DEID---SVGSKRGRVELSSYSVVEQTLNQLLAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA_sub.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR000642; Peptidase_M41.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed~8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00004; AAA; 1.
Pfam; PF01434; Peptidase_M41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000018; AAB95819.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77735 MW;
                                                                                                                                                                                                                                                                                                                                                      Mycoplasmataceae; Mycoplasma
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
709
275
490
491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
193
268
490
491
494
709 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M41.001;
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Singles 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae.
                                                                                                                                        FTSH_MYCPN P75120;
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DOMAIN
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METAL
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NP_BIND
METAL
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Best Local S
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                                                                                                               FTSH_MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=REUBER H35; TISSUE=Liver;
MEDLINE=93266517; PubMed=8496145;
Wu S., Gupta S., Chatterjee N., Hileman R.E., Kinzy T.G.,
Denslow N.D., Merrick W.C., Chakrabarti D., Osterman J.C., Gupta N.K.;
"Cloning and characterization of complementary DNA encoding the
eukaryotic initiation factor 2-associated 67-kDa protein (p67).";
J. Biol. Chem. 268:10796-10801(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                       01-0CT-1994 (Rel. 30, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
Methionine factor 2 associated 67 kba glycoprotein) (p67) (p67eIF2)
METAP2 OR MNPEP OR P67EIF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity). PTM: CONTAINS 12 O-LINKED GLCNAC. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C; ALSO KNOWN AS THE MAP FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS.
FUNCTION: PROTECTS EIF-2 ALPHA-SUBUNIT FROM INHIBITORY
PHOSPHORYLATION BY EIF-2 KINASES. PLAYS A CRITICAL ROLE IN THE
REGULATION OF PROTEIN SYNTHESIS. IT ALSO INTERACTS WITH THE
EIF-2 GAMMA-SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)0 = L-METHIONINE + PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95372350; PubMed=7644482; Meaver L.H., Stewart A.E., Aaffin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E., Matthews B.W., Bradshaw R.A.; Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent enzymes." proc. Natl Acad. Sci. U.S.A. 92:7714-7718(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-LYS.
COBALT 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARG/LYS-RICH (BASIC).
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00599; MAPEPTIDASE.
PROSITE; PS01202; MAP_2; 1.
Hydrolase; Aminopeptidase; Cobalt; Glycoprotein.
                                                                                                                                                                                                                               478 AA
99 DRTDQGLSLGSERAHADFDSH--LDDALNRSLAE 130
                                     327 DEID---SVGSKRGRVELSSYSVVEQTLNQLLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002468; MAP_2.
InterPro; IPR001714; Methamino_PTase.
InterPro; IPR000994; Peptidase_M24.
Pfam; PF00557; Peptidase_M24; 1.
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L10652; AAA41111.1; -.
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
106
251
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HSSP; P56218; 1XGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; M24.002;
                                                                                                                                                                                                                               AMP2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                     P38062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                              8
                                                                                                                                                              RESULT
AMP2_RAT
                                                                                                                                                                                                                                                              DDT HELD DD HE
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; 9

Gaps

16;

Indels

32;

Conservative

Matches 44

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GRELLVEGVLDAAGDGDVRVCPVGQ-TATREVHITLQVGSEQA--LFRVGK--APLLAFL 98

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                                                                                                                                                                         8;
COBALT 1 AND 2 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 AND 2 (BY SIMILARITY).
LRPTCKEVVSRGDDY -> CAQPVKKLSAEEMTIKT (IN
                                                                                                                                                                                                                                   242 LQYDDI----CKIDFGTHISGRIIDCAFTVTFNPKYDILLKAVKDATNTGIKCAGIDVRL 297
                                                                                                                                                                            Gaps
                                                                                                                                                                                                        17 LRYETVDPYAVRLTF--HLPG----DAPVTWVFG--RELLVEGVLDAAGDG------DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIJNE-9742617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                       Score 72.5; DB 1; Length 478; Pred. No. 6.9;
                                                                                                                                                                                                                                                                    64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Lyase; Complete proteome.
SEQUENCE 655 AA; 69399 MW; 208AF2F6DB39EE8B CRC64;
                                                                                            BEICOE91E0CB3D74 CRC64;
                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yagf.
                                                                                                                                                                       20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               655 AA
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002691; ILVD_EDD; 1.
PROSITE; PS00886; ILVD_EDD_1; 1.
PROSITE; PS00887; ILVD_EDD_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE000134; AAC73372.1; -. EMBL; U70214; AAB08650.1; -. ECGENE; EG13345; yagF. InterPro; IPR000581; ILVD_EDD. Pfam; PF00920; ILVD_EDD; 1.
                                                                                            MW;
                                                                                                                                        10.6%;
28.8%;
                                                                                            53052
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
   262
331
364
459
478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                          Query Match
Best Local Similarity
                                                                                            478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gregor J., Davis
Mau B., Shao Y.;
   262
331
364
459
464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAGE OR B0269
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997
01-NOV-1997
                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                              YAGE_ECOLI
P77596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YJHG.
                                                                                            SEQUENCE
                                                               CONFLICT
   METAL
METAL
METAL
                                               METAL
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                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEPLER COMPONENT PROTEINASE (POTENTIAL). 70 KDA PROTEIN. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AESLOFHVTDKRGVPGMWNILKAGRVYELLSLAADG-----------VGCE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 QALFRVGKAPLLAF-----LDRTDQGLSLGSERAHA---DFDSHLDDALNRSLAEE 131
                               Gaps
                                                         31 FHLPGDAPVTW----VFGRELLVEGVLDAAGDGDVRVCPVG-QTATREVHITLQVGSEQA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AVRLIFHLPG--DAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQTATREVHITLQVGSE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete nucleotide sequence and genome organization of barley
                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
6-COMPOND (PROPERTY OF COMPONDENTY OF COMPONDENT PROTECTIONS (EC 3.4.22.-) (HC-PRO); 70 kDa protein].
Barley mild mosaic virus (strain Nal) (BaMMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mild mosaic virus (Nal strain).";
Arch. Virol. 141:2077-2089(1996).
-!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
                                                                                                                                     86 LFRVGKAPLLAFLDRTDQGLSLGSERAHADFDS--HLDDA-----LNRSL 128
 Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE (BY HC-PRO PROTEASE)
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
A290247196822BE2 CRC64;
                               43;
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 891 AA
                               19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
Score 71.5; 1
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001337; TMV_coat.
Pfam; PF00721; TMV_coat; 1.
Polyprotein; Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-97128984; PubMed-8973524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97942 MW;
10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%;
28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D83409; BAA18954.1; -
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                             STANDARD;
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 891 AA;
                                                                                                                                                                                                                                                                                                                                                               Bymovirus.
NCBI_TaxID=103900;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kashiwazaki S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
189
229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 ONAG 284
                               32;
                                                                                                                                                                                                                             POL2_BAMMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
ACT_SITE
SITE
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                                                                                                                                                                                              RESULT 10
POL2_BAMMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                Matches
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                                                                                                                                                                                                                            MEDLINE=95372350; PubMed=7644482;
Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E.,
Matthews B.W., Bradshaw R.A.;
"Eukaryotic methionyl aminopeptidases: two classes of cobalt-dependent
                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
(Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2)
METAP2 OR MNPEP OR P67EIF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24C; ALSO KNOWN AS THE MAP FAMILY 2.
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEINS.
-1- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)0 = L-METHIONINE + PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 282:1324-1327(1998).
-!- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 109-478.
MEDLINE-99030697; PubMed-9812898;
Liu S., Widom J., Kemp C.W., Crews C.M., Clardy J.;
"Structure of human methionine aminopeptidase-2 complexed with fumagillin.";
                                                                                                                                                                                                                                                                                                                                                       Li X., Chang Y.; "Molecular cloning of a human complementary DNA encoding an initiation factor 2-associated protein (p67)."; Biophys. Acta 1260:333-336(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COBALT 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARG/LYS-RICH (BASIC).
ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001714; Methamino_Prase.
InterPro; IPR000994; Peptidase_M24.
Pfam; PF00557; Peptidase_M24; 1.
PRINTS; PR00599; MAPEPTIDASE.
PROSTTE; PS01202; MAP. 2; 1.
Hydrolase; Aminopeptidase; Cobalt; 3D-structure.
                                             478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-LYS.
                                             PRT;
                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
MEDLINE=95178556; PubMed=7873610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U29607; AAA82930.1; -. EMBL; U13261; AAC63402.1; -. PDB; 1159; 14-JAN-00. MEROPS; MA4.002; -. MIM; 601870; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002468; MAP_2.
                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
93
106
231
251
                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                     TISSUE=Brain;
                                            AMP2_HUMAN
P50579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
ACT_SITE
METAL
                                                                                                                                                                                                                                                                                  enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                  AMP2_HUMAN
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8;
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                                                                                                                                                                                                                                                                                                                                        242 LQYDDI----CKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIKCAGIDVRL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2)
(Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2).
METAP2 OR MNPEP OR P67EIF2.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                        17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG------DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6 x CBA; TISSUE-Liver;
Sekiquchi S., Suzuki E.;
Sekiquchi S., Suzuki E.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT PROTEINS (BY SIMILARITY).
FUNCTION: PROTECTS EIF-2 ALPHA-SUBUNIT FROM INHIBITORY PHOSPHORYLATION OF PROTEIN SYNTHESIS, IT ALSO INTERACTS WITH THE EIF-2 GAMMA-SUBUNIT (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)O = L-METHIONINE + PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: COBALT; BINDS 2 IONS PER SUBUNIT (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                       25;
       COBALT 1 AND 2 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 AND 2 (BY SIMILARITY).
5788E4BBB35E48F9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                                                                                                                  10.3%; Score 70.5; DB 1; Length 478; 28.8%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARC/LYS-RICH (BASIC).
ASP/GLU-RICH (ACIDIC).
POLY-LYS.
COBALT 2 (BY SIMILARITY).
                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002468; MAP_2.
InterPro; IPR001714; Methanino_Prase.
InterPro; IPR00194; Peptidase_M24.
Pfam; PF00557; Peptidase_M24; I.
PRINTS; PR00599; MAPEPTIDASE.
PROSITE; PS01202; MAP_2; I.
Hydrolase; Aminopeptidase; Cobalt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB003144; BAA19789.1; -.
                                                                                                              MW;
262
331
364
459
52891 N
                                                                                                                                                                                                                                       32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1929701; Metap2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46
93
106
251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
       262
331
364
459
478 AA;
                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1xgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAP FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMP2_MOUSE
008663;
                                                                                                           SEQUENCE
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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          METAL
METAL
METAL
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TRANSMEM
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                                                                                                                                                                                                                                                                ENTE_ECOLI STANDARD; PRT; 536 AA. P10378; P10378; P10378; P10478; P10479; P7777; Created) O1-MAR-1989 (Rel. 10, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 16-0cT-2001 (Rel. 40, Last annotation update) 2,3-dihydroxybenzoate-AMP ligase (EC 6.32.-) (Dihydroxybenzoic acidactivating enzyme) (Enterobactin synthetase component E) (Enterochelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
Lin D.,
                                                                                                                                               Gaps
                                                                                                                                   17 LRYETVDPYAVRLTF--HLPG---DAPVTWVFG--RELLVEGVLDAAGDG-----DVRV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-KIZ. 7 MG165;
STRAIN-KIZ. 7 MG165;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 393-546 FROM N.A. MEDLINE-89123155; PubMed-2521622;
Liu J., Duncan K., Walsh C.T.;
"Nucleotide sequence of a cluster of Escherichia coli enterobactin biosynthesis genes: identification of entA and purification of its product 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase.";
J. Bacteriol. 171:791-798(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elkins M.F., Earhart C.F., "Opacity factor from group A streptococci is an apoproteinase."; FEMS Microbiol. Lett. 56:35-40(1988).
                                                                                                                                                                                                                                                                                                                                                            ENTE OR B0594.
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M. Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                           25;
COBALT 1 AND 2 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 (BY SIMILARITY).
COBALT 1 AND 2 (BY SIMILARITY).
BBB9A2AFC19952E8 CRC64;
                                                                                                                                                                                               64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHA 114
                                                                                   10.3%; Score 70.5; DB 1; Length 478; 28.8%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staab J.F., Elkins M.F., Earhart C.F.; "Nucleotide sequence of the Escherichia coli entE gene."; FEMS Microbiol. Lett. 50:15-19(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                           35; Indels
                                                                                                           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89290355; PubMed=2525505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90236256; PubMed=2110093;
                                   459
52921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-8 FROM N.A.
                                                                                                           Conservative
 262
331
364
459
478 AA;
                                                                                              Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                    synthase E)
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                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 ITLQVGSEQALFRVGKAPLLAFLDRTDQGLS-----LGSERAHADFDSHLDDALN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000165; AAC73695.1; -.

REMBL; U82589; AAB40794.1; -.

REMBL; M24148; AAA16101.1; -.

REMBL; M24148; AAA16101.1; -.

REMBL; M36700; AAA18492.1; -.

REMBL; M36700; AAA18492.1; -.

REMBL; M36700; SYECEB.

RECGENE; EG10263; entE.

RecGene; EG10263; entE.
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                                                                                                                          OF ENTEROBACTIN SYNTHESIS.

PATHWAY: ENTEROBACTIN SYNTHESIS.

PATHWAY: ENTEROBACTIN BIOSYNTHESIS. ENTEROBACTIN IS AN IRON-
CHELATING. COMPOUND INVOLVED IN TRANSPORTING IRON FROM THE
BACTERIAL ENVIRONMENT INTO THE CELL CYTOPLASM.

SUBUNT: PROTEINS ENTE, ENTE, BYTE, AND ENTG FORM A MULTIENZYME
COMPLEX CALLED ENTEROCHELIN SYNTHASE.
FUNCTION: ACTIVATION OF THE CARBOXYLATE GROUP OF 2,3-DIHYDROXY-BENZOATE (2,3-DHB), VIA ATP-DEPENDENT PPI EXCHANGE REACTIONS, TO THE ACYLADENYLATE, PREPARING THAT MOLECULE FOR THE FINAL STAGES OF ENTEROBACTIN SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWA4_MOUSE STANDARD; PRT; 551 AA.
P97471; Q9CW36;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAEGNPLPOG -> ECRRKSTAAR (IN REF. F818942DFDD8DC99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inner membrane; Complete proteome TRANSMEM 86 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59112 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126. RSLAEEQS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
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DOMAIN
DOMAIN
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SMA4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Shibata Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Raned G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA Ruture 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disruption in mice.";
Cytokine Growth Factor Rev. 11:49-58(2000).
-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA
(TRANSFORMING GROWTH FACTOR) SUPERFAMILY; SWAD4 IS THE COMMON
SMAD (CO-SMAD) (BY SIMILARITY). REQUIRED FOR GASTRULATION. MAY ACT
AS A TUMOR SUPPRESSOR.
                                                                          Anna C.H., Devereux T.R.; "Sequence and chromosomal mapping of the mouse homolog (Madh4) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBUNIT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).
INTERACTS WITH C-SKI, MSG1 AND ATF2 (BY SIMILARITY).
-:- SUBCELLUIAR LOCATION: IN THE CYTOPLASM IN THE ABSENCE OF LIGAND, MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: UBIQUITOUS.
-i- SIMILARITY: BELONGS TO THE DWARFIN/SMAD FAMILY.
-i- SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
-i- SIMILARITY: CONTAINS 1 DWB/MH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              franscription regulation; Multigene family.
                                                                                                                                                   SEQUENCE OF 67-551 FROM N.A.
STRAIN-C57BL/6J; TISSUE=Lung;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20175825; PubMed-10708952;
                                            STRAIN=A/J; TISSUE=Lung;
MEDLINE=97311184; PubMed=9166592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q13485; 1DD1.
MGD; MGI:894293; Madh4.
InterPro; IPR001132; Dwarfin.
InterPro; IPR003619; Dwarfin.A.
                                                                                                       human DPC4/MADH4 gene.";
Mamm. Genome 8:443-444(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U79748; AAB57905.1; -. EMBL; AK004804; BAB23576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00968; Dwarfin; 1.
SWART; SM00523; DWA; 1.
SWART; SM00524; DWB; 1.
                               SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
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Zhang Y., Feng X.-H., Wu R.-Y., Derynck R.;
"Receptor-associated Mad homologues synergize as effectors of the TGF-
                                                                                                                                                                                                                                                                                                                                                303.VHNELAFQPPISNHPAPEYWCSIAYFEMD-VQVGETFKVPSSCPV------VTVDGYVD 354
                                                                                                                                                                                                                                                                                                                  5 VSEELAFRIPV------ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against
DPPP homolog 4) (Deletion target in pancreatic carcinoma 4) (hSMAD4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moskaluk C.A., Hruban R.H., Schutte M., Lietman A.S., Smyrk T., Fusaro L., Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Fetal brain;
MEDLINE-96144664; PubMed-8553070;
MADALINE-96144664; PubMed-8553070;
MADA S.A., Schutte M., Shamsul Hoque A.T.M., Moskaluk C.A.,
da Costa L.T., Rozenblum E., Weinstein C.L., Fischer A., Yeo C.J.,
Hruban R.H., Kern S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequencing of DPC4 in the analysis of familial pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suppressor in TGFbeta-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homínidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [5]
CHARCTERIZATION OF SAD DOMAIN.
MEDLINE=20102728; PubWed=10636916;
de Caestecker M.P., Yahata T., Wang D., Parks W.T., Huang S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hruban R.H., Kern S.E.;
"DPC4, a candidate tumor suppressor gene at human chromosome
18q21.1.";
                                                                                                                                                                                                            DB 1; Length 551;
                                                                         S -> A (IN REF. 2).
R -> P (IN REF. 2).
0835EF88D9C1C980 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       355' PSG-GD-RFC-LGQLS--NVHRTEAI--ERARLHIGK 384
                                                                                                                                                                                                                                                                                                                                                                                                                       55 AAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 AA
                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                          10.3%; Score 70.5; I
32.0%; Pred. No. 13;
                                                      POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu F., Pouponnot C., Massague J.;
"Dual role of the Smad4/DPC4 tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagn. Mol. Pathol. 6:85-90(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96371046; PubMed-8774881;
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  SAD.
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Genes Dev. 11:3157-3167(1997).
                                                                                                                                60417 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 271:350-353(1996).
                                                                                                                                                                                                                                                              31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 383:168-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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274
320
450
257
292
551 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q13485;
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                                                                         CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                        Best Local
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Miyazono K.;

"Tefe beta signaling by Smad proteins.";

"Teransporative Growth Factor Rev. 11.15-22(2000).

"TRANSPERIME GROWTH FACTOR SIGNAL TRANSDUCTION BY TGF-BETA

"TO DAN AND PROVIDES AN ACTIVATION FUNCTION REQUIRED POR SMADIOR

SMADZ TO STIMULATE TRANSCRIPTION. MAY ACT AS A TUMOR SUPPRESSOR.

"TO DNA AND PROVIDES AN ACTIVATION FUNCTION REQUIRED POR SMADIOR

SMADZ TO STIMULATE TRANSCRIPTION. MAY ACT AS A TUMOR SUPPRESSOR.

"INTERACTS WITH C-SKI, MSGI AND ATF2.

"INTERACTON TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD.

"ISBASSE: DEFECTS IN MADH4 ARE A CAUSE OF PANCREATIC CARCINOMA.

"ISBASSE: DEFECTS IN MADH4 ARE A CAUSE OF PANCREATIC CARCINOMA.

"ISBASSE: DEFECTS IN MADH4 ARE A CAUSE OF PANCREATIC CARCINOMA.

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"ISBASSE: DEFECTS IN MADH4 ARE A CAUSE OF PANCREATIC CARCINOMA."
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Hill C.S., Shioda T., Roberts A.B., Lechleider R.J.;
"The Smadd activation domain (SAD) is a proline-rich, p300-dependent transcriptional activation domain.";
J. Biol. Chem. 275:2115-2122(2000).
                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 285-552.
MEDLINE-20113477; PubMed-10647180;
Oin B., Lam S.S., Lin K.;
"Crystal structure of a transcriptionally active Smad4 fragment.";
Structure 7:1493-1503(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS) OF 273-552.
MEDLINE-21127490; Pubmed-11224571;
Chacko B.M., Qin B., Correia J.J., Lam S.S., de Caestecker M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'The L3 loop and C-terminal phosphorylation jointly define Smad
                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 319-543.
MEDLINE-97357157; PubMed-9214508;
Shi Y., Hata A., Lo R.S., Massague J., Pavletich N.P.;
"A structural basis for mutational inactivation of the tumour suppressor Smad4.";
Nature 388:87-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Verschueren K., Huylebroeck D.;
Remarkable versatility of Smad proteins in the nucleus of
Transforming growth factor-beta activated cells.";
Cytokine Growth Factor Rev. 10:187-199(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20175821; Pubmed-10708948;
Wrana J.L., Attisano L.;
The Smad pathway.";
Cytokine Growth Factor Rev. 11:5-13(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "TGF-beta signal transduction.";
Annu. Rev. Biochem. 67:753-791(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20175822; PubMed=10708949;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trimerization.
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Search completed: July 18, 2002, 14:31:54 Job time: 943 sec

EMBL; AF045447; AAC03051.1; -.

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304 VHNELAFQPPISNHPAPEYWCSIAYFEMD-VQVGETFKVPSSCPI------VTVDGYVD 355
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                     POLY-ALA.
D -> H (IN PANCREATIC CARCINOMA).
                                                                                                                                                                                                                                                 Transcription regulation; Phosphorylation; Multigene family; Disease mutation; 3D-structure.

DOMAIN 31 140 DWA.
                                                                                                                                                                                                                                                                                                                                                                                                    Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                              27; Indels
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7EE3C4647712DA90 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; Score 69.5; 1
30.9%; Pred. No. 16;
                                 EMEL, AF045441; AAC03051.1; JOINED. EMEL, AF045441; AAC03051.1; JOINED. EMEL; AF045443; AAC03051.1; JOINED. EMEL; AF045444; AAC03051.1; JOINED. EMEL; AF045445; AAC03051.1; JOINED. EMEL; AF045445; AAC03051.1; JOINED. EMEL; AF045446; AAC03051.1; JOINED. PDB: 1VGS; 08-NOV-98. PDB: 1DD1; 24-NOV-99. PDB: 1G088; 29-NOV-00.
           AF045439; AAC03051.1; JOINED. AF045440; AAC03051.1; JOINED.
                                                                                                                                                                                    InterPro; IPR001132; Dwarfin.
InterPro; IPR003619; Dwarfin_A.
                                                                                                                                                                                                                                                                                                                                                            60439 MW;
AAC03051.1;
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         AAC03051.1
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SMART; SM00524; DWB; 1.
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530
466
493
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Best Local Similarity
AF045438;
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DOMAIN
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043060 porphyridiu
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092tw5 rhizobium n
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098c85 rhizobium n
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09xa56 streptomyce
09y003 pseudomonas
09a2n4 caulobacter
09sty4 streptomyce
09sty4 streptomyce
09sty5 rhizobium n
09sty20 homo sapien
088967 mus musculu
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091950 pseudomonas
09nfk2 boophilus m
09v2c0 pyrococus
091ch7 streptomyce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
NCBL_TaxID=1888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. van Wezel G.P., Rousseau C., Kraal B.; van Wezel G.P., Rousseau C., Kraal B.; "Cloning and sequencing of the Streptomyces albus ssgA gene."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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100.0%; Pred. No. 1.2e-60;
ive 0; Mismatches 0;
           Q9NYQ8
069245
Q9W1Y0
Q9L950
Q9NEK2
Q9V2C0
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043060
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09PNH8
092TW8
09M3R9
09M3R9
09B2W34
09B3W4
09B3W3
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Best Local Similarity 100.
Matches 135; Conservative
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Streptomyces albus
                                     01-MAR-2001 (01-MAR-2001)
SEQUENCE
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091268 streptomyce
09x7m8 streptomyce
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09fc07 streptomyce
09tc9 streptomyce
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Q9ss82 arabidopsis
O34788 bacillus su
Q98dn9 rhizobium l
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166.638 Million cell updates/sec
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                          Compugen Ltd
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Listing first 45 summaries

    protein search, using sw model

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Q9F9B7
P95753
Q9F9B5
Q9L268
Q9S2F7
Q9X7M8
Q9FC07
Q9K7R1
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_human:*
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Maximum DB seq length: 2000000000
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van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces goldeniensis ssgA gene.";

submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF195770; AAG28481.1; -.

SEQUENCE 135 AA; 14843 MW; 32006CC86BDE4ED6 CRC64;
                                                                                                                                                                                                                                                                                 Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J., Rinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EEMBL, AL096823; CAB46964.1.;
SEQUENCE 136 AA; 14920 MW; 4B67CIFIEOBECC88 CRC64;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                       Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Last annotation update)
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75.6%; Pred. No. 6.9e-42;
tive 9; Mismatches 24;
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MEDLINE-97000351; PubMed-8843436;
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Matches 102; Conservative
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01-DEC-2001 (TrEMBI
PUTATIVE REGULATOR.
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                                         01-NOV-1999
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                                                                                                                                     Shinichi K., Ensign J.; "Ensign J.; "Control of a gene involved in sporulation and "Clonding and characterization of Streptomyces griseus."; Cell. division of Streptomyces griseus."; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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BIRL: D50051; BAA21558.1: -. SEQUENCE 136 AA; 14783 MW; C6A28A7823AD7C8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.5%; Score 464; DB 2; Length 136; 65.9%; Pred. No. 1.6e-38; ive 18; Mismatches 28; Indels
        Length 135;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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01.MAY-1997 (TrEMBLrel. 03, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
     Score 481; DB 2;
Pred. No. 3.3e-40;
Ouery Match
Best Local Similarity 71.1%; Pred. No. ...
...trhes 96; Conservative 14; Mismatches
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MEDLINE=97286526; PubMed=9141673;
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Matches 89; Conservative
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SEQUENCE FROM N.A.
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL096852; CAB51005.1;
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                  Redenbach M., Kieser H.M., Dengaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MAINDL MICTOBIOL 21:77-96(1996).
EMBL; ALI37778; CAB10943.1;
SEQUENCE 159 AA; 17472 MW; BA41013F940D7315 CRC64;
                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Last annotation update)
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40.2%; Pred. No. 1.6e-14;
iive 12; Mismatches 64
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MEDLINE=97000351; PubMed=8843436;
    MEDLINE=97000351; PubMed=8843436;
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Submitted (JUL-1999)
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Best Local Similarity
Matches 51; Conserv
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"Cloning and sequencing of the Streptomyces netropsis ssgA gene.";
submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195772; AAG28483.11; -
SEQUENCE 145 AA; 15838 MW; 92AC0F30DF3D2620 CRC64;
                                                                                                                                                                                                                                                                                                                                  Streptoverticillium netropsis (Streptoverticillium flavopersicus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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Seeger K.J., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, PUTATIVE REGULATOR.
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Cerdeno A.M., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : || : ||||:||
131 EAALGKILAEEQNAG 145
                                                                                 :||| | ||||:||
122 EDALGRILAEEQNAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDALNRSLAEEQSAG 135
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                           DDALNRSLAEEQSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Best Local S
Matches 85
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SEQUENCE FROM N.A.
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                     STRAIN-A3(2);
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MEDLINE-97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Rinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049587; CAB40672.1;
 77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLGIDDGL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 LVEGVLDAAGDGDVRVCPVGQTAT-REVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 LIAGMOEPNGHGDVRVRPYAYDRTVLEFH----APEGTAVIHVRSGELRRFLQAAGELVP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSTVIEQSVEARLVAAAPRMPSIPATLHYDRADPFAVRMTFPAPATLEGVEVCWTFSREL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSFLVSEELAFR-----IPVELRYETVDPYAVRLTFHLPG---DAPVTWVFGREL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1902;
                                                                                                                                                                         Streptomyces coelicolor.

Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.

NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 138;
                                                                                                                                                                                                                                                                                                              Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels
                                                                                                                                                                                                                                                        Oliver K., Harris D.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             138 AA; 15261 MW; F531BA295144ABA5 CRC64;
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Last annotation update)
                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 22.6%; Score 155; DB 2; Local Similarity 31.2%; Pred. No. 7.5e-08; les 44; Conservative 16; Mismatches 63.
                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 AA
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                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 VGLEHLQLDLDHDLAELMRGS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 LGSERAHADFDSHLDDALNRS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, PUTATIVE REGULATOR.
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                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                        121 DDALNR 126
                                           137 AELLAR 142
                                                                                                                                                                                                                                                                                                    STRAIN-A3(2);
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Matches
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                                                                                                                                                                                                                                                                                                               Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-9596).
EMBL; AL391041; CAC01575.1; -.
SEQUENCE 156 AA; 17188 MW; 7181972EE7F33FB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physical map
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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"A set of ordered cosmids and a detailed genetic and physical methe 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049863; CAB42928.1; --
SEQUENCE 142 AA; 15741 MW; E24AA52C00AF40F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 156;
                                                                                                                    STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 EVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 TAWLQVNAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
19.5%; Score 134; DB 2; Length 15
Best Local Similarity 31.5%; Pred. No. 1.1e-05;
Matches 34; Conservative 18; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                    STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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Length 142;

DB 2;

17.0%; Score 117;

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RESULT 11

Q9RKC9

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL: A1049628; CAB40869.1;

ATP-binding.

SEQUENCE 862 AA; 94537 MW; B380462A621C7BDB CRC64;
                                                                        STRAIN—ATCC 15692 / PAO1;
STRAIN—ATCC 15692 / PAO1;
MEDLINE—204373737; Pubmed—10984043;
Stover C.K., Pham X.-Q.T. Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger R.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E., W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 AVRLIFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVGQ----TATREVHITLQV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Oliver K., Harris D.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 1 protein; Complete proteome.
741 AA; 79979 MW; 2C17D3850CEB98D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
PUTATIVE LARGE ATP-BINDING PROFEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 GSEQALFRVGK --- APLLAFLD-RTDQGLSLGSERAHADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 82; DB 16; 32.7%; Pred. No. 9.7; tive 8; Mismatches 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 79; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   862 AA
                                                                                                                                                                                                                                                                         opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004724; AAG06372.1; -.
Interpro: IPR001279; Beta_lactam_met.
Pfam; PF00753; lactamase_B; 1.
Hypothetical protein; Complete proteon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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MEDLINE=97000351; PubMed=8843436;
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Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1902;
                                       NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2);
                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                            10 AFRIPV--ELRYETVDPYAVRLTFHLPGDAPVTWVFGRELLVEGVLDAAGDGDVRVCPVG 67
                                                                                                                    19 ADRFPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRPES 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A set of ordered cosmids and a detailed genetic and physical map
the B Mb Streptcomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL: AL132674; CAB59654.1; -.
                                                                                                                                                                                  68 QTATREVHITLQVGS-----EQALFRVGKAPLLAFLDRTDQGLSLGSERAHAD 115
                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 107.5; DB 2; Length 126; 36.1%; Pred. No. 0.0035; tive 13; Mismatches 34; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2);
Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 126 AA; 13742 MW; D54AB574D28B4D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
HYPOTHETICAL PROTEIN PA2984.
                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: | :: | | | | GR----VQAVVEFHSPQGCSVVQFENKALIRFLRRT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GQTATREVHITLQVGSEQ -- ALFRVGKAPLLAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              741 AA.
                                                                                                                                                                                                                                                                                                    126 AA
            31.3%; Preu. ....
+ive 15; Mismatches
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                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL 13.7 KDA PROTEIN
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                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor
                Best Local Similarity
Matches 36; Conserv
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Matches 35; Conserv
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O9HZMO;

PA2984

Q9HZM0

RESULT 12

09HZM0

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       9
                                       LRYAAEVAPTVRGRVEDGLATHVP---PTTFEAAREVARAGGDLVLGLLPGPEDGID--- 699
                                                       64 CPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGSERAHADFDSHLDDA 123
                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                              50 EGVLDAAGDGDVRVCPVGQTATREVHITLQVGSEQALFRVGKAPLLAFLDRTDQGLSLGS 109
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                              40 DGTSDSDSDPDPPK-PEGDTRRQELLARI-----AMIQTSKVRLTDFLDERSEYLTKFA 92
         Gaps
                       LRYETVDPYAVR-----LIFHLPGDAPVIWVFGREL-----LVEGVLDAAGDG-DVRV 63
                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                               DB 10; Length 258;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.; DNA Res. 0:0-0(1997).
        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              110 ERAHADFD-----SHLDDALNRSL-----AEEQSAG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                      6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 AA
                                                                                                                                                 258 AA
                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
Pred. No. 23;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                              11.4%; Score 78; 29.7%; Pred. No. (
                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
31.7%; Pred.
                                                                                                                                                 PRT;
                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, MZB10.8 PROTEIN.
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05,
19,
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Matches 30; Conservative
        39; Conservative
                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-MARBURG 168;
Best Local Similarity
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RA Kunst E- 304440.3)

RA Kunst F. Ogasawara N. Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galieron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandl G.,

RA Ghiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kurita K., Leylne A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Leylne A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Setiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,

RA Setor V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Varita R., Wambutt R., Wadler E., Woshikawa H., Danchin A.;

RA Winters P., Wambutt R., Yamamoot H., Yamane K., Yasumoto K., Yasumoto K., Yate R.,

RA Prescone E., Wapat A., Yamamoot H., Yamane K., Yasumoto K., Yate R.,

RA Hile C., Wambutter R., Wadler E., Woshikawa H., Danchin A.;

RA The complete genome sequence of the gram-positive bacterium Bacillus
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: REQUIRES ZINC FOR ITS ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VSEELAFRIPVELRYE---TVDP----YAVRLTFHLPGDAPVTWVFG---RELLVEGVL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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Pred. No. 9.8;
6; Mismatches 29; Indels
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PROSITE; PS00059; ADH_ZINC; 1.
Complete proteome; Oxidoreductase; Zinc.
SEQUENCE 346 AA; 37341 MW; 5E327192D678F8A2 CRC64;
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InterPro; IPR00238; ADH_zinc.
InterPro; IPR002085; Adh_zn_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 KAAGATDIYAVELSPEROOKAEEL 212
MEDLINE-98044033; PubMed-9384377;
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HSSP; P07846; 1SDG.
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Best Local Similarity 39.3
Matches 33; Conservative
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

nucleic search, using sw model

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ou:

1797656 seqs, 10463268293 residues hits satisfying chosen parameters:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

US-09-749-185-6 407

Perfect score:

Sequence:

Scoring table:

Listing first 45 summaries

gb_ba:* GenEmbl:*

Database

9b_htg: 9b_in:* 9b_om:* 9b_ox:* 9b_ph:* 9b_pl:* 9b_pl:* 9b_r:*

em_fun:* em_hum:*

em_ba:*

em_om:* em_or:* em_in:*

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em_pat: em_ph:*

em_pl:* em_ro:*

em_ov:*

gb_sy:* gb_un:* gb_vi:*

Minimum Match 0% Maximum Match 100%

Post-processing:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of

Searched:

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(NL); WEZEL GILLES PHILIPPUS
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                                                                                                                                                                                                                  U52907 Thermus agu
AL556162 Streptomy
AL646086 Ralstonia
AL049587 Streptomy
AL391751 Streptomy
L14612 Pseudomonas
AE004898 Pseudomonas
AE001952 Dainococc
AL163003 Streptomy
AL589708 Streptomy
Continuation (3 of
               AX007218 Sequence
AX007218 Sequence
D50051 Streptomyce
AX007224 Sequence
AX07220 Sequence
AX07220 Sequence
AX08303 S.albus bet
AL137778 Streptomy
AL37778 Streptomy
AL37778 Streptomy
AL13778 Streptomy
AL13778 Streptomy
AL159178 Streptomy
AL159178 Streptomy
AL45629 Streptomy
AX089416 Sequence
AX089418 Streptomy
US2307 Thermus agu
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AE005987 Caulobact
AL592292 Streptomy
AL049863 Streptomy
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AL079356 Streptomy
AL359988 Streptomy
AC078894 Oryza sat
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1. .407
/organism="Streptomyces goldeniensis"
/db_xref="taxon:121022"
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                                                                                                                                                                                                                                                                                                               LMFLCHR16_02
LMFLCHR16_03
LMFLCHR36_31
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Sequence 7 from Patent W00000613.
AX007222 GI:9995088
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SCBAC16H6
AL646086
SCSF2A
SC9E12
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AF195771
SCE19A
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AF195770
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13.3 40901
13.2 110000
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259.8
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110.4
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DEFINITION
ACCESSION
VERSION
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AX007222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                               4444
                                                    July 18, 2002, 11:22:05; Search time 4085.76 Seconds (without alignments) 2084.582 Million cell updates/sec
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                                                                                                               1 atgagcttcctcgtctcgga......gaggagcagaacgccggctg 407
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SUMMARIES

em_htg_inv:*
em_htg_other:* em_htgo_inv:*

em_htg_hum:*

em_vi:*

em_sts:* em_un:*

A

Query Match Length DB

Score

Result

1,2

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abaB; bidA regulation; cysA; cystathionine/methionine gamma-synthase/lyase; gntR-family; integrated element; korSA; lysK-family; membrane protein; phosphotyrosine protein phosphatase; pray, psAM2; ptpA; ssgA; thiamine biosynthesis; thiC; transcriptional regulator; traSA.
                                                                                     Streptomyces griseus SsgA; possible cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 15441)
Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 acctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacc 120
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Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 407; DB 1;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 407; Conservative 0; Mismatches 0;
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          /db_xref="taxon:121022"
/db_xref="ATCC:21386"
                                                                        /gene="ssgA"
/note="similar to
division protein"
                                                                                                                     /codon_start=1
                                            /gene="ssgA"
1. .408
                                                        .408
                                . 408
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                                                                //oden_start=...
/coden_start=...
/toden_start=...
/transl_table=11
/transl_d="Cac07387.1"
/product="SsgA"
/protein_id="Cac07387.1"
/db_xref="c1:9995689"
/translation="MSFLVSEELSFRIPVELRYETCDPYAVRLFHLPGDAPVTWAFG
RELLIDGGPRPCGDGDVHIAPADPEFFGEVLFRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPIGGERSLADFPALLDEALDRILAEEQNAG"
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van Wezel,G.P., Rousseau,C. and Kraal,B.
Cloning and sequencing of the Streptomyces goldeniensis ssgA gene (pubblished)
2 (bases 1 to 408)
van Wezel,G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 acctgigaiccciacgccgigcggcigacciticaictgcccggagaigcccggigacc 120
                                                                                                                                                                                                                                                                                                                                                                                        61 ACCTGTGATCCCTACGCCGTGCGGCTGACCTTTCATCTGCCCGGAGATGCCCCGGTGACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 tgggcgttcgggcgggagttgctcatcgacggaggtccgcgggccgtgcggggacgggac 180
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Submitted (18-OCT-1999) Biochemistry, University of Leiden,
9502, Leiden 2300 RA, Netherlands
1. .408
                                                                                                                                                                                                                                                                                                                                1 ATGAGCTTCCTCGTCTCGGAAGAACTCTCCTTCCGTATTCCGGTGGAGCTGCGTTACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
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                                                                                                                                                                                                                                                                                                                  atgagetteetegteteggaagaaeteteetteegtatteeggtggagetgegttaegag
                                 1. .>4vɔ
/gene="ssgA"
/note="strain ATCC of Streptomyces goldeniensis"
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                        Length 407;
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                                                                                                                                                                                                                                                      Score 407; DB 6;
Pred. No. 5.3e-42;
Mismatches 0;
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Streptomyces goldeniensis SsgA
AF155770.1 GI:11066158
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Local Similarity 100.0%;
les 407; Conservative 0
                "ssgA"
                           .>405
                   /gene='
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08-JUL-1999

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Indels

Length 408

JOURNAL MEDLINE REFERENCE REFERENCE

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COMMENT

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SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLW
   complement(1, .4279)
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'gene="SCO11.01c" hypothetical protein, partial CDS, len:
'note="SCO11.01c" hypothetical protein, partial CDS, len:
'95 aa; unknown function, previously sequenced as

TR:053870 (EMBL:U37580), S.coelicolor hypothetical protein

ORF5 downstream of phosphotyrosine protein phosphatase
(159 aa). Weak similarity to the N·terminus of TR:06988

(EMBL:AL023797) Streptomyces coelicolor hypothetical

ECD:0.00036, 46.2% identity in 65 aa overlap. Continues
as SCH24.40c in cosmid H24 (EMBL:AL049826)"
                                                                                                                                                                                                                                                                Submitted (08-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.nih.go.jp/
jun/Gqi-bin/frameplot.pl. CAUTION: We may not have predicted the
jun/Gqi-bin/frameplot.pl. or correct initiation codon. Where possible we choose an initiation
codon (atg, gtg, ttg or (att)) which is preceded by an upstream
ribosome binding site sequence (optimally 5-13bp before the
initiation codon). If this cannot be identified we choose the most
upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mrvrpvvkrtararavLLDGDHLILIKRTKPGVDPywvrpGGGVEP
DDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ದ
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Cosmid Q11 Cosmid Q11 lies between H24 and D78 on the AseI-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                  Barrell, B.G. and Rajandream, M.A.
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/organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
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/protein_id="CAB46956.1"
/db_xref="G1:5457268"
Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available on the World Wide Web.
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Location/Qualifiers
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complement(1. .289)
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                                                                                                                                                                         3 (bases 1 to 15441)
James, K.D., Parkhill, J.,
Direct Submission
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                                                                                                         Seeger, K. and Harris, D.
                                                                       (bases 1 to 15441)
                                                                                                                                                  Unpublished
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                                                                                                         AUTHORS
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TITLE
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gene

CDS

FEATURES

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transcriptional regulator, len: 301 as; previously sequenced as TR:053869 (EMBL:037580) S.coelicolor lysR-like protein (301 aa). Highly similar to SW:ARAB_STRAT (EMBL:037580), arab, Streptomyces antibioticus transcriptional regulatory protein (301 aa), fasta socres; opt: 1581 z-score: 1813.2 E(::0, 80.3% identity in 300 aa overlap. Similar to many other transcriptional regulators. Contains probable helix-turn-helix motif at aa 17-38 (Score 1659, 44.84 SD). Contains Pfam match to PF00126 HTM_1, Bacterial regulatory helix-turn-helix protein, lysR family and PS00004 Bacterial regulatory proteins, lysR family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MOLALIRTFVTVHRAGSFTRAAALLGLSQPAVTSQIRTLERQLG
RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAETGLEDDSTLRTLHLAGPPEFTA
ERALPALGELTGEDGQAFALRASFGNAEFTLEGLAAGHHDLAIGTTRPRGALHTATPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDEVHVLVATPHWAERAGVEDVRDTDASALKHVPVVEVHESLPFVGRYWASVFDARPA
SPATVVAPDLRAVLACAVAGAGLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and PS00868 Cys/Met metabolism enzymes pyridoxal-phosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1518. .2696)
/gene="SCQ11.03c"
/note="SCQ11.03c, cysA, probable cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces antibioticus hypothetical protein found upstream of the aban gene (322 am) (87.1% identity in 232 am overlap). Contains Pfam match to PF01053 Cys_Met_Meta_PP, Cys/Met metabolism PLP-dependent enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative lysR-family transcriptional regulator"
/protein_id="CAB46957.1"
/db_xref="GI:5457269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="PS00044 Bacterial regulatory proteins, lysR family
note="sequence corresponding to EMBL: U37580 from 1 to
                                                              7...98
/note="overlap with Streptomyces coelicolor cosmid H24
(EMBL-AL049826) from 41528 to 41625"
complement(360. 1265)
/gene="SC011.02c"
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/gene="SCQ11.02c"
/note="Match to PF00126 HTH_1, Bacterial regulatory
helix-turn-helix protein, lysR family Score 145.96"
complement(1125. .1217)
/gene="SCQ11.02c"
                                                                                                                                                                                                                                                                                                                                 /gene="SCO11.02c"
/note="SCO11.02c, abaB, probable lysR-family
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/db_xref="G1:5457270"
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/gene="SCO11.03c"
                                                                                                                                                                                                                                                                                                      .1265)
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                            /note="abaB'
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PAT 06-SEP-2000
                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomyceso.

(bases. 1 to 407)

Kraal,B., Luiten,R.G. and Van Wezel,G.P.

Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms
patent: WO 0000613-A 3 06-74N-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLE GIJSBERTUS MARI
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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                                                                                                          Streptomyces griseus.
Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pred. No. 1e-23;
0; Mismatches 92;

    .407
    /organism="Streptomyces griseus"
/db_xref="taxon:1911"

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Sequence 3 from Patent WO000613.
AX007218
AX007218.1 GI:9995084
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/protein_id="CAC07385.1"
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/note="strain ATTC
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llarity 77.4%;
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Best Local S:
Matches 315,
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/gene="SCO11.04c"
//gene="SCO11.04c"
//gene
                                     TGHGDVILGYVAGRDAGAMAAVRRWRKIVGAIPGPMEAWLAHRSIATLQLRVDRODST
ALKVAEALRTRPEITGLRYPGLPDDPSHKVASQQMLRYGCVVSFTLPSRARADRFLDA
LRLVEGATSFGGVRSTAERRGRWGGDAVPEGFIRLSVGAEDPDDLVADLLRALDETTE
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GWHECEGADPRTEAVLADHGYGLDBAARQFQSWFGRLDLVVALDAGHLRALRRLAPT
ERDAKVRLLRSYDPAVAGGDLDVPDPYTGGRDGFEECLEMVEAASTGLLAAVREQVE
GRAA"
              IETPSNPGLDVCDVRRLVEAAHAGGALVAVDNTLATPLGQRPLELGADFSVASGTKQL
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                                                                                                                         complement(1533. .2624)
/gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
/gene="SCQ11.03c"
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                                                                                                                                                                                                                                                                         /note="PS00868 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
complement(2693, .3187)
/gene="SCQ11.04c"
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Pred. No. 1.6e-28;
); Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-tyrosine-phosphatase"
/protein_id="CAB46959.1"
/db_xref="G1:5457271"
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82.8%;
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/translation="MMSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAF
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DKLVPLGGEHTLGDFDGNLEDALGRILAEEQNAG"
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Shitchi, K. and Ensign, J.
Cloning and characterization of a gene involved in sporulation and cell division of Streptomyces griseus
Unpublished (1995)
Chases 1 to 1513)
Shinichi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-APR-1995) Kawamoto Shinichi, National Food Research Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2, Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996) Location/Qualifiers 1.1513
                                                                                                              Streptomyces griseus (strain:B2682) DNA.
Streptomyces griseus
Streptomyces griseus
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Actinomycetales; Streptomycineae; Streptomyces.
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Rawamoto,S. and Ensign,J.C.
Cloning and characterization of a gene involved in regulation sporulation and cell division of Streptomyces griseus
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/protein_id="BAA21558.1"
/db_xref="G1:2281004"
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                                                                                                                                                                                                                          Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 1 06-JAN-2000;
UNIV. LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS VAN (NL)
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GDAPVTWAFGRELLLDCLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTA
PLVAFLDRTDKLVPLGOEHTLGDFDGNLEDALGR"
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llarity 77.4%; Pred. No. 9.8e-24;
Conservative 0; Mismatches 92;
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/organism="Streptomyces griseus"
/db_xref="taxon:1911"
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/codon_start=1
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/db_xref="GI:9995083"
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/db_xref="G1:11066163"
/db_xref="G1:11061163"
/db_xref="G1:110G1NE061163"
/db_xre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF195772 438 bp DNA linear BCT 01-NOV-2000
Streptomyces netropsis SsgA (ssgA) gene, complete cds.
AF195772
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                                                                                                                                                                                                                                                                                     301 acggacaagatcgtgccgctggggcaggagcgttccctcgccgacttcgacgcctgctc 360
                                                                                                                                                                                                                                                                                                                                                          301; ACGGACAAGTCGGTGCCGCTCGGTCAGGAACAGACTCTGGGTGACTTCGAGGACAGCCTG 360
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                                                                                                                                              241 gggagcgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgc
       181 giccacategegecegecegaceegaagaegiteggegaggiecigateegeetgeaggig
                                                                        181 GTCCACATCGCCCCGACCGACCCCGAGGGCCTGTCGGACGTCTCCATCCGGCTCCAGGTG
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Submitted (18-OCT-1999) Biochemistry, University of
9502, Leiden 2300 RA, Netherlands

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Streptomyces netropsis

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 407)

Kraal, B., Luiten, R.G. and Van Wezel, G.P.

Reducting branching and enhancing fragmentation in culturing

Filamentous microorganisms

Patent: WO 0000613-A 9 06-JAN-2000;

UNIY LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA

(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS

VAN (NL)
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/db_xref="G1:995091"
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RELLLDGINRPSGGDOTVHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTD
KSVPLGQEQTLGDFEDSLEAALGKILAEEQNAG"
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    .407
    /organism="Streptomyces netropsis"
/db_xref="taxon:55404"

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Best Local Similarity 75.7%;
Matches 308; Conservative
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/translation="MSFLVSEELAFRIPVEERYETVDPYAVRLTFHLPGDAPVTWVFG
TELLVBCVLDAAGDGDVRVCPVGQTATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
CGLSLGSERAHADPSHLDDALNRSLAEEGSAG"
192 9 80 t
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van Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces albus ssgA gene
                                                                                                                                                                                                                                                                                                         Leiden, PO
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  gggagcgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgc
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9502, Leiden 2300 RA, Netherlands
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Pred. No. 8.9e-22;
0; Mismatches 102;

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    /organism="Streptomyces albus"
    /db_xref="taxon:1888"

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/db_xref="GI:11066161"
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/transl_table=11
/product="SsgA"
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Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms
Patent: WO 0006013-A 5 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLE GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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Bacteria; Firmicutes; Actinobacteriae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                       gacgaggcgctggaccgcatcctggccgaggagcagaacgccggctg 407
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Pred. No. 9.7e-22;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Streptomyces albus G"
/db_xref="taxon:1962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5 from Patent WO0000613. AX007220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρ
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74.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 305;
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Best Local
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ACCESSION
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ORGANISM
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jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (ady, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGVTFÄENALLKAHALAEATGLPAVADDSGLCVDVLNGAPGIFSARWAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGQLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTAEEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement(892. .1296)
Agene-"SCE194.03c,
//note-"SCE194.03c,
possible secreted protein, len: 134 aa;
unknown function, probable CDS suggested by GC frameplot,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCE19A.01"
/note="SCE19A.01"
/note="SCE19A.01, hypothetical protein, partial CDS, len:
>31 aa; unknown function, similar to members of the alkyl
hydroperoxide reductase C/thiol-specific antioxidant
family e.g. TR:053226 (EMBL:AL021185), bcp, Mycobacterium
tuberculosis bacterioferritin comigratory protein (157
aa), fasta scores; opt: 124 z-score: 238.1 E(): 6.2e-06,
63.3% identity in 30 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 aa; unknown function, similar to many e.g.
SW:Y030_MYCTU (EMBL:Z73902) Mycobacterium tuberculosis
hypothetical protein (204 aa), fasta scores; opt: 633
z-score: 743: 6E(1: 0. 52.0% identity in 200 aa overlap.
Similar to SW:YGGV_ECOLI (EMB:U28377), yggV, Escherichia
coli hypothetical protein (197 aa) (49.5% identity in 198
                             Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(243. .845)
/gene="SCE19A.02c"
/note="SCE19A.02c, conserved hypothetical protein, len:
                                                                                                                                                                                                                                                                                                                                       upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequence coverlapping sections once, or longer, because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid E19A lies between and overlaps cosmids E6 and E56 on the Asel-E genomic restriction fragment.
      where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="tRNA Leu anticodon TAG, Cove score 69.78"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="IVVDEOGKVERALYNVRATGHVAKIIKDLGI"
140. .226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"hypothetical protein"
/protein_id-"CAB50982.1"
/db_xref-"GI:5531350"
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/transl_table=11
/label=SCE19A.02c
/product="hypothetical protein"
/protein_id="CAB50983.1"
/db_xref="G1:5531351"
                                                                                                                                                         http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
correct initiation codon. Where po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="tRNA-Leu"
complement(243. .845)
/gene="SCE19A.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=2
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCT 16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Streptomycineae, Streptomycetaceae; Streptomyces.

(bases 1 to 35284)

Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.

A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL: http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 787 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4-hydroxyphenylpyruvate dioxygenase; ABC transporter; amino acid permease: asnC-family; cysteine synthase; nicotinamidase; osmorogulation; osmotolerance; oxidoreductase; permease; phosphoenolpyruvate-dependent; protease; regulator; ribonuclease PH; rph; sugar phosphotransferase system; transcriptional regulator; transposase; tRNA Leu; zinc metallopeptidase. Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                             265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 ACCGACCAGGGCTTGTCGCTCGGCAGCGAGCGGCACACGCCGACTTCGACAGCCACCTC 385
TGGTCTTCGGGCGTGAACTGCTGGTCGAGGGAGTCCTGGACGCCGGGGGGGACGCGAC
                                                                                                                                                                                                                           gtccacatcgcgccgaccgagagacgttcggcgaggtcctgatccgcctgcaggtg
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James,K.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
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Streptomyces coelicolor cosmid E
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Seeger, K. and Harris, D.
Unpublished
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SOURCE

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362 acgaggcgctggaccg 377
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                                                                                                                                                                                                                     /product="putative secreted protein"
/protein.id="CAB5094.1"
/brotein.id="CAB50994.1"
/d_xsref="G1:5331354.1"
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ADAIADSVTELQQAVENADDPTQWEESLNSIDKNLDRIGDQTDNTDVNKAVDDLGKAV
DNVRTSVENDETPDLSPYTDAAGELTKVCTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative ribonuclease PH"
/product="putative ribonuclease PH"
/db_xref="di="CABSO985.1"
/db_xref="di="S31353"
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/translation="MORIDGRTPQQLRPVTIERGWSKHAEGSVLVSFGDTKVLCNASV
/TEGVPRWRKGSGEGWYTAETAMLPRATUTRGDRESVKGRIGGRTHEISRLIGRSLRAV
IDYKALGSWTVVLLDCDVLQABGGTTRAAITGAYVALADAVAMAQGRKLIKANRKPLTG
TVSAVSVGIVDGTPLLLDLRYEEDVRAATDAMVVCTGDGRFVEVQGTAEAEPFRABELN
TLLDLATAGCTELAELQRKALDATLER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown function, similar to parts of many sugar permeases eg. TR:P96159 (EMBL:165013), malx, vibrio furnissii pTS (phosphoenolpyruvate-dependent sugar phosphotransferase system) permease for glucose (523 aa), fasta scores; opt: 217 z-score: 287.9 E(): 11-6.08, 48.1% identity in 77 aa overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCE19A.04c, rph, probable ribonuclease PH, len: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MASKAEKIVAGLGGIDNIDEIEGCITRLRTEVNDPALVNEAALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as; highly similar to many e.g. SW:RNPH_ECOLI (EMBL:X00781), rph, Escherichia coli ribonuclease PH (238 as), fasta scores; opt: 916 z-score: 1116.8 E(): 0, 60.8% identity in 240 as overlap. Contains Pfam match to entry PF01138 RNBse_PH, 3' excribonuclease family and PS01277 Ribonuclease PH signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF01138 RNase_PH, 3'
exoribonuclease family, score 266.70, E-value 3.1e-76"
complement(1805. 1843)
/note="SCE19A.04c"
/note="PS01277 Ribonuclease PH signature"
complement(2268. 2550)
/gene="SCE19A.05c"
complement(2268. 2551)
/gene="SCE19A.05c"
/note="SCE19A.05c"
/note="SCE19A.05c"
positional base preference and amino acid composition. Contains probable N-terminal signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PS00013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB, score 43.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAHGVVKMGTAIQVVIGTDADPIAAEIEDMM complement(2385...2489)
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/protein_id="CAB50986.1"
/db_xref="GI:5531354"
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                                                                                                                                                                                                                                                                                                                                                                      complement(1201. .1233)
/gene="SCE19A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1454. .2191)
/gene="SCE19A.04c"
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/gene="SCE19A.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1454. .2191)
/gene="SCE19A.04c"
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                                                                                                                                                                                                    /label=SCE19A.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                attachment site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="rph"
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BCT 29-JAN-2000
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Submitted (28-JAN-2000) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elongation factor; endodeoxyribonuclease; GTP pyrophosphokinase; membrane protein; membrane transferase; protein-export membrane protein; regulator; secreted protein; sugar transferase; threonine-tRNA synthetase; transport system inner membrane protein. Streptomyces coelicolor A3(2).

Streptomyces coelicolor A3(2).
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Actinomycetales; Streptomycineae; Streptomyces.
1 (bases 1 to 3840)
Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
Kinashi, H. and Hopwood, D.A.
Ast of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                              (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20202 CGGACGATCCCTACGCCGTGCACATCACCTTCCACATCGACTCCGGCCACCCGGTGCACT 20261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20322 TGCGGGTGTGGCCCGTCGAAGACGGAGGCCGCAGCGTCGTACTCGTCGTCGTCGAGCAGCC 20381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20142 TCAGGCTCGTCCTGTCGCCCGAGAGCGGCATTCCGGTGCCGGCCCGGCTCGGCTACCACA 20201
                                                                                                                        possible PTS transmembrane component,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20262 GGACGTTCGCCCGCGACCTTCTGGTGGAGGCGTCTTCCGGCCGTCCGGGCACGGGGACG 20321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 38640)
Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                   2 tgagcttcctcgtctcggaagaactctccttccgtattccggtggagctgcgttacgaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgcccggtgacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tecacategegecegecegaeceggagaegtteggegaggtectgateegeetgeaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggagcgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cggacaagatcgtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gggcgttcgggggggggttgctcatcgacggaggtccgcggggccgtgcggggacg
                                                                                                                                                                                                                                          Length 35284;
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                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                     len: 431 aa; similar to many PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                             1e-05;
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                              Score 110.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor cosmid L2. AL137778 AL137778.1 GI:6822206
                                                                                                                                                                                                                                                                             Pred. No.
                                                            2660. .3955
/gene="SCE19A.06"
/note="SCE19A.06,
2660. .3955
/gene="SCE19A.06"
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Seeger, K.J. and Harris, D.
                                                                                                                                                                                                                                          27.1%;
55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20502 CCGAGCTGCTCGCCAG 20517
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COMMENT

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/note="SCL2.03c, relA, GTP pyrophosphokinase, len: 847 aa; identical to previously sequenced SW:RELA_STRCO (EMBL.18926) Streptomyces coelloclor GTP pyrophosphokinase (EC 2.7.6.5) RelA, 847 aa and highly similar to SW:RELA_STRAT (EMBL:AF072829) Streptomyces antibhoticus RelA protein, 841 aa; fasta scores: opt: 4969 z-score: 4906.2 E(): 0; 90.38 identity in 848 aa overlap and to SW:RELA_CORGL (EMBL:AF038651) Corynebacterium glutamicum GTP pyrophosphokinase (EC 2.7.6.5) RelA, 760 aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.78 identity in 774 aa overlap. Contains Pfam match to entry PF01842 ACT, ACT domain and match to Prosite entry PS00017 ATP/GRP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / CEARS LATER OF THE STATE OF ARK PARAMETER DOAKNOTHED IN HAP AND THE STATE OF A STATE O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //note="PS00017 ATP/GTP-binding site motif A (P-loop)"
complement(3273. .7460)
Anote="Previously sequenced region SW:SCSECAPT EMBL:X85969
S.coelicolor secD, secE apt genes"
complement(3778. .3781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRGRGRKRRANADPGVVVKGVEDVWVKLARCCTPVPGDPIJGFVTRGSGVSVHRSDCV
NVDSLSREPERILEVEWAPTQSSVFLVAIQVEALDRSRLLSDVTRVLSDQHVNILSAA
VQTSRDRVATSRFTFEMGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //octe-"Pfam match to entry PF01842 ACT, ACT domain, score 63.10, E-value 6e-15" complement(2378. .2401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SCL2.04c, apt, adenine phosphoribosiltransferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3904. .4568)
/note="previously sequenced region SW:SCAPTRELA EMBL: x87267 S.coelicolor apt & relA genes" complement(3956. .4453)
                                                                                       /note="previously sequenced region SW:SCAPTRELA
EMBL:X87267 S.coelicolor apt & relA genes"
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/product="adenine phosphoribosiltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="GTP pyrophosphokinase"
/protein_id="CAB70915.1"
/db_xref="G1:6822209"
                                                                                                                                                                                                                                                                                                                    /gene="relA"
/note="SCL2.03c, relA, GTP
                                                                                                                                                                               complement(1229. .3772)
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                                                                                                                                                                                                                                                                      complement(1229. .3772)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="apt
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                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Juny our wing frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

The position of possible ribosome binding site sequences are given for sosition of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nfi-go.jb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to TR:033256 (EMBL:298209) Mycobacterium (Luberculosals hypothetical 49.8 kD protein MTCY174.11, len: 450 aa; fasta socres: opt: 843 z-score: 874.7 E(): 0; 45.9% identity in 296 aa overlap. Contains possible
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YOHINKQVDAHAYGDLEALRAKLOGIVALVETRREEKKAQARAKQSDEAKGAKEALV
AEAEELARSDQWRAAGERLESIVOTWKGLPRLDKSDELWHRPEAHAEAFSKRKQH
FAQLDAQREEARRIKERLVSEAEALSNSTDWGPTAARYRDLMSEWKAAGRAGKEHEDD
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SVNERWEAIGHVPRDARPKSRGGCTRSSGPSRRPRRPSGAGPTPRHARVPRA"
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                                                                                                                                     Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                           (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
    David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
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/organism="Streptomyces coelicolor A3(2)"
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/protein_id="CaB70913.1"
/db_xref="G1:6822207"
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/protein_id="CaB70914.1"
/db_xref="G1:6822208"
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/gene="SCL2.02"
/note="SCL2.02, unknown, len: 46 aa"
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/note="SCL2.01, hypothetical
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/gene="SCL2.01"
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/gene="SCL2.02"
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                                /translation="wadypeegvvekditplladpgaraltdalaegagrtgatkvv
GLEARGFILGAPVALRAGLGFIPVRKAGKLPGATLSQAYDLEYGSAEIEVHAEDLTAG
DRVLVVDDVLATGGTAEASLELIRRAGAEVAGLAVLMELGFLGGRARLEPALAGAPLE
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Debottay,P., Dusart,J., De Meester,F., Joris,B., Van Beeumen,J.,
Erptoum,T., Frere,J.-M. and Ghuysen,J.-M.
Nucleotide sequence of the gene encoding the Streptomyces albus G
                                                                                                                                                                                                                                                                                                                                                /gene="sece"
/note="SCL2.05c, secF, protein-export membrane protein,
len: 373 aa: identical to previously sequenced
SW:SECF_STRC0 (EMBL:R85969) Streptomyces coelicolor
protein-export membrane protein SecF, 373 aa and similar
                                                                                                                                                                   E-value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 cctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgcccggtgacct 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 tccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 ggagcgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgca
                                                                                                                                              PF00156 Pribosyltran,
domain, score 150.30,
                                                                                                                                                                                                                     /gene="apt"
/note="PS00103 Purine/pyrimidine phosphoribosyl
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Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
Bacteria; Firmicutes; Actinobacteriae.
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                                                                                                                                              /note="Pfam match to entry
Phosphoribosyl transferase
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'protein_id="CAB70916.1"
                                                                                                                                                                                                                                                          transferases signature"
complement(4468. .4503)
complement(4501. .5622)
                                                                                                                                                                                                                                                                                                               /gene="secF"
complement(4501. .5622)
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                                                                                                       complement(3980. .4429)
/gene="apt"
                                                                                                                                                                                                    complement(4103. .4141)
                     /db_xref="GI:6822210'
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LDRNGEFLSRRILYTQDDVEQADGAGPETGKPONLANAQLTVEELCEVSITASDNCAA
NUALRELGGPAVTREVRSLORVYLENDRWEPERLNSABEGRYDDTTSPRALTRYGRL
VLGDALNPRDRRLISWILLANTTSGDRERAGLPDDWTLGDKTGAGRYGTNNDAGVTWP
PGRAPIVLTVLTAKTEQDAARDGLVADAARVLAETLG
                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
SVSDAERRLAGLERASGARLGVYAYDTGSGRTVAYRADELFPMCSVFKTLSSAAVLRD
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ATP-binding protein; branched amino acid transport system permease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         integral membrane protein; ion transport integral membrane protein; polysaccharide biosynthesis protein; requlator; regulatory protein; secreted amidase; secreted protein; sigma factor; transcriptional regulator; transcriptional regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyce
1 (bases 1 to 32704)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGCTCGCCTTCCGCATCCCGGTGGAGCTGCGTACGAGACCGTCGATCCGTACGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 gaactctccttccgtattccggtggagctgcgttacgagacctgtgatccctacgccgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94.6; DB 1; Pred. No. 0.0023;
                                                                                                                                   /organism="Streptomyces albus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor cosmid 8A11. AL391041
cod ractamase precursor
Eur. J. Biochem. 166, 345-350 (1987)
87275916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAA26775.1"
/db_xref="GI:153339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="inverted repeat"
1230. .1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="inverted repeat"
540 c 496 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-lactamase"
                                                                                                                                                                                                                             /gene="beta-lactamase"
243. .1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1204. .1216
/gene="beta-lactamase"
                                                                                                                                                                                                                                                                                      /gene="beta-lactamase'
                                                                                                                                                                                 /db_xref="taxon:1888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 ctcatcgacggaggtccgcgg 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CTGGTCGAGGGAGTCAAGGGG 141
                                                                                                                                                                                                                                                                                                                /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL391041.1 GI:9716211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.2%;
79.4%;
                                                                                                                                                             /strain="G"
                                                                                                                                                                                                              243. .1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 79.4
Matches 112; Conservative
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2787. .3257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (adg. query) which is preceded by an upstream cribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If may be shorter because we only sequence in the sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are also included but some of these may be fortuitous.

The length in codons is given for each CDS.
Usually the highest scoring match found by fasta o is given for
USS which show significant similarity to other CDS in the database.

The position of possible ribosome binding site sequences are given
where these have been used to deduce the initiation codon.
Gene prediction is based on positional base preference in codons
using a specially developed Hidden Markov Model (Krogh et al.,
Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot
program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC8A11.01"
/note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                               Direct Submission
Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial regulatory proteins, luxR family and match to prosite entry P800622 Bacterial regulatory proteins, luxR family signature. Also contains a possible helix-turn-helix motif at residues 699. 720 (+3.25 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SC8A11.01"
//note="SC8A11.01"
/note="SC8A11.01, possible transcriptional regulator (fragment), len: >750 aa; similar to TR:095124 (EMBL:AL109747) Streptomyces coelicolor probable (EMBL:AL109747) Streptomyces coelicolor aa; fasta scores: opt: 818 z-score: 913.7 E(): 0; 32.6% identity in 775 aa overlap. Contains Pfam match to entry PF00196 GerE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative transcriptional regulator (fragment)" /protein_id="CAC01573.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                            Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre is fu by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                        Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                    Colney, Norwich, Norfolk NR4 7UH, UK Notes:
Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
correct initiation codon. Where pc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="A3(2)"
/db_xref="taxon:100226"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                    Saunders, D.C. and Harris, D.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC8A11.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=2
                                                                                                                                                                        (bases 1 to 32704)
                                                                   (bases 1 to 32704)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 2254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strand
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                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                    AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                   MEDLINE
   JOURNAL
                                                                       REFERENCE
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complement(3297...7058)

Gene="SC8A11.04c"

complement(3297...7058)

Gene="SC8A11.04c"

complement(3297...7058)

Gene="SC8A11.04c"

complement(3297...7058)

Gene="SC8A11.04c"

foote="SC8A11.04c"

foote="SC8A11.04c"

foote="SC8A11.04c"

foote="SC8A11.04c"

aa; similar to TR:09RL54 (EMBL:AL151596) Streptomyces

coelicolor probable secreted peptidase SCF31A.10, 1245

aa; fasta scores: opt: 1872 z-score: 1848.3 E(): 0; 37.2%

identity in 1300 aa overlap, to TR:995684 (EMBL:D8367)

Streptomyces albogitaseolus subtilisin-11ke protease, 1102

aa; fasta scores: opt: 1365 z-score: 1380.6 E(): 0; 33.4%

identity in 1268 aa overlap and to Streptomyces coelicolor probable secreted peptidase SC8A11.16c, 1239 aa; fasta scores: opt: 1835 z-score: 1467.4 E(): 0; 46.9% identity in 1279 aa overlap. Contains from matches to entries probable secretes to probable secreted periodiase family and PF02225 PA, PA domain and matches to Prosite entries SCORES PROBABLE SCO
                                                                                                                                                                    YTRATVADRILSTHRALAETILEGSPGRRLVHLAAATLGPDDELAGOLERFADDAQKRGG
ALAAAVPALGAGGILLINBADAEGPTER
ALAAAVPALGAGGILHINBADAEGPTER
ARAAVPALGAGGILLINBADAEGPTER
RVRQAAAELDRWKPDPDEQRRTQDMIDAAAGAFDVGSTSVARRLLWRAAARCFFODGDA
RVRQAAAELDRWKPDPDAPHVLTVRAYTEPYRGTDLIARLEKLRPDREDGRLLHYL
GISCARAIGDWGRATRYLAQAASWWRSOGRIGLIARSLAGSWRRLYGDGAGAREESAE
GISCARAIGDGAGAREESAA
GISCARAIGDGAGARESSAA
OVEGILAALFDSRAVEARABASVRRCWPRASVWAO
OVEGILLAALFDSRAVEAYDALARAFDKTDPHYHSTSRWLLVPDLVDAAAAAGRNEGARE
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/gene="SC8A11.03"
/gene="SC8A11.03, possible regulator, len: 156 aa; similar to TR:Q9S2F7 (EMBLAL096852) Streptomyces coellcolor putative regulator SC19A.24, 142 aa; fasta scores: opt: 272 z-score: 353.0 E(): 3.4e-12; 36.9% identity in 130 aa
/trānslation="IGAARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
VRARILQRAAGNPLALVELPRAAQGISPPLDDLPLTQRLETAFASRTDSLTRECRTFL
LVLAABPTAPLNQLLDVASRLAGSEVTVYALQEAVDAGLVVLTGRTPEFRHPLMRSAI
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PDHPLLVTIRFAPEGAPPVTWHVGRDLLHEGLRTTSGLGDVQVWADTPTDRETAWLQV
NAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLVELPELADRLPSEMMIVARTYSTAVLAPDDTAEDCYDSALSALPDTWPLARARHL
QHGRRLRRQRRNVDARKPLRLARDEFDRVGAQPWADMAREQLRAAGESDGRRRPSKGE
SLTVQERQIAELASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2093. .2176
/gene="SCBA11.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteases, subtilase family, aspartic acid active site, PS00137 Serine proteases, subtilase family, histidine active site and PS00138 Serine proteases, subtilase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2042. .2239
/gene="SC8A11.01"
/note="Pfam match to entry PF00196 GerE, Bacterial
regulatory proteins, luxR family, score 49.10, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTVTVDQVRAEVAQLMGATEEEFTRPRSAGRLRARPAPRRACRGW"
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/product="hypothetical protein SC8A11.02c"
/protein_id="CAC01574.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2184. .2453)
/gene="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
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/protein_id="CAC01575.1"
/db_xref="G1:9716214"
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/gene="SC8A11.02c"
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2787. .3257
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97000351
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                                                          ORGANISM
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JOURNAL
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JOURNAL
                                                                                                                                                 REFERENCE
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                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                   GSLSGTSMATPHVAGAAALLAAEHPDWTGQRIKEALVGTTAGTGRFSPFDAGSGRVDV
AAAVRSTLLASGDAFAQAHYPYTPGQTVRRDVTTNSGPAPVALDLALSPAELPEGLF
TLSEAQVTVPAHGTASVGYTHLDABEDNGAVATRIVASGADGAVLARTPVGVGVKEGR
RATLALTARDHHDKFLSGTVILKDVERNTARKYSVDASGRLDLRLSPSTSSYWMNSA
VPGVDGTHTLGFAMFTAPEVVLDADRTVAFDADDLRKAAAVTPRATANQFLRIDQYRG
                                                                             /transl_table=11
/product="putative secreted peptidase"
/protein_id="cacl1576.1"
/db_xref="GI:9116215"
/translation="MPIPWSRGRGLIVGIAALLVLTATAPAASALPGTVPPAPPAPA
                                                                                                                                                                                                                                 GPTRVLTLITGDRVTVTGEDGAETVLSVTDPHGRSGGAHVMTVGSDTYVYPDAAVPLL
GSGALDERLFNVTELLEDGYDDARADELPLIVTYTDTAARSLGARTPEGARRTRALSS
IRGAAISAEHSRAADFWTSLTGTGDAAAGGSAARSATSGGRLAGGIAKVWLDGKVRAT
                                                                                                                                                                                                                                                                                                                    LSDTTAQIGAPDVWSGGNTGEGVGVAVLDTGVDAGHPDFAGRIAATASFVPDQDVTDR
NGGTHVASSTVAGTGAASGGVFKGVAROSAGSLHGVLDNSGSGQDSWALAGMBRAVRD
QHAKIVSMSLGDSPPTGTPDLSEAVNMLSAERGALFVVAAGNGPEAVTVGTPAADA
ALTVGAVNGPGKGVDQIADFSSRGPRVGDNAVKPDLTAPGVGVLAARSRVAPEGEGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTGLFPFMDSYVAEYWRYDSLWVTPTPEVRTGSYTFATRWRQIQPPLIFSAGSQTFDD
VTVQSRSPQLPEGTRAYRAVWAGDGSATEFRGAEVRDRVAVVRRSDTVAPTDQAAAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAGARQLLILNDGYGKFDPWADLPPAAPLPVASLGTDDSARLLARFRGAGTTTLRVVS
HPVPRYAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSQGRAVEYRQDISLLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLGIVPTQVRAQGELTSWVTADDDVRWVSFASRPDLGQRGVARSYEPRSTTRETWFAP
IQHPRLLSDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGEDVNERIVWYGGLSPGPKPYRLYLEGSRNLPDRPYSTRTRTWWDFTSATTDFTRL
TPLPLVQLDYAVAVDLSGRAHRRTELTVTASHLEGAAGAGAIRTATVEVSYDDGATWH
RTALRKSADGWTARLDAPGRARYASLRTTAKDTEGNGVGQTLIRAFGLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Pfam match to entry PF02225 PA, PA domain, score 19.00, E-value 0.058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3016 GCACCACGAGCGGCCTGGGGGAACGTCCAGGTGTGGGCCGACACCCCCACCGGGAGA 3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2896 TICCGCCGCGAGTICCGTTACGATCCCGACCACCCCCTCCTCGTCACGATCCGCTTCGCCC 2955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2956 CCGAGGCCCCCCACCGGTCACCTGGCATGTCGGCCGTGACCTGCTGCACGAGGGCCTGC 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3076 ccecerescriccassicaacecacassicataascarasicaretroascerecessis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 tgcccggagatgccccggtgacctgggcgttcgggcgggagttgctcatcgacggaggtc 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 cgctggtggccttcctggaccgcacggacaagatcgtgccgctgggggcaggagcgttccc 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttccggtggagctgcgttacgagacctgtgatccctacgccgtgcggctgacctttcatc 97
family, serine active site. Also contains possible N-terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgcggccgtgcgggacgggacgtccacatcgcgcccgccgacccggagacgttcggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 aggtcctgatccgcctgcaggtggggagcgaccaggcgatgttccgggtcggcacggcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 32704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 tegeegacttegaegeeetgetegaegaegaegetggaeegeateetggee 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.11;
0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4374. .4613)
/gene="SC8A11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL159178.1 GI:7210989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.4
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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SCH22A/c
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VERSION
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strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1984) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Inn/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon gig, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most upstream initiation codon.

IMPORTANT: This sequence (optimally 5-13bp before the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid H22A Lies between neighbouring submissions.

Cosmid H22A Lies between and overlaps with cosmids H35 and H63 on the Asel-H genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-MAR-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //note="SCH22A.01, possible regulatory protein (fragment),
len: >465 aa; similar to TR:CAB59599 (EMBL:AL132662)
Streptomyces coelicolor hypothetical regulatory protein
SCF11.22, 877 aa; fasta socres: opt: 708 z score: 765.1
E(): 0; 34.5% identity in 466 aa overlap. Contains Pfam
match to entry PF01590 GAF, GAF domain and possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSKY and Beowulf Genomics.

Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
transmembrane transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                             A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                             Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBIO ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3. (bases 1 to 29625)
Cerdeno,A.M., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
                                                                                                                      Actinobacteridae;
                                                                                                                                                              Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 29625
/organism="Streptomyces coelicolor A3(2)"
                                                                                                                  Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
1 (bases 1 to 29625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:100226"
                              Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCH22A.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 29625)
Murphy, L. and Harris, D.
Unpublished
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/note="SCH22A.05, possible stress response protein, len:
194 aa; similar to TR:AAR11772 (EMBL.AE002055) Deinococcus
radiodurans tellurium resistance protein Terz, 195 aa;
fasta scores: opt: 300 z-score: 364.6 E(): 6.8e-13; 31.5%
identity in 178 aa overlap and to SW:TERZ_SERMA
(EMBL:138824) Serratia marcescens tellurium resistance
protein Terz, 193 aa; fasta scores: opt: 263 z-score:
321.2 E(): 1.8e-10; 28.2% identity in 195 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative stress response protein"
/product="putative stress response protein"
/protein_id="CAB76974.1"
/db_xref="cd::7210994"
/translation="MTLTKEGPADLDGVFHLSIGVSWDPTAGSSGGVLGKLRRKTG
TDLDLAVAMQGGDPVRLAGLDSLDPMGNGSLLHSGDNQTGHGDGDDETVTVEFARLP
SAITSIVFVAAAYKKGSSFQKARNISFKVYDATGGSSEQVADIWPSLLSQDNGCAVAK
AVRVGGTWKLEVVNETGKIKQGDEHALMRFAVSK"
complement(4798 . 5529)
/gene="SCH22A.06c"
complement(4798 . 5529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MGTDGFATWTRRFEDERERRAAGGDPDWERGAVLHRAVWAGIOR
ROGGBDGGDANLVAREEGGDADVARRVNEWPREDGNHALLARLLARGDRPALGSGHW
SDTVEWRLRELIGLEFELLVILMIAEVVALRYYRALROGTDDALTSEVAGRILADERRH
VPFHCERLHHSLAGELPAVTRRPVMVLMRLLLLAATVVVAADHGAGLRRLGVGRRRFAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4798. .5529)
/gene="SCH22A.06c"
/note="SCH22A.06c, possible membrane protein, len: 243 aa.
Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"SCH22A.07c, possible regulatory protein, len: 260 aa; similar to SW:BRPA_STRHY (EMBL:M64783) Streptomyces hygroscopicus bialaphos biosynthetic pathway regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28755 CCGGCGTCGACGCGGCCGTGAGCCTGCAGGACGCAGGTGCTGGTGCCGGTCCGGGGCG 28696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28815 ACGICGICACCGCCCGGCCGGCCTGCCCGCCGACGCCGACCGGGCCGCCCGGGCCCGGGCGC 28756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28695 GCGGCGAGACCTCGTTGCAGGGGACGGCGACCCAGGGCATCTCGGGCTCCGGCGCCGAAC 28636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 acgiccacaicgcgccgaccggagagacgitcggcgaggiccigaiccgcctgcagg 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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complement(5539. 5545)
complement(5637. 6419)
/gene="SCH22A.77c"
complement(5637. 6419)
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Best Local Similarity 54.9%; Pred. No. 23;
Matches 117; Conservative 0; Mismatches
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Job time: 13755 sec
            4088. .4672
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4088. .4677
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/transl_table=11
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GNPSWLVGRAVEATGAVGEHILDWYVQLAVAAVVVALYQLRGVAAERRFPRHHLVRT
FLLIGLLGPAIYMIFPVVGPVRAXGTGARGTGGEMALADLWPHTLPPVGPPHAFTYD
GVYFRNCWMSLHTAMATVIFIHSKRGPVLRWAGAFWLVATLTATLGFGYHYAIDLIA
GVVFAYTVAGGLRSLDRGWDRGSSLLVAHGALVFTAILASTRYLSLEWARNPWYFGPL
LLLAMASVIHGYVRTYKSWEPVTAAPPALPERAL
                                                                                                                                                                                                                                                                                                                                GDVVGHDLRAAADMSQIRNMIRALYYDPGAAPSTSLARLDRIWAAALDEAPVATALLA
ELEPAGGTWGURWSSAGHPPELVLLPDGRVRVLDMEPGLPLGYAPDLPREPDHGRPLPV
DSTVILFTDGLVEVPGQPLDRGLDALAVTASRLVGLAPEDLCHALVAHRPGNGHDDKA
VIALRTPPLTSYGS?
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/gene="SCH22A.02c"
/note="SCH22A.02c"
/inite="SCH22A.02c, hypothetical protein, len: 160 aa;
/inite="SCH22A.03c, EMBL.AL049587) Streptomyces
coelicolor hypothetical 17.1 kD protein SC5F2A.32, 161 aa;
fasta scores: opt: 256 z-score: 310.3 E(): 7.3e-10; 39.4%
identity in 160 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MLGPRVRGQPRTGFPCGDAMSTLLQPMPHRHVLTLPAAPPAVRL
ARETAEQALAEWGVNPGHPAVAPALLILSELVTNSVRHASPPSEGVTVTYAAGDDCLA
FAVHDRHPHQPRLHGARTTGRTGGLATVMELTGTLGGTAVVRGDGDGRGKSIWVTLPL
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RETITELVAVAQPGNVDALFAAVDAGAYULKAPASIMGYGGVVRAPDGTVWQLATSA
KRDTAPVTRDVDETVLLLGVEDVARTKRFVYEQGLTVGKSFGGKYVEFATGFGTVKLS
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                                                                                                                                                                                    /translation="EGPGSGPAQGSGEGPAAAPGRGGDDEPYASLLDLPLSSDLNRIG
EQLHALARAQRTLQELLQAVVNITGELELPAVLRRIVRTAMDLVGARYGAMGVLDQEG
                                                                                                                                                                                                                                             RILEEFIPLGLTTKELADLEGVELPRGRGLLGHLIHHPEPLRVKDISRHPESAGFPPG
                                                                                                                                                                                                                                                                                HPPMKSLLGVATSVRGRIYGNLYLSERKDGQPFDRHDEGVIRALAGTAGVAIENARLY
QQVRNSSEQFQRLLLPRLPDLRPFTAGAAYRPASAPAAVGGDWYDAMLLPGGACAAVI
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complement(1969. .3258)
/gene="SCH22A.03c"
/note="SCH2A.03c, possible membrane protein, len: 429 aa.
Contains possible hydrophobic membrane spanning regions"
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aglalimyvlimrqrlvaaavavgvdlitvalvrmaapatasgshsfgngalmyvlggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF01590 GAF, GAF domain, score 89.60, E-value 6.5e-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .130
/gene="SCH22A.01"
/note="nominal overlap with S. coelicolor cosmid StH35"
                                                                                           /product="putative regulatory protein (fragment)"
/protein_id="CAB76970.1"
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/db_xref="G1:7210991"
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/gene="SCH22A.04c"
/note="SCH22A.04c, unknown, len: 206 aa"
      at residues 48. .60"
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/product="putative membrane protein"
/protein id="CAB76972.1"
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complement(3337..3957)
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/gene="SCH22A.02c"
complement(1435, 1917)
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coiled-coil region
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/gene="SCH22A.01"
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S. clavuligerus cl
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N. magadaii bacter
Platenolide syntha
                          Sequence encoding
Micromonospora DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ssgA; liquid culture; filamentous bacteria; secondary metabolite;
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                                                                                                                           AAH52046
AAI99683
                                                                                                                                                                                                             AAF30757
AAS88065
AAS87399
AAN70466
AAT03572
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AAD14501
AAS51470
AAQ91580
                                                       AAV21187
AAZ32020
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AAA58471
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AAQ46806
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AAA11992
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AAD17184
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                                         4AS08693
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 AAD17184
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/label= SsgA_protein
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AAZ49730;
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S. spinosa DNA fra
S. spinosa DNA fra
Pseudomonas aerugi
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Streptomyces netro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDSS/gcgdata/geneseq/geneseqn-embl/NA2000:DAT:*/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001.DAT:*/
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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AAZ49728
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63.8
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Platenolide syntha Pseudomonas sp. WF

Streptomyces

98EP-0202148

26-JUN-1998;

(UYLE-) RIJKSUNIV LEIDEN

P. aeruginosa accB

45624 50000 1350 2760

2259.8 2259.8 2248.6 243.8 58.8 58.8 54.4

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Result No.

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361 gaggacgcactgggccgcatcctcgccgaggagcagaacgccggctg 407
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mycelium; antiblotic, antitumour agent; immunosuprressive agent;
hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent;
herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345;
bioinsecticide; receptor agent; antagonist; blomass; ds.
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                                                                                             enhancing fragmentation in filamentous improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                        Length 407;
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                                                                                                                                                                                                                                                                                               Sequence 407 BP; 56 A; 135 C; 145 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 407; DB 21; 100.0%; Pred. No. 2.3e-66;
                                                                                                                                                                                                                                                                                                                                                                      ö
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                          Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    griseus ssgA gene-2.
                                                                                                                                    English.
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                                                                                                                                   60pp;
                                                                                                                                                                                                                                                                                                                                                                 407; Conservative
                          B,
                                                                                           Reducing branching and
                                                                                                         microorganisms used to
                          Kraal
                                                    2000-147269/13
                                                                                                                                    Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                  P-PSDB; AAY44651
                         Van Wezel GP,
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Pred. No. 2.2e-39;
0; Mismatches 92; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                      ONDERZO
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NEDERLANDSE ORG WETENSCHAPPELIJK
                                                                                          /*tag= a
/label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     Luiten RGM;
                                               Location/Qualifiers
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77.48;
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Best Local Similarity 77.4
Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Wezel GP, Kraal B,
Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147269/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY4649
                                                                                                                                                                   WO200000613-A1
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                                                                                                                                                                                                                                                                                                               26-JUN-1998;
                                                                 mat_peptide
                                                                                                                                                                                                                  06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                             (UYLE-)
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gacgaggcgctggaccgcatcctggccgaggagcagaacgccggctg

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151 tgggcgttcggccgcgagctgctgctgacgggctcaacagcccgagcggcgacggcgat 210
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                                                                                                                                                                                                  mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bloinsecticide; receptor agonist; antagonist; blomass; ds.
                                                                                                                                                                                  liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 259.8; DB 21;
Pred. No. 2.2e-39;
); Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                       /product= "SsgA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luiten RGM;
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
31..438
                                                                                                                                                       griseus ssgA gene-1.
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                                                              BP.
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llarity 77.4%;
Conservative
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                                                            AAZ49727 standard; DNA; 438
                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                               Streptomyces griseus.
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                                                                                                                                                       Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 315;
                                                                                                                         18-APR-2000
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                                                                                         AAZ49727;
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The present sequence is a DNA (ATCC 23940) encoding S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparaslit agents, runniant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                   300
                                                                                                                                          acggacaagatcgtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctc 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                                                     271 ggcgcggaccgtgcgctgttccgggcggggacggcaccgctggtggcgttcctcgaccgg
181 gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
                                   211 gigoacateggeeegaeegageeegaggeeiteggagaigiteeaeateeggeiteeaggie
                                                                     gggagcgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgc
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                                                                                                                                                                                                                                     gacgaggcgctggaccgcatcctggccgaggagcagaacgccggctg 407
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/label= SsgA_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces netropsis ssgA gene.
                                                                                                                                                                                                                                                                                                                                              BP.
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P-PSDB; AAY44652.
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Gaps

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Indels

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Similarity

gtcggcgatccgtatgccatccggatgacgttccaccttcccggcgatgccctgtgacc 150 tgggcgttcgggcgggagttgctcatcgacggaggtccgcgggccgtgcggggacggggac 180

121

31 atgagetteetegteteegaggagetetegtteegtatteeggtggageteegataegag 90 atgagottcctcgtctcggaagaactctccttccgtattccggtggagctgcgttacgag

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08-MAR-2001
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                                      Gaps
                                                             1 atgagetteetegteteggaagaacteteetteegtatteeggtggagetgegttaegag 60
                                                                                                                 tgggcgttcggggcgggagttgctcatcgacggaggtccgcgggccgtgcgggggacggggac
                                                                                                                                              gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
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                       Length 407;
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 0 other;
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2.5e-37;
99;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                      Score 248.6; I
Pred. No. 2.5e-
0; Mismatches
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BP; 63 A; 151 C; 131
                                                                                                                                                                                                                                                                                                                                         albus G ssgA gene.
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                       61.18; 75.78;
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                               Best Local Similarity 75.7
Matches 308; Conservative
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 Sequence 407
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The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraline agents, herbicides, antiparasilic agents, runnant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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transgenic plant; insect resistance;
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Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                          59.9%; Score 243.8; DB 21; 74.9%; Pred. No. 1.9e-36; ive 0; Mismatches 102;
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                                                                           Disclosure; Fig 5; 60pp; English.
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Best Local Similarity
Matches 305; Conserv
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spinosa DNA fragment SEQ ID 1.

28-AUG-2001 (first entry)

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyne. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of III). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in forosamine and trimethylrhamnose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for recombinant production of insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                            Salas JA;
                                                                                                                                                                                                                                                                            Velten R,
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99DE-1057268
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                                                                                                                                                                                 (FARB ) BAYER AG.
29-NOV-1999;
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ij 21031 GTGGAGCTGCGGTACGACACGCGCAATCCGTACGAGATCTCCATGAAGCTCAACGTAGGC 20972 gtggagctgcgttacgagacctgtgatccctacgccgtgcggctgacctttcatctgccc 102 Gaps 3; Length 45624; Indels 0; Mismatches 167; DB 22; Score 58.8; DB Pred. No. 0.01; Query Match
Best Local Similarity 50.3%;
Matches 172; Conservative Query Match Best Local S 43 ò

Sequence 45624 BP; 7933 A; 14913 C; 14940 G; 7838 T; 0 other;

163 ccgtgcggggacgggacgtccacatcgcgccggccgacccggagacgttcggcgaggtc QΩ õ δ

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20854 GTGATCGAGATGAGCTCGCCGTCGGGGCAGGCCTCCTTCGAGGTGAATGCTGACCAGCTT 20795 ctgatccgcctgcaggtggggagcgaccaggcgatgttccgggtcggcacggcgctg 20911 GAGGCAGGCGAAGGCGATGTGCGGATCGGCCCTCGA---CGGGGTTTTCCGGGGTTGGTC 223 g g ò

20794 GCGGACTTCTTGAACGACACCTACGACGTGGTCGAACCTGGTGATGAACACCGGTGGATG 20735 gtggccttcctggaccgcacggacaagatcgtgccgctggggcaggagcgttccctcgcc 342 283 g ð

20734 AACGICGACGAGGIGCIGAGCCAGCIGCICTCGCACAACCIG 20693 343 gacttcgacgccctgctcgacgaggcgctggaccgcatcctg 384 අ ò

AAF88312 standard; DNA; 50000 AAF88312 AAF88312 XXXX

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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic cactivity involved in blosynthesis of spinosyns. (I) are used (I) to identify, inactivate or modulate genes involved in the blosynthesis of dentify, inactivate or modulate genes involved in the blosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylthamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of (II), their precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce the significantly increased levels or produce new derivatives of
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                                                             ....smille; trimethylrhamnose; polyketide synthase; biosynthesis; spinosyn; polyketide aglycone; transgenic plant; insect resistance; macrolide; insecticidal; ds.
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recombinant production of
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24594 gtggagetgeggtacgacagecgeaatecgtacgagatetecatgaageteaaegtagge 24653 24714 gaggcaggcgaaggcgatgtgcggatcggcctcga---cgggggttttccgggggttggtc 24770 24771 gigaticgagaigagetegeegteggggeaggeeteettegaggigaaigetgaeeageti 24830 24713 giggagotigogitacgagacotgigatocotacgocgigoggotgacotitoatotgoco 102 103 ggagatgccccggtgacctgggcgttcgggcgggagttgctcatcgacggaggtccgcgg 162 24654 acggacggtcaggtggactgggtgatcgcccgcgacctgctggccgacgggctgatcgcc 163 ccgtgcggggacgggacgtccacatcgcgcccgccgacccggagacgttcggcgaggtc ctgatccgcctgcaggtggggagcgaccaggcgatgttccgggtcggcacggcgccgctg Length 50000; ., m Score 58.8; DB 22; Length Pred. No. 0.01; 0; Mismatches 167; Indels 14.4%; 50.3%; Matches 172; Conservative Similarity Query Match Best Local S 223 qq Dp g ò ŏ δ

283 giggcetteciggacegeaeggacaagategigeegeiggggeaggagegtteeetegee 342

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Sequence 50000 BP; 8484 A; 16290 C; 16535 G; 8691 T; 0 other;

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Length 1350;

AAS54328

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13.48;
47.68;
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-1994;
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  Query Match
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                          Best Local
Matches 10
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AAQ79921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The protein salso useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part form the printed specification, but was obtained in electronic
                          24831 gcggacttcttgaacgacacctacgacgtggtcgaacctggtgatgaacaccggtggatg 24890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa DNA for cellular proliferation protein #459.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; ds; prokaryotic cellular proliferation gene;
antibiotic; antibacterial; drug design.
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                                                                                                                   24891 aacgtcgacgaggtgctgagccagctgctctcgcacaacctg 24932
                                                                       343 gacttcgacgccctgctcgacgaggcgctggaccgcatcctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Seq ID No 7965; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL, Zyskind JW,
Xu HH;
    AAS54328 standard; DNA; 1350
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2000US-253625P.
2000US-257931P.
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2000US-207727P.
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P-PSDB; AAU36469.
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27-NOV-2000;
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26-MAY-2000;
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1064 agcacttccacgccccgggcggcaacggcgtgcgcgtcgactcgcacctctacaggggct 1123
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                                                                                                                                                                                                                                                                                                                         284 tggccttcctggaccgcacggacaagatcgtgccgctggggcaggagcgttccctcgccg 343
                                                              44 tggagetgegttacgagacetgtgatecetacgecgtgeggetgacettteatetgeecg 103
                                                                                             824 tegagitectetacgagaaeggeegettetacticategagaigaacaetegegigeagg 883
                                                                                                                             104 gagatgccccggtgacctggggcgttcgggcgggagttgctcatcgacggaggtccgcggc 163
                                   Gaps
                                                                                                                                                             884 tggagcacccggtatctgagatggtcaccggtgtcgacatcgtcaaggagatgctgcgca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing lipid levels in plants by modulating malonyl-CoA levels - partic. for ollseed crops, also nucleic acid
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                                   Indels
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/label= accC
/note= "encodes biotin-carboxylase"
Score 54.4; DB 23;
Pred. No. 0.087;
); Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                      1124 acagcgtgccgccgaactacgactcgctggtcggca 1159
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1349..2701
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/label= accB
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16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DZIE) (ZOTC) (ZOTC) (SEKU/) (FJAE/) (BRAU/) (STRO/) (
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(ALPH-)
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                                                                                                                                                                                                                                                                                                                                          44 tggagctgcgttacgagacctgtgatccctacgccgtgcggctgacctttcatctgcccg 103
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                        The accB and accC genes of Pseudomonas aeruginosa PaO encode the biotin carboxyl carrier protein (BCCP, given in AAR66743) and biotin-carboxylase (BC, given in AAR66744) components, respectively, of acetyl-COA-carboxylase. The genes may be used to modulate lipid accumulation in transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcgcctccggcgagaagctctcgatccgccaggaggacgtggtcatccgcggccatgcgc
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                                                                                                                                                                                                                                                                                                     . (0
                                                                                                                                                                                                                                                               Length 2760;
constructs for expressing acetyl-CoA carboxylase, transgenic
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                                                                                                                                                                                                                                                                                                     Indels
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/note= "CDS does not include stop codon"
                                                                                                                                                                                                        Sequence 2760 BP; 530 A; 962 C; 835 G; 433 T; 0 other;
                                                                                                                                                                                                                                                               13.4%; Score 54.4; DB 16; 47.6%; Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                   0; Mismatches 176;
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16550..49840
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6952..16530
/*tag= d
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                                                       Fig. 4A-E; 48pp; English
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2806..6906
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                 plants and peptide prods
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                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 160; Conserv
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The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrollide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130, AAE10131, AAE10132, AAE10133, AAE10137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nystatin polyketide synthase polynucleotides and polypeptides. useful as antibiotics and antifungals ^{\circ}
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                                                                                                                                                                                  protein"
not include start codon"
                                                                                                                                                                                                                                                                                                                              (short) protein"
not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "CDS does not include start codon" (3765..64961
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Gulliksen O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
SINTEF STIFTELSEN IND TEK FORSK.
ALPHARMA AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "CDS does not include complement (62551..63615)
                                                                                                         /*tag= g
/product= "NysR1 protein"
                                                                                                                                                                                                                                                                    /product= "NysR3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                /product= "NysR5 protein"
                                             /product= "NysE protein"
51405.54305
/*tag= q
"NysC protein"
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/product= "ORF1 protein"
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Sletta H,
                                                                                                                                                                                                                                                                                                                                                      "CDS does
                                                                                                                                                                                  /product= "NysR2
                                                                                                                                                                                                        "CDS does
                                                                                                                                                                                                                                                                                                                                 /product= "NysR4
                                                                                                                                         54329..57190
/*tag= h
                                                                                                                                                                                                        /note= "CDS d
57180..59963
                                                                                                                                                                                                                                                                                      60415..61047
/*tag= j
/product= "N)
50260..51015
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10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
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Ellingsen TE,
                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                   /*tag=
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DZIEGLEWSKA H.
ZOTCHEV S B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
STROM A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-557614/62.
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RESULT 12
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         NAME OF THE PARKET OF THE PARK
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                                                                                                                                                                   52186 tecggeeggaegeeggeggggagegeeggggeegeegaggteggeagteaegteetegeee 52245
                                                                                                                                                                                                                                                                                                                                                                                                                                          52246 gctcggtgcgctgcctgttggagcgccggccgcctgggtgcgcggcggggtggccgtgcca 52305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52306 tegeogracteggeeeggagtgeacegagttgetggeggegetegeeggegteeeggeeg 52365
                                                                                                                             98 tgcccggagatgccccggtgacctgggcgttcgggcgggagttgctcatcgacggaggtc 157
                                                                                                                                                                                                                                                      217
                                                                                                                                                                                                                                                                                                                                                                                218 aggtectgatecgeetgeaggtggggagegaceaggegatgtteegggteggeaeggege 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 cgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcaggagcgttccc 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;
   Length 65140;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (60238..61296)
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces noursei nystatin PKS gene cluster DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= g
/product= "NysD2 complete protein<sup>†</sup>
120628..121308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
Product= "NysI complete protein"
84792..51099
      Score 52.2; DB 22;
Pred. No. 0.16;
                                                                0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= h
/product= "NysR4 (long) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Nysk protein"
57503.,58687
/*tag= d
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complement (58786..58980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "NysJ protein"
51155..57355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "NysM protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
6337..34771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD17186
ID AAD17186 standard; DNA; 125401 BP.
12.8%;
ilarity 48.5%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001; 2001WO-GB00509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ပ
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                                Similarity
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                                                                Matches 144;
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      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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Db 112387 tytocygcygcaatccyctygccetcyccocycctcotcyacyaactccycycycyayyycy 112446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antibiotics. The present sequence is a Streptomyces noursel nystatin PKS gene cluster DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 aggteetgateegeetgeaggtggggagegaceaggegatgtteegggteggeaeggege 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 cgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcaggagcgttccc 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 tgcccggagatgccccggtgacctgggcgttcgggcgggagttgctcatcgacggaggtc 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-557614/62.
P-PSDB; AAE10143, AAE10144, AAE10145, AAE10146, AAE10147, AAE10148,
AAE10149, AAE10150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338' tegeegaettegaegeeetgetegaegaegaegeetggaeegeateetggeegaggage 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nystatin polyketide synthase polynucleotides and polypeptides, ful as antibiotics and antifungals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 cgcggccgtgcgggggacggggacgtccacatcgcgccgccgccggagagacgttcggcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 125401 BP; 15664 A; 49692 C; 42871 G; 17174 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                    Strom AR;
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                                                                                                                                                                                                                                                                                                                                                                 Brautaset T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52.2; DB 22;
Pred. No. 0.15;
0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                     Fjaervik E, Brautase
Jetta H, Gulliksen O;
                                                                                          NORGES TEKNISK NATURVITENSKAPELIGE.
F STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 188-254; 266pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                        Ellingsen TE, Sletta H,
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Best Local Similarity 48.5%;
Matches 144; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1879
                 10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
2000GB-0002840
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                                                                                                                                                                                                                                                                                                                                                                    Sekurova ON,
                                                                                                                                                                SINVENT AS.
DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
FJABRVIK E.
BRAUTASET T.
                                                                                                                                               ALPHARMA AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                    STROM A R.
                                                                                                                     SINTEF
                                                                                               VINU (-ONYU)
                                                                                                                                                                                                                                                                                                                                                                    SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ11126
                                                                                                                                                                                                                                                                                                                                                                                          Valla S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ11126
                                                                                                                (SNTF)
(ALPH-)
(SINV-)
(DZIE/)
(ZOTC/)
(SEKU/)
(FJAE/)
                                                                                                                                                                                                                                                                                                                  (STRO/)
                                                                                                                                                                                                                                                                                                                                                                 Zotchev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
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Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
                                                                                                                               Everninomicin; antibiotic; bottle-neck gene; orthomicin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /partial
/note= "No start codon"
complement (12108..13022)
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                                                                                                                                                                     Micromonospora carbonacea var. africana
                                                                                                                                                                                                                                                  complement (1389. 1394)
                                                                                                                                                                                                                                                                         complement (1490..2611)
                                                                                                                                                                                                                                                                                                                complement (2618..2622)
                                                                                                                                                                                                                                                                                                                                           complement (2622..3860)
                                                                                                                                                                                                                                                                                                                                                                                complement (3867.3870)
                                                                                                                                                                                             Location/Qualifiers
complement (132..1382)
             AASO8693/c
ID AASO8693 standard; DNA; 109519 BP.
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/product= "EvdJ"
12027..12455
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/product= "EvdL"
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/product= "EvrA"
                                                                                                                                                                                                                                   /product= "EvdA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "EvdF"
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/product= "EvdI"
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                                                                                                                                                                                                                                                                                                                                                                    "EvdC"
                                                                                                                                                                                                                                                                                                                                                                                                                                     "EvdD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "EvdE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "EvdH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= p
.0424..11176
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/*tag= r
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/*tag= h
5309..6235
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6232..7275
/*tag= j
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/*tag= g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence contains the coding information for (a) the cytochrome P450 enzyme, P450RII; and (b) the electron donor iron sulphur protein FeS-B. It is contained in a recombinant plasmid which is used to transform host Streptomyces species which in turn are used to coost a plant seed to transform the plant. The resultant transsee also AQIII27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 cacggcgccgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcagga
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/product= FeS-B protein
                                     Location/Qualifiers
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1369..1575
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Best Local Similarity 50.6
Matches 125; Conservative
             Streptomyces griseolus.
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11-SEP-1989;
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282 ggtggccttcctgggaccgcacggacaagatcgtgccgctgggggcaggagcgttccctcgc 341 222 octgatccgcctgcaggtggggagcgaccaggcgatgttccgggtcggcacggcgcgct 281 0; Gaps Length 109519; Score 51.6; DB 22; Length 1 Pred. No. 0.2; 0; Mismatches 119; Indels /*tag= be complement (45767..45770) /*tag= be /*tag= bf /*tag= bf complement (45952..45956) /*tag= bg /*tag= ax /product= "EvrU" complement (41679..42707) complement (42714..42717) /*tag= az /*tag= ba /product= "EvrW" complement (43807..43811) /*tag= bb complement (43799..44866) /*tag= bc /product="Evrx" complement (45014..45760) /*tag= bd complement (47156..49234) complement (55135..56094) complement (56100..56103) complement (56184..56813) complement (40899..40902) complement (40887..41576) complement (42810..43799) /*tag= bh //*tag= bh //*product= "EvsB" | /*tag= bi //*tag= bi //*tag= bi //*tag= bi //*tag= bk //* /product="Evsc" 53554..54207 /*tag= bl /product="EvbA" /*tag= bq /product= "EvbC2" 56961..58709 /product= "Evrv" 'product- "Evry" /product= "EvbC" Query Match 12.7%; Best Local Similarity 50.8%; Matches 123; Conservative p /*tag- bo Α /*tag= ay /*tag= CDS RBS CDS RBS CDS RBS RBS RBS CDS CDS RBS CDS CDS CDS CDS RBS CDS CDS CDS RBS CDS Op q g ò ò

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Iruela-Arispe L, Hastings GA,
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       The present sequence represents a Amycolatopsis mediterranei rifamycin synthesis gene cluster DNA fragment from the present invention. The DNA fragment comprises a DNA region involved directly or indirectly
342 cgacttcgacgccctgctcgacgaggcgctggaccgcatcctggccgaggagcagaacgc 401
                                                                                                                          Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.
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                                                                                                                                        Amycolatopsis mediterranei; rifamycin; synthesis; gene cluster; polyketide synthase; actinomycete; ansamycin; ds.
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/label= ORF B
/product= "polyketide synthase"
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/product= "polyketide
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in the gene cluster responsible for rifamycin synthesis, including the adjacent DNA regions to the right and left which, by reason of their function in connection with rifamycin biosynthesis, qualify as constituents of this rifamycin gene cluster, and functional fragments, derivatives or constituents of these. The Amycolatopsis mediterranel rifamycin synthesis gene cluster DNA fragment can be used for producing rifamycin, rifamycin analogues or precursors. It can also be used for inactivating or modifying genes involved in ansamycin or rifamycin biosynthesis. The DNA can be used for constructing mutant actinomycetes strains from which the natural rifamycin or ansamycin biosynthesis gene cluster has been partly or completely deleted. The DNA fragment can be used for assembling a library of polyketide synthases, which can be used for assembling a library of polyketides. A hybridisation probe of the invention can be used for identifying DNA fragments involved in the biosynthesis of ansamycins.
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pred. No. 0.27;
0; Mismatches 110; Indels 0
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51.5%;
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Matches 117; Conservative
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RUBEN S M.
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WPI; 1999-590684/50.

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AAE32000 and AAE32001 encode, and AAE49501 and AAE49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2 and METH2 have been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, sometic, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZ32002 to AAZ32000, and AAY49503 to AAX49511 represent sequences given in the exemplification of the present
                                                                      New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                      Disclosure; Page 296-321; 457pp; English.
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Gaps 12.1%; Score 49.4; DB 20; Length 38734; 51.6%; Pred. No. 0.55; 1ve 0; Mismatches 106; Indels 0; Query Match 12.1 Best Local Similarity 51.6 Matches 113; Conservative

Sequence 38734 BP; 6142 A; 13140 C; 13585 G; 5867 T; 0 other;

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2535 cggctgacctccgacgagggcgccgtcgacgacttcggcttcgacccggagctgaccgac 2594 217 gaggtcctgatccgcctgcaggtggggagcgaccaggcgatgttccgggtcggcacggcg 276 QQ ò

gactacctgctccccgccctgcgcctgtacgagaagtacttccgggtcgacctggag 2654 2595 pp

2655 ggactggagaacgtgccggccgagggggggcgcactcctggtcgccaaccactccggcacc 2714 336 ccgctggtggccttcctggaccgcacggacaagatcgtgccgctggggcaggagcgttcc 277 Ωp ò

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Search completed: July 18, 2002, 11:37:34 Job time: 11319 sec

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CITY: Menlo Park
STATE: California
COUNTRY: US
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US-08-074-121-4
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603.847 Million cell updates/sec
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Patent No. 5212296
Patent No. 5212296
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Sequence 13, Appl
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                                                                        July 18, 2002, 11:25:01; Search time 165.56 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-453-695A-109
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Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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978 4
11604 4
15079 4
20235 1
20235 1
4411529 3
36519 44377 2
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ALIGNMENTS

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US-GN-074-121-4

US-GN-074-121-4

Sequence 4, Application US/08074121

PETCHI No. 5767362

GENERAL INFORMATION

APPLICANT: Reauf, Vic C.

TITLE OF INVENTION: Lipid Content of Plant Tissues

NUMBER OF SEQUENCES: 15

CORRESPONDERS:

ADDRESSEE: Fish Richardson

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STATE: California

COUNTRY: 1200 Sand Hill Road, Suite 100

CITY: Menlo Park

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menlo Park

STREET: 200 Sand Hill Road, Suite 100

CITY: Menlo Park

STREET: 200 Sand Hill Road, Suite 100

CITY: Menlo Park

STREET: 200 Sand Hill Road, Suite 100

CITY: Menlo Park

STREET: 200 Sand Hill Road, Suite 100

CITY: Menlo Park

STREET: 200 Sand Hill Road, Suite 100

COUNTRY: 1200 SATER: Sand Hill Road, Suite 100

COUNTRY: Babbale FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Babenton Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: 05/08/074,121

FILLING DATE: 08-UNN-1993

CLASSIETARION NUMBER: 32/50

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 05/985

TELEFRAM: (415) 854-0875

TELEFRAM: (415) 854-0875

TELEFRAMISCHISTIGS:

LENGTH: 321 base pairs

TELEFRAURE: CASSIET CASSIE
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12.7%;
50.6%;
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Best Local Similarity 50.69
Matches 125; Conservative
; LOCATION: 1349..2695
PCT-US94-06447-4
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                                                                           44 tggagctgcgttacgagacctgtgatccctacgccgtgcggctgacctttcatctgcccg 103
                                                                                                                                              104 gagatgccccggtgacctgggcgttcgggcgggagttgctcatcgacggaggtccgcggc 163
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                                            Gaps
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0
     13.4%; Score 54.4; DB 1; Length 3231; 47.6%; Pred. No. 0.0045; Live 0; Mismatches 176; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Calgene, Inc.
TITLE OF INVENTION: Methods and Compositions for Modulating
TITLE OF INVENTION: Lipid Content of Plant Tissues
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Well, Gotshal & Manges
STREET: 2882 Sand Hill Road, Suite 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06447
FILING DATE: 06-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 acttcgacgccctgctcgacgaggcgctggaccgca 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CGNE-097/WO TELECOMNUNICATION INFORMATION: TELEPHONE: (415) 926-6200 TELEFAX: (415) 854-3713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9406447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                        Best Local Similarity 47.6
Matches 160; Conservative
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STATE: California
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PCT-US94-06447-4
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                                                                                                                             44 tggagctgcgttacgagacctgtgatccctacgccgtgcggctgacctttcatctgcccg 103
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                                                              Gaps
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Length 3231;
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Pred. No. 0.015;
0; Mismatches 122; Indels
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Patent No. 9212296
Query Match 13.4%; Score 54.4; DB 5; Best Local Similarity 47.6%; Pred. No. 0.0045; Matches 160; Conservative 0; Mismatches 176;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
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ORGANISM: Mycobacterium tuberculosis
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CITY: Chicago
STATE: Illinois
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                                                                                       US-09-103-840A-2
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1879;
                                                                                                                                        5212296-5
Patent No. 5212296
APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
                                                                                                                                                                                                :J.; O'KEEFE, DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES A.;TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 122;
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Pred. No. 0.015;
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION UNBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 465,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
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50.6%;
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Matches 125; Conserv
                                     390 ggagcag 396
                                                                     432 cgacctg 438
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LENGTH: 1879
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LENGTH: 4403765
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  positions throughout the sequence \mathfrak g
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                                                                                                                                                                                                                                                                  67 gatccctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacctgggcg 126
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                                                                                                                                                        Length 4403765;
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TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, &
                                                                                                                                                          Score 49.2; DB 4; Length 4
Pred. No. 0.042;
0; Mismatches 178; Indels
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PatentIn Release #1.0, Version #1.25
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t, c or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 109, Application US/08453695A Patent No. 5708143 GENERAL INFORMATION:
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NAME: No. 5708143and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32658
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,
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IBM PC compatible
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46.7%;
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LENGTH: 3353 base pairs
                                                                                                                                                        Query Match 12.19
Best Local Similarity 46.7
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
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2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCTGCAGGCTTTCGAGTTCCGCGTGGGCGC 2360
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                                                                                      Score 47.6; DB 1; Length 3353;
Pred. No. 0.096;
0; Mismatches 99; Indels 0
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TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAPA:
APPLICATION NUMBER: US/08/453,702A
FILING DATE:
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Pred. No. 0.096;
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Chicago
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; Sequence 109, Application US/08453702A
; Patent No. 5891706
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: No. 5891706and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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51.9%;
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51.98;
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                                                                                    Query Match
Best Local Similarity 51.9°
Matches 107; Conservative
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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Best Local Similarity
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    ; LOCATION: 7
US-08-268-161A-109
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Sequence 109, Application US/08268161A
Patent No. 5798224
GENERAL INFORMATION:
APPLICANT: SUZUKI, Shintaro
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun.
ADDRESSEE: Borun.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: June 27, 1994
CLASSIFICATION: 435
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CITY: Chicago
STATE: Illinois
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NAME: Young J. Suh
REGISTRATION NUMBER: p-41,337
REFERENCE/DOCKET NUMBER: 27866/32149
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENOTH: 3353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                               NAME/KEY: CDS
LOCATION: 763..3123
TYPE: nucleic acid
STRANDEDNESS: sing
                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                            ; LOCATION: 7
US-08-453-695A-109
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2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGGGCGC 2360
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                                      186 catcgcgcccgccggagacgttcggcgaggtctgatccgcctgcaggtggggag
                                                                                                                        246 cgaccaggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacgga
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                                                                                                                                                                                                                                                                                                           RESULT 10
PCT-US95-08071-109
Sequence 109, Application PC/TUS9508071
GENERAL INFORMATION:
APPLICANT: SIZUKi, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEGURNCES: 115
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
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Pred. No. 0.096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Sears Tower, 233 S. Wacker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12588
FILING DATE: 23 DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: NOLARM, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT/US95/08071
                                                                                                                                                                                                                                                 2481 CGAGCTGGTGCCCCGGGCGCCGAGC 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS: LENGTH: 3353 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
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milarity 51.9%;
Conservative 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicago
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PCT-US95-08071-109
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                                                                             2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGGGCGC 2350
                                                                                                                      catcgcgcccgccggacccggagacgttcggcgaggtcctgatccgcctgcaggtggggag 245
                                        126 gttcgggcgggagttgctcatcgacggaggtccgcgggccgtgcggggacggggacgtcca 185
  Gaps
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-hes 99; Indels
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APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEGUENCES: 115
CORRESPONDENCE ADDRESS:
99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, STREFF: 233 South Wacker, 6300 Sears Tower CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47.6; DB
Pred. No. 0.096
0; Mismatches
Mismatches
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TELECOMONICAPTON INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,639
FILING DATE: 18 JUN 1998
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/263,161
FILING DATE: 27 JUN 1994
ATTORNEY/AGENT INFORMATION:
MANNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              2481 CGAGCTGGTGCCCCGGGCGCCGAGC 2506
                                                                                                                                                                                                                                                                                          306 caagatcgtgccgctggggcaggagc 331
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 109, Application US/09099639 Patent No. 6262237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Greta E. No. 6262237and REGISTRATION NUMBER: 35,302
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INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 51.9%;
Matches 107; Conservative C
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Conservative
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763..3123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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; LOCATION:
US-09-099-639-109
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US-09-099-639-109
Matches 107;
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2301 GTTCGCTCTCCAGTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGGGCGC 2360

126 gttcgggcgggagttgctcatcgacgaggggggggcgtgcgggggacgggcgtcca 185

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5146 ceseccentricalcecalerectersers 5205
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                                          313 gigocgotiggggcaggagcgitcoctcgccgacticgacgccctgctcgacgaggcgctg 372
                                                                                                                                                             748: GCCCATCTGTCCCAGGCGCTCGACGATGTGACCGTCGGGGTGAACTCGTCCCCGGTGAC 807
628 GTCGACGAÇCCGGGCGCGATCGCCAACGTCAAGCCGCTCTACGGGGACGCGAACGACCCG 687
                                                                               688; TTCCTCGGGTACGACCGCGAGCTGCTGGCGCCGGAGGACCCCGCGGACAAGGAGGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aldoo
APPLICANT: Ashish S. Paradkar
ATPLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
TITLE OF INVENTION: Acid Biosynthesis
TITLE OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 11604;
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Pred. No. 0.1;
0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
": The Jenifer Buliding, 400 Seventh Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
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APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09385028 Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
E: DNA (genomic)
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TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 13:
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LENGTH: 11604 base pairs
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US-09-385-028-13
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                                                                           2361 CACAGACCGCGGCTTCCCGGCGCTGAGCAGCGAGGCGCTGGTGCGAGTGCTGGTGCTGGA 2420
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                                     categegecegecegaeceggagaegtteggegaggteetgateegeetgeaggtggggagg
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
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49.0%; Pred. No. 0.11;
tive 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: D. Douglas Price
REGISTRATON NUMBER: 24,514
REGISTRATON NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-666
TELEPHONE: (202) 39305350
TELEPRICE RA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    2481 CGAGCTGGTGCCCGGGCGGCCGAGC 2506
                                                                                                                                                                                                         306 caagategtgeegetggggeaggage 331
                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/09385028 Patent No. 6232106 GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 126; Conservative
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US-09-385-028-18
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                                                                                                                                                          253 gcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggacaagatc 312
                                                                                                                                                                                                                                                   313: gtgccgctgggggcaggagcgttccctcgccgacttcgacgccctgctcgacgaggcgctg 372
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for
                                                                      193 cccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtggggagcgaccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: Donadio, J
APPLICANT: Malpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
CORRESPONDENCE 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Abbott Laboratories D377/AP6D-2 One Abbott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharopolyspora erythraea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/07642734C Patent No. 5824513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 20235 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                          373 gaccgcatcctggccga 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 19..10722
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T: Park Rd
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: NRRL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-07-642-734C-3
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326 TTCCTCGGGTACGACCGCGAGCTGCTGGCGCCGGAGGACCCCGGGGACAAGGAGGCCGTC 5325
                                                                                                                                                                                                  5326 GCCCATCTGTCCCAGGCGCTCGACGATGTGACCTCGGGGTGAAGCTCGTCCCCGGTGAC 5385
                                                                 253 gegatgiteegggteggeaeggegeegetggtggeetteetggaeegeaeggaeaagate 312
                                                                                                                                                        313 gtgccgctggggcaggagcgttccctcgccgacttcgacgccctgctcgacgaggggcgctg 372
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49.0%; Pred. No. 0.1;
tive 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: JACOBSON, PRICE, HOLMAN & STERN, PPLC
The Jenifer Buliding, 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELEFAX: (202) 33905350
TELEFAX: (202) 33905350
TELEFAX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Acid Blosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         5386 GICCICALCATCGACAA 5402
                                                                                                                                                                                                                                               373 gaccgcatcctggccga 389
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Best Local Similarity 49.0°
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: The Jeni
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
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) ORGANISM: Str

US-09-385-028-1
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STRANDEDNESS:
TOPOLOGY: lir
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LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 4471..5847
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and enoylreductase domains
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
FEATURE:
                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 97..1482
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module
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LOCATION: 10723..20235
LOCATION: 10723..20235
OTHER INFORMATION: /codon_start= 10723
OTHER INFORMATION: /function= "gene =erya"
OTHER INFORMATION: /product= "orf3 encoding modules
OTHER INFORMATION: 6-deoxyerythronolide B formatio"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 9433..9984
LOCATION: 9433..9984
OTHER INFORMATION: /function= "approximate span OTHER INFORMATION: beta-ketoreductase of module 4"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
CACION: 1693..2670
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 4171.4428
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
                                           NAME/KEY: misc_feature
LOCATION: 19..4470
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 3"
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LOCATION: 4471.10722
OTHER INFORMATION: function= "approximate span
OTHER INFORMATION: module 4"
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LOCATION: 10723.15165
OTHER INFORMATION: _______approximate span
OTHER INFORMATION: _______dudle 5"
OTHER INFORMATION: 6-deoxyerythronolide B
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6644 cccceeaagreecececarceaecacceecrcececceacceaecreegecaccarcaccecc 6703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 aggogatgiticogggitoggoacggogocgciggitggocttcciggaccgcacggacaaga 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 ggcgggagttgctcatcgacggaggtccgcggccgtgcggggacggggacgtccacatcg 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 cctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacctgggcgttcg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 tegigoegetgggggaggagegtteeetegeegaettegaegeeetegaegaeggege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATTON: 15172..16569
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
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LOCATION: 18379..18921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module
FEATURE:
                          LOCATION: 12379.13350
OTHER INFORMATION: /function- "approximatr span of
OTHER INFORMATION: acyltransferase domain of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

) CCCATION: 19492..20235

COCATION: /function= "approximate span of

OTHER INFORMATION: /function= nof module 6"

US-07-642-734C-3
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LOCATION: 1857...13114
OCCATION: 7 / function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 5"
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COCATION: 19149..19398
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LCGATCON: 15166..20235
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 6"
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                                                                                                                                                                        LOCATION: 14062..14610
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: beta-ketoreductase of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47.4; DB 1;
Pred. No. 0.1;
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Best Local Similarity 47.2%;
Matches 144; Conservative (
misc_feature
12379..13350
                                                                                                                                                misc_feature
  NAME/KEY:
LOCATION:
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NAME/KEY: misc_feature
LOCATION: 4471..5847
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
FEATURE:
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LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and encylreductase domains m"
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LOCATION: 10831..12174
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
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/function= "gene =eryA"
/product= "orf3 encoding modules 5 & 6-deoxyerythronolide B formatio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
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LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 4171..4428
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 3"
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LOCATION: 14857..15114
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5"
                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 4471...10722
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 9433..9984
OTHER INFORMATION: __function= "approximate span
OTHER INFORMATION: __beta-ketoreductase of module 4"
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LOCATION: 14062..14610
COCHER INFORMATION: /tunction= "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
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LOCATION: 10723..15165
OTHER INFORMATION: _____approximate span
OTHER INFORMATION: _____module 5"
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OTHER INFORMATION: /codo
OTHER INFORMATION: /func
OTHER INFORMATION: /Func
OTHER INFORMATION: 6-deo
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LOCATION: 12379..13350
OTHER INFORMATION: /fur
OTHER INFORMATION: acyl
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LOCATION: 19.10722
OTHER INFORMATION: /codon_start= 19
OTHER INFORMATION: /function= "gene eryA"
OTHER INFORMATION: /product= "eryA ORF2 encoding modules 3 & 4 for OTHER INFORMATION: 6-deoxyerythronolide B"
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COGATION: 97..1482
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
                                                                                                                                                                                                                               APPLICANT: Donadio, S
APPLICANT: Katz, L
APPLICANT: Mcalpine, J B
APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
ADDRESSEE: Steven F. Weinstock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1693..2670
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
                                                                                                                                                                                                                                                                                                                                                         STATE: 1L
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
SUBTRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/439,009A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
ATTORNEY AGENT INPORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 4952.US.D1
REFERENCE/POCKET NUMBER: 4952.US.D1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 19..4470
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: module 3"
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STRAIN: NRRL 238
                                                                                                                               US-08-439-009A-3

Sequence 3, Application US/08439009A

Patent No. 6004787

GENERAL INFORMATION:
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 15172...15569
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
PEATURE:
NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
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FEATURE:
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COCATION: 18379-.18921
COTHER INFORMATION: Cluction= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
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NAME/KEY: misc_feature
LOCATION: 19149..19398
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 6"
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NAME/KEY: misc_feature

LOCATION: 19492..20235

O'THER INFORMATION: /function= "approximate span of O'THER INFORMATION: thioesterase domain of module 6" US-08-439-009A-3
                         OTHER INFORMATION: /function- "approximate span of OTHER INFORMATION: module 6"
LOCATION: 15166..20235
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                                                    0; Gaps
Query Match 11.6%; Score 47.4; DB 3; Length 20235; Best Local Similarity 47.2%; Pred. No. 0.1; Matches 144; Conservative 0; Mismatches 161; Indels 0;
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tggac 375 371

⁶⁷⁶⁴ TGGAC 6768

Search completed: July 18, 2002, 11:34:02 Job time: 11432 sec

AL106054 Drosophil AQ85231 LMA_FEV1_1 AQ85231 LMA_FEV1_1 AQ834356 Zr72b09.s AQ846145 LMA_FEV1_1 BI39919 pgplc.pk0 BI39919 pgplc.pk0 BI39435 pgpln.pk0 BM485736 pgpln.pk0 BM485736 pgfn.pk0 BM42660 pgf2n.pk0 AG041031 Pan trog1 AG04103 Pan trog

BM370573 EBROO8_SQ AJ282193 4A3A-AAQ-AQ847078 LMAJFV1_1 AL528164 AL528164 AW746434 WS1_53_G0

Sednence:

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Searched:

Jatabase

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Submitted (02-JNN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JNN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitliy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecor Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecor individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   935 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACK14N09 of RPCI-98 library from Drosophila melanogaster (fruit AL066051 AL066051 GI:4945019
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Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 935)
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AQ846145
BI389979
BI392194
BI394352
AI981707
BM426660
AG041031
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CNS078QL
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BG274749
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AJ282193
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VERSION
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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AL066051 Drosophil
AL053013 Drosophil
AU088650 AU088650
C97336 C97336 Rice
AG146122 Pan troep
AC146122 Pan troep
AC14612 Pan troep
AC14612 Broophil
BI778054 EBroO7_SQ
AC851336 LMA_FVI_l
AL250274 Terraodon
BE125039 DG1_14_CO
BE125039 DG1_14_CO
BE125039 DG1_11_CO
                                                                                                                          July 18, 2002, 10:12:49; Search time 4821.96 Seconds (without alignments) 1139.217 Million cell updates/sec
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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CMS0072Q
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/organism="Drosophila melanogaster"

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FEATURES

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Result . 9 υ /db_xref="taxon:7227 /clone_lib="RPCI-98"

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KEYWORDS
SOURCE
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- Web: www.genoscope.cns.fr.
- Web: www.genoscope.cns.fr.
- Ollaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2: cn bw sp, the same strain used for the BDGP's
Pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"

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Liber Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see hittp://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammeoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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/clone="BACR19D16"
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1 (bases 1 to 723)
Sasaki, T. and Yamamoto, K.
Rice CDNA from mature leaf (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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/clone="S20147"
                                                                                                /organism="Drosophila
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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Fax: 81-298-38-7468
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- Web : www.genoscope.cns.fr)

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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                       melanogaster"
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      1. .935
/organism="Drosophila m
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N09"
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170 c 162
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SM Orizea sativa.

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ehrhartoideae; Oryzeae; Oryzeae;
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/db_xref="taxon:4530"
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C97336 Rice callus Oryza sativa cDNA clone C60023_11A, mRNA
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                                                                                                                                                                                                                                                                                                  23 ACTTCGTCGGAGTCGGAGTCCGAGTCCACCGCCTCGCCGGAGATGGAGCACGCCTCCTCG
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                                                                                                                                                 Length 723;
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                 0; Mismatches 188;
                                                                                                                                                 DB 9;
/clone_lib="Rice mature leaf"
/tissue_type="mature leaf"
197 c 270 g 129 t
                                                                                                                                                 Score 56.2;
Pred. No. 3.
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/organism="Oryza sativa"
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Location/Qualifiers
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Best Local Similarity 47.3%;
Matches 169; Conservative
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C97336.1 GI:3760078
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Submitted (02-40G-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
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AG146122.1 GI:16675800
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-007K01.TJ.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                   167 gcggggacgggacgtccacatcgcgcccgacccggagacgttcggcgaggtcctga 226
                                                                                                                                    294 GCGAGGGCGTGGTGTTCGCCACGGCGAGGGTCCGGCCATACGCGCTCGACGACGGTGATGG 353
                                                                                                                                                                                                                                                          354 GCGAGTTCGTGCCGTGCGACGAGATGCGCGACTTCTTCGTGCCCGGGGGGCGCGGGGGGG 413
                                                                                                                                                                                                              227 tecgeetgeaggtggggagegaceaggegatgtteegggteggeaeggegeegetggtgg 286
                                                 Gaps
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Pan troglodytes DNA, clone: RP43-007K01.TJ, genomic survey
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
404 c 455 g 25 t 61 others
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  Length 558;
                                                 Indels
Query Match 13.1%; Score 53.2; DB 10; Best Local Similarity 51.1%; Pred. No. 9.4; Matches 121; Conservative 0; Mismatches 116;
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No. 9.4;
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/clone="RP43-007K01.TJ"
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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194 747

Matches

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DEFINITION

RESULT CNS0072Q

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

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AWDD4221
LG1_289_A06.b1_A002 Light Grown I (LG1) Sorghum bicolor CDNA, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoleae; Andropogoneae; Sorghum.
1 (bases 1 to 633)
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/db_xref="taxon:4558"
/db_xref=brayn:10-to 14-day-old light-grown (greenhouse)
/note="lorgan: 10- to 14-day-old light-grown (greenhouse)
seedlings; vector: Lambda Zap; Site_1: XhoI; Site_2: Ecoi
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                    255 gatgttccgggtcggcacggcgcgctggtggccttcctggaccgcacggacaagatcgt 314
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The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 033)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An EST database from Sorghum: light-grown seedlings
  ggagttgctcatcgacggaggtccgcgggccgtgcggggacggggacgtccacatcgcgcc
                                        195 egecgaeceggagaegtteggegaggteetgateegeetgeaggtggggagegaecagge
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184 c 226 g 108 t
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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POLYA=No.
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Fax: 706 542 1805
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Web: Wave, genoscope.ons.fr.

Web: Wave, genoscope.ons.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp. the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence T7 end of BAC # BACR44809 of RPCI-98 library from Drosophila melanogaster (fruit AL066742
                                                                                        ggcacggcggctggtggccttcctggaccgcacggacaagatcgtgccgctggggcag 327
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14B09"
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/strain="Friedlin strain V1"
/db.ref="taxon:5664"
/clone="LMAJFV1_m15c01"
/clone="LMAJFV1_m15c01"
/clone="LMAJFV1_m15c01"
/clone="taxon:5664"
/lab_host="TOP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's EcoRV site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
                                                                                                                                                                                                                                                                                                                                                                       AQ846145
LMAJFV1_Im15c01.y1 Leishmania major FV1 random genomic library
Leishmania major genomic clone LMAJFV1_lm15c01 5' similar to
contains element 212bp.2 leishmania repetitive element ;, DNA
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1 (Dases I to 390)

Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., I., Bennett, J., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Barvey, N., Mccann, R., Tsagareishvili, R., Willams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishhania major Friedlin strain vI genome by shotgun sequencing: a resource for DNA microarrays and expression
248 accaggogatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggaca 307
                                                                                             agategtgeegetgggggagggtteectegeegaettegaegeeetgetegaegagg 367
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4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                              134 rececaagregrecrearcateateacecececaegregecegececregregeres
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Location/Qualifiers
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Seq primer: -40RP from Gibco
Class: shotgun
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7.1

BASE COUNT

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Eukaryota; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 440)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D. F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Uppublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 252 ggcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggacaagat 311
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                                                                                                             72 ctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacctgggcgttcgg 131
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/clone="EBroO7_S0002_B16"
/clone=lib="IGF Barley EBroO7 library"
/tissue_type="Etiolated root and shoot"
/lab_host="DH10B"
Score 51.4; DB 12;
Pred. No. 18;
0; Mismatches 166;
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Invergownie, Dundee, DD2 5DA, Scotland,
111: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality score 
Seq primer: Ml3 reverse.
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Query Match 12.6%;
Best Local Similarity 47.6%;
Matches 151; Conservative
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Unit of Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 GCTCCGCGCCGTCGGCG
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/strain="Friedlin strain V1"
/db_xref="taxon:5664"
/clone="LMAJFV1_lm29c04"
                                                                                                      /organism="Leishmania major"
               class: shotgun
High quality sequence stop: 399.
Location/Qualifiers
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                          204 g
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Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
If using this information please cite:
N.S. Akopyants and S.M. Bewerley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(hatalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMAJFV1_lm29c04.y1 Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm29c04 5' similar to contains element V1-ch1_type_II.2 V1-ch1_type_I leishmania repetitive element ;, DNA sequence.
                                                                                                                                                                                                                                                                                                   133 cgggagttgctcatcgacggaggtccgcgggccgtgcggggacgggacgtccacatcgcg 192
                                                                                                                                                                                                                                   113 CGGATGGTGGCCGATGCCGTGGTGCAGGCGTCGTCGTGTTCGCCGCCTTCGACAAGGAC 172
                                                                                                                                                                                                                                                                                                                                                                gcgatgttccgggtcggcacggcgccgctggtggccttcctggaccgcacggacaagatc 312
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                                                                                                                                                    Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                               cccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtggggagcgaccag
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                         Length 440;
    Gene Function) project."
34 q 59 t 3 others
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21192569
                                                                                                                          Pred. No. 25;
0; Mismatches 137;
                                                                                                           DB 10;
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                                                                                                           Score 50.6;
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                     184 g
    (Investigating
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                                                                                                         Query Match 12.4
Best Local Similarity 48.9
Matches 131; Conservative
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                                           ORIGIN
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/clone_lib="Leibmania major FVI random genomic library"
/lab.host="TOP10 (Invitrogen)"
/note="Vector: pZero-2 (Invitrogen); Site_l: ECGRV;
Genomic DNA was isolated from stationary phase cells. For
this library, DNA was sheared to give a tight size
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's ECGRV site."
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Petraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
Weissenbach, J.
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                                                                                                                                                         Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracdon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracdon.
Location/Qualifiers
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[ pases 1 to 397)

Cordonnier-Pratt, M. -M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                   Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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   Bouneau, L., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fish
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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                                                                                                                                                                                                                                                                                 /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="037G07"
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Pred. No. 27;
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Best Local Similarity 42.9%;
Matches 147; Conservative
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ывызырны 473 bp mRNA linear EST 20-JUL-2000 DG1_121_C03.bl_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA sequence.
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         The University of Georgia
The University of Georgia
Plant Schences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1805
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below phred quality 16. The threshold for highest quality sequence
is 20.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
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Pred. No. 33;
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High quality sequence stop: 382
POLYA-No.
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Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                                                                                                                        Location/Qualifiers
Contact: Cordonnier-Pratt MM
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Sorghum bicolor
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BE355969.1
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Tel: 706 542 1860
Fax: 706 542 1805
Faxi: 706 542 1805
Famil: mumprattenga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 472
POLXA-NO.
                                                                                                                             122 gggcgttcggggcgggagttgctcatcgacggaggtccgcgggccgtgcgggggacgggacg 181
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Best Local Similarity 48.4%; Pred. No. 33;
Matches 138; Conservative 0; Mismatches 147;
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Streptomyces netro
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115.010 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Maximum DB s
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AAG35779 AAY81644 AAG92682 AAB79361 AAG14865 AAR38156	AAG11249 AAG11248 AAG11247 AAB93677 AAY21669	AAY84894 AAW81867 AAU56274 AAB96344 AAB31257 AAB31555 AAB91557	AAY42167 AAB47047 AAB479027 AAB41315 AAG82257 AAG8035	AAC80043 AAU46702 ABB66811 AAB6618 AAV85963 AAU35343 AAU79061 AAU36303
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ALIGNMENTS

Streptomyces goldeniensis SsgA protein. AAY44651 standard; Protein; 135 AA (first entry) 18-APR-2000 AAY44651; AAY44651

mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antinigraine agent; herbicide; antiparestici agent; ruminant growth promoter; biolissecticide; receptor agonts; antagonist; blomass. SsgA; liquid culture; filamentous bacteria; secondary metabolite;

Streptomyces goldeniensis.

WO200000613-A1

06-JAN-2000.

99WO-NL00395 25-JUN-1999;

98EP-0202148 26-JUN-1998;

(UYLE-) RIJKSUNIV LEIDEN

Luiten RGM;

(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.

Van Wezel GP, Kraal B,

WPI; 2000-147269/13. N-PSDB; AAZ49730.

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us-09-749-185-7.rag

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Best Local Similarity 78.5
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces netropsis.
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                                                                                                                             135 AA;
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                                                                                                                                                              Query Match
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                                                     The present sequence is S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents,
                                                                                                                                                                                                                                                                                                             VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
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                                                                                                                                                                                                                                                      1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD 60
                                                                                                                          hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                  SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antihigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                           Length 135;
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                                                                                                                                                                                                         Score 701; DB 21;
Pred. No. 3.4e-75;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                 Mismatches
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                                  60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces griseus
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                                  Fig 5;
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                         135 AA;
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                                  Disclosure;
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The present sequence is S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, rumninant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.3%; Score 556; DB 21; Length 135; 78.5%; Pred. No. 5.6e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SsgA: liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
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                                                                                                                                                                                                                                          Length 135;
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                                                                                                                                                                                                                                          Score 544; DB 21;
Pred. No. 1.5e-56;
                                                                                                                                                                                                                                                                                         Mismatches
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77.8%;
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                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                   135 AA;
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Matches 105
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #17671.
                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS,
                                                                                                                68.6%; Score 481; DB 21; 71.1%; Pred. No. 4.5e-49; ive 14; Mismatches 25
                                                                                                                                                                                                          Mitcham JL, Wang S
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; SEQ ID No 17970; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU56775 standard; Protein; 400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                               Best Local Similarity 71.1
Matches, 96; Conservative
                                                                                                                                                                                                                                                                                                                                                      121, DEALDRILAEEQNAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating acne vulgaris
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                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS59578.
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                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
         and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel receptor type protein tyrosine phosphatase beta protein used to modulate normal cellular processes of differentiation, metabolism, cell cycle by competing with endogenous transmembrane receptors for ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; protein tyrosine phosphatase; PTPase; vulnerary; cytostatic; antlinflammatory; antidiabetic; viral infection; inflammation; cancer; receptor-type protein tyrosine phosphatase beta; RPTPbeta; carbonic anhydrase; CAH; diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                              72 GEVLIRLQVGSDQAMFRVGTAPLVA---FLDRTDKIVP-----LGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                                 12 RIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPETF 71
                                                                                                                                                                                                                                        Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schlessinger J;
                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                    10.8%; Score 76; DB 2 ilarity 25.2%; Pred. No. 2.2; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human carbonic anhydrase isoform #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barnea G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB59590 standard; protein; 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 7; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-0551270.
91US-0654188.
92US-0961235.
93US-0015973.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-070117/08.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 eagldrv 176
                                                                                                                                                                                                                                                                                                                                                                                                                          121 DEALDRI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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15-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59590;
                                                                                                                                                                                        Sequence
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receptor-type protein tyrosine in a special control or all and stated sets of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is given in a specification relating to a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 6642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.8%; Score 75.5; 28.2%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB59950 standard; Protein; 736 AA.
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31; Conservative
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N-PSDB; ABL04053.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 AA;
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11-JUL-2000;
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Rosen CA, Ruben SM,
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                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                         222 AA;
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                                                          (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed the specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
   and
                                                                                                                                                                                                                        272 fttsngsvfriglgngvev-dpeeinvtfedvkgcdeakgelkevveflkspekfsnlgg 330
                                                                                                                                                                                                                                                                    331 klp-----kgvllvgpp---gtgktllaravageakvpffhaagpe-fdevlvgggarr 380
                                                                                                                                                                           60; Gaps
                                                                                                                                                                                                                                             DAPVTWAFGRELLIDGGPRPCGDGDVHIA------PADPETFGEVLIRLQVGS 82
                                                                                                                                                                                                                                                                                          83 DQAMFRV--GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE----EQNAG 135
                                                                                                                                                                                                                                                                                                       Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                    DB 22; Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bhatia A;
                                                                                                                                                                           53; Indels
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, Jen S, Carter D;
                                                                                                                                                   Score 74; DB 2
Pred. No. 8.6;
5; Mismatches
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                                                                                                                                                    10.6%; 22.9%;
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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e J, Zhang Y,
                                                                                                                                          Query Match
Best Local Similarity 22.9%;
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                                                                                                                   736 AA;
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07-JUL-2000;
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AAU55550
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the treatment, prevention and diagnosis of medical conditions caused by Paches. The disorders include SAPHO syndrome (synovitis, acre, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by cargin linked immunoscibent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----vqvapadmgsasygdiltrmapgaaliprggvgsyalrrwlaagalavclddv 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 lvddkvsfalpvaanrevld--alrqagipaapdalt---pnevraawgagada---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 RPCGDGDVHIAPAD--PETFGEVLIRLQ------VGSDQAMFRVGTAPLVAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein BLAST search protein SEQ ID NO: 154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%; Score 71.5; DB 22; 25.3%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 lygdacedgivsalrercrsylqyyadada 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DKIVPLGQERS-----LADFDA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB45480 standard; Protein; 160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1999; 99US-0128697.
20-JAN-2000; 2000US-0176929.
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The invention relates to the isolation of genes AAC81710-C81758 encoding the human secreted proteins AAB45386-B5434. This sequence represents a fragment of the protein encoded by the gene given in the descriptor inc. The sequence is used as a query sequence for doing BLASTX searches to determine homologous sequence to the protein. The genes and proteins are susful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, and other cancers of the adrenal gland, bone, bone marrow, breast, astrointestinal tract, liver, lung, or urogenital; (b) immune disorders autoimmune thyroiditis, diabetes mellitus, Crohn's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple cardiovascular disorders such as myocardial ischaemias; (d) wound halling; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 plgpldfgnvvatldpgaarhltlachydsklfpsgstp---fvgatdsavpcalllela 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 71; DB 21; Length 16(
Pred. No. 2.6;
7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #16938.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatological; osteopathic; neuroprotectant
                                                                                  Disclosure; Page 513-514; 521pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU56042 standard; Protein; 540 AA.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 27; Conserv
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by content and acceptance of the treatment, prevention and diagnosis of medical conditions caused by publications. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, Mypertosis and osteonyelitis), uveitis and endophthalmitis.

Contervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies percipic for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and cherefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contact fink assay (ELISA).

Contagned linked immunosorbent assay (ELISA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 VLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAEEQN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ELRYETCDPYAVRLTFHLPGDA--PVTWAFGRELLIDGGPRPCGDGDVHIAPADPETFGE 73
                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.1%; Score 71; DB 22; Length 540; 27.9%; Pred. No. 13; Live 14; Mismatches 54; Indels
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Carter D;
                                                                                                                                                                                                                 Claim 3; SEQ ID No 17237; 1069pp; English.
L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG35780 standard; Protein; 257 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 27.9
Matches 34; Conservative
                                                                                                                                                                      treating acne vulgaris
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                                             2001-616774/71.
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28-JUN-1999;
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990S - 0156596 - 990S - 0156596 - 990S - 0157753 - 990S - 0157753 - 990S - 0157753 - 990S - 015929 - 990S - 016098 - 990S - 0161360 - 990S - 0161393 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651493 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 01651483 - 0
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99US-0123180.
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es 31; Conserv
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18 - OCT - 1999;

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29-SEP-1999;
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05-MAR-1999;
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57 GDG--DVHIAPADPETFG----EVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis; pneumococcal disease.
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Best Local Similarity 30.7%; Pred. No. 6.4;
Matches 31; Conservative 11; Mismatches
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               990S - 0158029
990S - 0158132
990S - 0159239
990S - 0159294
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990S - 0159329
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99US-0161920.
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99US-0161404.
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99US-0161993.
99US-0162142.
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99US-0125164.
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                 007-0CT-1999;
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19-MAR-1999;
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25-OCT-1999;
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25-OCT-1999;
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99US-0155486.
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990S-0156458.
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990S-0157117.
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04-OCT-1999;
05-OCT-1999;
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sequences from the Coryneform bacterium Corynebacterium glutemicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, consideration point of a gene derived from a mutant of coryneform bacterium, measuring expression ment and enrived from coryneform bacterium, coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium of a gene derived amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                        mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 LIDGGPRPCGDG------DVHIA--PADPETFGEVLIRLQVGSDQAMFRVGTAPLV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: || : | | | | | | | | : | | | | 6 mvtggaqqigrgiseklaadgfdiavadlpqqeeqaaetiklleaagqkavf-vg---- 59
                                                                                                                                                                                                        The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum SMP protein sequence SEQ ID NO:238.
                                                                                                                                                                   Claim 17; SEQ'ID NO: 6436; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%; Score 69; DB 22; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 8.5;
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99DE-1031413.
99DE-1031419.
99DE-1031420.
99DE-1031424.
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                   2001-376931/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 AA;
                                    N-PSDB; AAH67901
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08-JUL-1999;
08-JUL-1999;
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08-JUL-1999;
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                                                                                                                                                                               AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antilifiammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens and/or antigens. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                       New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 lpgtmiedylvefngkrfeavdggmkpnepvevvirpedlritlpeeg-----klqvkvd 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 QAMFRVGTAPLVAF-----LDRTDKIVPLGQERSL-------ADFDAL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 386;
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Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C glutamicum protein fragment SEQ ID NO: 6436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.0%; Score 70; DB Best Local Similarity 27.2%; Pred. No. 11; Matches 37; Conservative 18; Mismatches
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                                                                                                                                                Claim 1; Page 87; 108pp; English.
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Senoh A, Ikeda M,
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 teeyve---ieeqeag 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 LDEALDRILAEEQNAG 135
 Hansbro PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coryneform bacterium;
                                    WPI; 2000-195300/17.
Gilbert CFG,
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03-AUG-2000;
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
                                                                                                                                                            Schroeder H, Zelder O,
                                                                                                                                                                                                                     Claim 20; Page 479-480; 1246pp; English.
                                                                               99DE-1040765.
99US-0151572.
99DE-1042076.
                                                   99DE-1032230
99US-0143208
                           99DE-1031562
99DE-1031634
                                        99DE-1032180
                                                                    99DE-1032973
99DE-1033005
                                                               99DE-1032924
                                                                                                 99DE-1042079
                                                                                                                                    99DE-1042125
                                              99DE-1032227
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Best Local Similarity 26.1%
Matches 24; Conservative
                                                                                                                                                           Pompejus M, Kroeger B,
                                                                                                                                                                       WPI; 2001-061975/07.
                                                                                                                                                                                                                                                                                                                                              258 AA;
                                                                                                                                                                             N-PSDB; AAF71478
                                                                                                                                                (BADI ) BASF AG.
                                                                                                                                    03-SEP-1999;
                                                                                                                  03-SEP-1999
03-SEP-1999
                                                                                                                                                                                                                                                                                                                                               Sequence
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03-SEP-1
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Search completed: July 18, 2002, 14:15:03 Job time: 10333 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haberhauer G;
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22; Indels 30; Gaps

DB 22; Length 258;

9.8%; Score 69; DB; 26.1%; Pred. No. 8.5; iive 16; Mismatches

48 LIDGGPRPCGDG------DVHIA--PADPETFGEVLIRLQVGSDQAMFRVGTAPLV 95

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96 AFLDRTDKIVPLGQERSLADFDALLDEALDRI 127

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Sequence 12, Appl
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Sequence 6, Ag
Sequence 6, Ag
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Sequence 234,
Sequence 11,
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Sequence 11
Sequence 6,
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                                                                        July 18, 2002, 14:16:07; Search time 51.31 Seconds
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/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-015-973-6

US-08-446-363-10

US-08-448-164-6

US-08-08-109-512-11

PCT-US92-08756A-11

US-09-040-774-2

US-09-012-710-12

US-09-012-710-12

US-09-55-273-12

US-09-56-273-12

US-09-56-273-12

US-09-56-273-12

US-09-56-273-12

US-09-56-273-12

US-09-56-273-12

US-09-56-273-12

US-09-1013-11

US-09-1013-11

US-09-056-56-234

US-09-056-58-981-11

US-09-228-986-118

US-09-228-986-118

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US-09-228-986-118

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                                                                                                                                                                                                                 231628 seqs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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6, Appli 3, Appli 3, Appli Appli Appli Sequence 6, Al Sequence 53, I Sequence 4, Al Sequence 4, Al Sequence 4, Al Sequence 80, I Sequence Sequence Sequence Sequence Sequence S Sequence Sequence Sequence Sequence Sequence US-08-015-986A-10
Sequence 10, Application US/08015986A
Sequence 10, Application US/08015986A
Sequence 10, Sp3123
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-GAMMA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,986A
FILING DATE: 10-FEB-1993
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18 872
REGISTRATION NUMBER: 7683-028
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
FEMALE: FEMALE STATES US-08-701-240-2 US-09-138-236-2 US-09-130-878-2 US-09-105-537-6 US-08-715-554-3 US-08-583-118-3 US-08-6-570A-6 PCT-US-6-01314-53 US-08-070-165F-4 US-08-061-465-4 US-08-061-465-4 US-08-061-465-4 US-08-061-465-4 US-08-061-465-4 US-08-481-985B-80 US-08-370-476-80 US-09-056-556-236 US-07-857-224B-44 ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas CITY: .New York STATE: New York COUNTRY: U.S.A. 306 694 694 3739 3739 11877 106 253 388 388 388 388 388 290 290 290 290 290 290 290 290 290 STRANDEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: protein amino acid

7;

Gaps

33;

Indels

Length 259;

DB 1;

10.8%; Score 75.5; DB 28.2%; Pred. No. 0.23; ive 13; Mismatches

Conservative

Local Similarity nes 31; Conserv

Query Match Best Local S: Matches 31,

δ Q

US-08-015-986A-10

24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75

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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 62141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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28.2%;
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Best Local Similarity 28.24
Matches 31; Conservative
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LENGTH: 259 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                           COMPUTER READABLE FORM:
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                                      New York
                                                        U.S.A.
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                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
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                                                        COUNTRY:
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                   CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 75.5; DB 1; Length 259; 28.2%; Pred. No. 0.23; tive 13; Mismatches 33; Indels 3
                                      76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 RDGIAVIGIFLKIGHENGEFQI------FLDALDKIKTKGKEAPFTKFD 178
                                                                                                                                            Sequence 6, Application US/08015973
: Patent No. 5604094
: GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: U S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIAL
COMPUTER: IBM PC COMPATIAL
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,973
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
ATCHREY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,78
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7683-021
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Patent No. 5891700
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 7683.
TELECOMUNICATION INCORMATION:
TELEPHONE: (212)790-9030
TELEFAX: (212)869-864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 31; Conservative
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86 PYRLR-OFHL-----HWGSSDDHGSEHTVDGVKYA---AELHLVHWNPKYNTFKEALKQ 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08448164
Patent No. 592536
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Indels
SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/446,363 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATE: US/08/448,164 FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75.5; DB 2;
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/015,986
FILING DATE: 10-FEB-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: PENNIE & EDMONDS
1155 Avenue of the Americas
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Gaps

33;

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24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                              10.8%; Score 75.5; DB 4; Length 259; 28.2%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                             76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tal, Ronny
APPLICANT: Benziman, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: General Benzind, David H.
APPLICANT: Calhoon, Roger D.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/309,512
                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,218
FILLING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: BOTLNEY, SCOLT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08309512 Patent No. 5759828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acetobacter xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (6141) 854-3694
'TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENT INFORMATION BORTNER, Scott R. Scott R. Scott R. Strumber, 34,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                    Best Local Similarity 28.2
Matches; 31; Conservative
                     SS: single
unknown
                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-081-929-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Tal, R
                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94025
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-309-512-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM:
US-08-309-512-11
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                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 RDGIAVIGIFLKIGHENGEFQI-----FLDALDKIKTKGKEAPFTKFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schlessinger, Joseph
APPLICANT: Barnea, Gilad
APPLICANT: Grumet, Martin H.
APPLICANT: Margolis, Richard U.
TITLE OF INVENTION: A NEW CLASS OF RPTPASSES: THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,929
FILING DATE: 23-JUN-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 75.5; 28.2%; Pred. No. 0.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                NAME: Misrock, S. Leslie
RECISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
                       US 08/015,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08081929
Patent No. 6160090
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: COTUZZI, LAURA A. REGIGSTRATION NUMBER: 30742 REFERENCE/DOCKET WUMBER: 76 TELECOMMUNICATION INFORMATION: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                       APPLICATION NUMBER: US 06
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Conservative
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-448-164-6
                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York COUNTRY: U.S.A.
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US-08-081-929-6
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APPLICANT: Wong, Albert J.
APPLICANT: Holgado-Madruga, Marla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 97,8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
                                                                                                                                                  US-09-040-774-2; Sequence 2, Application US/09040774; Patent No. 6207811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.5%;
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Kestila, Marjo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.6%
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (312)913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
     173 EPQAL-VMFDLDGFKPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-040-774-2
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                      ADDRL.
STREET: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199
                                                                                                                                          RESULT
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                                               5.
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 DPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE---TFGEVLIRLQ 79
                                                                                   23 DPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE---TFGEVLIRLQ 79
                                                                                                                                                                                    80 VGSDQAMFRVGTAPLVAFLDRTDKIVP----LGQERSLADFDALLDEALDRI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.8%; Score 69; DB 5; Length 493; Best Local Similarity 27.7%; Pred. No. 3.5; Matches 31; Conservative 16; Mismatches 37; Indels
       9.8%; Score 69; DB 1; Length 493; 27.7%; Pred. No. 3.5; tive 16; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: WEYR 20050 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
TELEFX: 278356
INFOREMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CYCLIC DIGUANYLATE TITLE OF INVENTION: METABOLIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08756A
FILING DATE: 19921014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,218
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
SOFTWARE: Version #1.25
                                                                                                                                                                                                                                                                                             Sequence 11, Application PC/TUS9208756A GENERAL INFORMATION:
APPLICANT: Tal, Ronny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach and Limbach
STREET: 201 Ferry Building
CITY: San Francisco
                                                                                                              :| |: : | | | | |
173 EPQAL-VMFDLDGFKPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); ORGANISM: Acetobacter xylinum PCT-US92-08756A-11
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tal, Ronny
APPLICANT: Benziman, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: Ben-Bassat, Arie
APPLICANT: Calhoon, Roger D.
APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 493 amino acids
AMINO ACID
                                                 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                           Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                           RESULT 7
PCT-US92-08756A-11
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             Query Match
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GAB1, A GRB2 BINDING PROTEIN, AND COMPOSITIONS FOR MAKING AND METHODS OF USING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1241;
80. VGSDQAMFRVGTAPLVAFLDRTDKIVP----LGQERSLADFDALLDEALDRI 127
                     30; Indels
                                                                                                                                                                                                                                                                                                                                       E: McDonnell Boehnen Hulbert & Berghoff
300 S. Wacker Drive, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/040,774
FILING DATE: 18 MAR 1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                          APPLICANT: Lenkkeri, Ulla
APPLICANT: Mannikko, Minna
TITLE OF INVENTION: Nephrin Gene and Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66.5;
Pred. No. 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 LVAFLDRTDKIVPLGQERSLADFDALLDEA 123
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Sequence 4, Application US/09138236

Sequence 4, Application US/09138236

Patent No. 6133428

GENERAL INFORMATION:

APPLICANT: Wong, Albert J.

APPLICANT: Wong, Albert J.

APPLICANT: Wong, Albert J.

APPLICANT: Wong, Albert J.

TITLE OF INVENTION: CAMPOSITIONS FOR MAKING AND METHODS OF USING THE SAME NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

MUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

STREET: One Liberty Place, 46th floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 PVRSPITRSFARDSSRFPMSPRPDSVHSTTSSSDSHDSEENYVPMNPNLSGE------600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 SDQAMFRV----GTAPL----VAFLD---RTDKIVPLGQERSLADFDALLDEALD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| ::| ::| | ::| | ::| | 601 -DPNLFASNSLDGGSSPMNKPKGDKQVEYLDLDLDSGKSTPPRKQKSSGSGSSMADERVD 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 PGDAPVTWAFGRE-LLIDGGPRP-------CGDGDVHIAPADPETFGEVLIRLQVG 81
                    Woodcock Washburn Kurtz Mackiewicz & No. 5912160ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 695;
                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.2%; Score 64.5; 21.3%; Pred. No. 19
                                      STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TJU-2032
                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,240
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,641
FILING DATE: US 60/002,641
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATMAKE: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TJT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 21.38
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-701-240-4
                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
CORRESPONDENCE ADDRESS:
                                                                                    Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 RILAEEQ 132
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                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 PGDAPVTWAFGRE-LLIDGGPRP------CGDGDVHIAPADPETFGEVLIRLQVG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
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Fatent No. 6087478
GENERAL INFORMATION:
APPLICANT: Woarefi, Ismail
APPLICANT: Moarefi, Ismail
APPLICANT: Maryan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.2%; Score 64.5; DB 4; Length 69
21.3%; Pred. No. 19;
tive 23; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,710
                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
CMDUPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701,240
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MAIK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 21.3%
Marches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-138-236-4
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 RILAEEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999 QQVVVY 038
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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SEQUENCE CHARACTERISTICS:
         INFORMATION FOR SEQ ID NO:
                                                                                                 linear
                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
US-09-556-273-12
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                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 119
LENGTH: 190
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                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 ----GDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAP----LVAFLDRTDKIV---- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 EELSFRIPV-ELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLID---GGPRPCGD---- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-TERMINAL DOMAIN OF A METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                        Ouery Match 9.2%; Score 64.5; DB 3; Length 837; Best Local Similarity 25.3%; Pred. No. 25; Matches 41; Conservative 17; Mismatches 59; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 PLGQE-----PRSLADFDALLDEAL-----DRILAEEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/556,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09556273
Patent No. 6312887
GENERAL INFORMATION:
APPLICANT: Vinkemeier, Uwe
APPLICANT: Vinkemeier, Uwe
APPLICANT: Variyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-T
TITLE OF INVENTION: STAT PROTEIN AND MET
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,710
                               REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                          12:
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                                                                                                                                                             LENGTH: 837 amino acids TYPE: amino acid
                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-3
TELEX: 133521
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                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New COUNTRY: US ZIP: 07601
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US-09-556-273-12
                                                                                                                                                                                                                                                                         US-09-012-710-12
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: Us/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 PRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLD---RTDKIVPLGQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 -----GDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAP----LVAFLDRTDKIV---- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 EELKFTTPLGRLHHRVRETRLLRESLHL---GPKTGQVSLONLIDPPLNGPGPSEDLPTI 182
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 PSPCGSEDVHVLAVDDSLVDRKVI------BHLLKISSCKVTA-VDSGIRALQFLGLDE 83
                                                                                                                                                                                                                                                                                                                                                      7 · EELSFRIPV - ELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLID - · · · GGPRPCGD - · · · 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LEUNG-TACK Patricia
APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree
APPLICANT: AUDONNET Jean-Christophe, Francis
APPLICANT: RIVIERE Michel, Emile, Albert
TITLE OF INVENTION: Mutants and vaccines of the Infectious
TITLE OF INVENTION: Bovine Rhinotracheltis virus
                                                                                                                                                                                                                                                Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 QLHQEIGAASGELEPKTRASLISRLDEVLRTLVTSSFLVEKQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106' PLGQE-----RSLADFDALLDEAL-----DRILAEEQ 132
                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 23.5%; Pred. No. 3.9;
Matches 19; Conservative 18; Mismatches 3(
                                                                                                                                                                                                                                             9.2%; Score 64.5; D: 25.3%; Pred. No. 25; tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 119, Application US/09228986 Patent No. 6359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08924345; Patent No. 6224878; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110. ERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 EKAAGDFNGL---KVDLIITD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Eucalyptus grandis
US-09-228-986-119
LENGTH: 837 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                               Best Local Similarity 25.3%
Matches 41; Conservative
                                                                                          protein
NO
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47 PHRGRADQHLGLDARLCAAACNVLLVDGVQHRPQRHGPGPRFGFPRVVVACG---IRQAR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 PYAVRLTFHLPGDAPVTWAFGRELLIDG------GPRP------CGDGDVHIAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 ADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVP----LGQE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.0%; Score 63; DB 4; Length 182; Best Local Similarity 30.3%; Pred. No. 4.9; Matches 33; Conservative 7; Mismatches 37; Indels
                        NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO. 234:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: July 18, 2002, 14:16:08
Job time: 9698 sec
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          LENGTH: 182 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: protein US-09-056-556-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
                                                                                                                                                                 STATE: AKLINGTON
STATE: AKLINGTON
STATE: AKLINGTON
ZIF: 22202

COUNTRY: USA
ZIF: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPU
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Pred. No. 4.1;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/09/056,556
FILING DATE: 07-APR-1998
                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LARSON AND TAYLOR
STREET: 727 SOUTH TWENTY-THIRD STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GGYVPVPAADADCYYSESDSETAGEFLIRM 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GG--PRPCGDGDVHIAPADPETFGEVLIRL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: XI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 920-7200
TELEFAX: (703) 892-6428
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.0%;
Best Local Similarity 46.7%;
Matches 14; Conservative
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LENGTH: 158 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-924-345-4
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 0
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-09-056-556-234
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein July 18, 2002, 14:17:35; Search time 73.98 Seconds (without alignments) 175.345 Million cell updates/sec Run on:

Perfect score:

US-09-749-185-7 701 1 MSFLVSEELSFRIPVELRYE......FDALLDEALDRILAEEQNAG 135 Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

283138 segs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable requiator			probable regulator	peroxisome assembl	hypothetical prote	carbonate dehydrat	probable transcrip	peroxisome biogene	cytochrome c-type	carbonate dehydrat	MHC class I RT1.C-	purine-binding che	probable peroxidas	mixed-lineage prot	hypothetical prote	carbonate dehydrat	peptidylprolyl iso	deoxyribonuclease	probable secreted	choline monooxygen	probable peroxin-6	probable basal-bod	penicillin-binding	penicillin binding	hypothetical prote	probable alcohol d	conserved hypothet	medium-chain acyl-
SUMMARIES	ID	T37179	T36147	T35247	T35319	A53121	H70678	A43641	T29420	S71090	D83460	CRHU3	I69009	B82380	T09164	S68178	T16511	A22612	S55383	JC1483	T44873	T08550	T37816	AD0089	G97472	AC2691	C87687	н69789	н87608	н84176
	DB	7	7	~	~	~	7	7	7	~																			N	7
	Query Match Length DB	136	142	138	142	1025	291	260	892	980	407	260	343	175	323	954	1387	259	559	230	387	426	948	218	757	757	966	346	289	600
dР	Query Match	84.0	30.7	24.0	18.7	12.0	11.6	11.2	11.2	11.1	11.1	10.8	10.7	10.6	10.6	10.6	10.6	10.5	10.4	10.3	10.3	10.3	10.3	10.3	10.2	10.2	10.2	10.1	10.1	10.1
	Score	589	215	168	131	84	81.5	78.5	78.5	78	77.5	75.5	75	74	74	74	74	73.5	73	72.5	72.5	72.5	72.5	72	71.5	71.5	71.5	71	70.5	70.5
	Result No.	1	7	e	7	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote hypothetical prote	late expression fa molybdenum cofacto	naringenin-chalcon peroxisomal assemb	quinone oxidoreduc hypothetical prote	hypothetical prote hypothetical prote	DnaA-related prote probable ATPase	hypothetical prote	probable sensol/re nodulation control
F95161 E98027	T10360 G84282	SYZMCC A48667	G83766 E89958	T05873 E70980	C87461 S42826	T01461	A39017
2.2	000	7 - 7	77	7 -	77	~ ~	7
385 385	163	400 1165	322	398 143	230	859	237
10.0	0.00	, o o	ω. α. α.	8.6 8.8	8. 6. 8. 8.	8.0	9.7
; 70 70	70.69.5	9 69	69	68.5	. 68.5 68.5	68.5	68
30 31	33.2	36.3	37	39,: 40	41.42	43	45

ALIGNMENTS

RESULT T37179

probable regulator - Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Species: G3-Dec-1999 #sequence_revision G3-Dec-1999 #text_change G3-Dec-1999 C:Accession: T37179

A; Gene: ssgA; SCOEDB:SCQ11.09

Gaps ; Length 136; Indels Score 589; DB 2; Pred. No. 5.1e-52; 7; Mismatches 13 Query Match
Best Local Similarity 85.2%;
Matches 115; Conservative

ö

2 MSFLVSEELSFRIPVELRYETRDPYAVRLTFHLPGDAPVTWAFGRELLVDGVGRPCGDGD 61 1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD 60 ò

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δλ g

121 DEALDRILAEEQNAG 135 δ

q

probable regulator - Streptomyces coelicolor (;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor (;Decies: Streptomyces coelicolor (;Dec-1999 #text_change 09-Jun-2000 (;Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000 (;Decesion: T36147 ()Decesion: T36147 ()Decesi

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12.0%;
27.8%;
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                         123 ALDRILAE 130
                                                                                                                                                                                                                                                                                                                                                                                                               134 FLAELTAE 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A53121
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    C;Genetics
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R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-138 <OLI>
A;Cross-references: EMBL:AL049587; PIDN:CAB40672.1; GSPDB:GN00070; SCOEDB:SC5F2A.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  М.А.
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A;Molecule type: DNA
A;Residues: 1-142 < OLL>
A;Residues: 1-142 < OLL>
A;Residues: BMBL:AL049863; PIDN:CAB42928.1; GSPDB:GN00070; SCOEDB:SC5H1.03
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, May 1999
A;Reference number: 221575
A;Accession: T35319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Accession: T35319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                             VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
                                                                                                                                                                                                                                                                                    48 LIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIAGMOEPUGHGDVRVR---PYAYDRTVLEFHAPEGTAVIHVRSGELRRFLQAAGELVPV 117
                                                                                                                                  Gaps
                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSFLVSEELSFR-----IPVELRYETCDPYAVRLTFHLPG---DAPVTWAFGREL 47
                                                                                                                               ;
0
A;Gene: SCOEDB:SCE19A.24
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: SCOEDB:SC5F2A.05c
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                       Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 138;
                                                                                                                               Indels
                                                                                                                               60;
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                                                                                   30.7%; Score 215; DB 2;
38.1%; Pred. No. 2.1e-14;
iive 18; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.0%; Score 168; DB 2; Best Local Similarity 31.4%; Pred. No. 1.1e-09; Matches 43; Conservative 17; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable regulator - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain A3(2)
                                                                                                     Similarity 38.1%
48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 GLEHLQLDLDHDLAELM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z21573
A; Accession: T35247
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                                                                                     Query Match
Best Local Simi
Matches 48;
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peroxisome assembly protein PAY4 - yeast (Yarrowia lipolytica)
C;Species: Yarrowia lipolytica, Candida lipolytica
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 02-Feb-2001
C;Accession: A53121
R;Nuttley, W.M.; Brade, A.M.; Eitzen, G.A.; Veenhuis, M.; Aitchison, J.D.; Szilard, R
J; Blol, Chem. 269, 586-566, 1994
A;Title: PAY4, a gene required for peroxisome assembly in the yeast Yarrowia lipolyti
A;Reference number: A53121; MUID:94103271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Rv2426c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
C;Accession: H70678
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon ; Connor, R.; Davies, R.; Parkhill, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Accession: H70678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 MWDELRIEL-LGDGRADGERHRAVVFVWAAAVEAFIRETHAVVRPGRE-----EVRVDD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TFGEVLIRLQVGS------DQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALLDE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 PCGDGDVHIAPADPETF-----GEVLIRLQVGSDQAMFR-----VGTAPLVAFLDR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761 PPGTGKTLLAKAIATTFSLNFFSVKGPELLNMYIGESEANVRRVFQKARDAKPCVVFFDE 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <VATP>
                                                                                                                                                                                                                                                                                                                                                                                             1 RPPVLAHLAYDAADPFALTVVFSHDGRVLARWTLDREMVAEGLTRPVGVGDVRLRPESRG 80
                                                                                                                                                                                                                                                                                                                                             12 RIPV---ELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: FtsH/SEC18/CDC48-type ATP-binding domain homology C;Keywords: ATP; nucleotide binding; P-loop; peroxisome biogenesis E;734-946/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology E;760-767/Region: nucleotide-binding motif A (P-loop)
A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                             Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 84; DB 2; Length 1025; Pred. No. 3.2; 12; Mismatches 37; Indels
                                                                                                                                                                        Query Match 18.7%; Score 131; DB 2; Length 14 Best Local Similarity 30.5%; Pred. No. 5.8e-06; Matches: 39; Conservative 20; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA A; Residues: 1-1025 <NUT> A; Cross-references: GB:L23858; NID:9393290; PID:9393291 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101"TDKIVPLGQERSLADFDALLDEALDRILAE 130
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Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   Query Match
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                                             GB:AL123456; NID:93261662; PIDN:CAB03770.1; PID:91666159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 11-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 22-Jun-1999
C;Accession: A43641; A45400
Biochem. Genet. 27, 17-30, 1989
A;Title: Muse carbonic anhydrase III: nucleotide sequence and expression studies. A;Reference number: A43641; MUID:89227981
                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                        87 PYRLR-QFHL-----HWGSSDDHGSEHTVDGVKYA---AELHLVHWNPRYNTFGEALKQ 136
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                 24 TGYLPDTATATAVFLADRLGKPLLVEG---PAGVGKTELARAVAQATGSGLVRLQCYEGV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADP--ETFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:9309127
as Leu
                                                                                                                                                                                                                                                                                          30 TFHLPGDAPVTWAF----GRELLIDGGPRPCGDGDVHIAPADPETFGEVLIRLQV--GS
                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: carbonate dehydratase; carbonic anhydrase homology Keywords: carbon-oxygen lyase; hydro-lyase; zinc 5-259/Domain: carbonic anhydrase homology <CAH>
                                                                                                                                                                                                     Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDGIAVVGILLKIGREKGEFQI-----LLDALDKIKTKGKEAPFTHFD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-260 < CTMED.
A; Cross-references: GB:M27796; NID:g192331; PIDN:AAA37355.1;
A; Note: the authors translated the codon TAC for residue 114; R; Stanton, L.W.; Ponte, P.A.; Coleman, R.T.; Snyder, M.A.
Mol. Endocrinol: 5, 860-866, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecule type: protein
A; Residues: 79-85, (6', 87-93, 'X', 95-96 <STA>
A; Residues: 79-85, (6', 87-93, 'X', 95-96 <STA>
A; Note: sequence extracted from NCBI backbone (NCBIP:57846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription regulator - Streptomyces coelicolor C; Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Expression of CA III in rodent models of obesity. A;Reference number: A45400; MUID:92017893 A;Accession: A45400
                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 78.5; DI
; Pred. No. 2.3;
13; Mismatches
                                                                                                                                                                                                   Score 81.5; DI
Pred. No. 1.3;
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - mouse
                                                                                                                                  Superfamily: hypothetical protein MTH1814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carbonate dehydratase (EC 4.2.1.1) III
                                                                                                                                                                                                                                              14;
                A; Residues: 1-291 <COL>
A; Cross-references: GB:281451; GB:AI
A; Experimental source: strain H37Rv
C; Genetics:
C; Superfamily: hypothetical protein
C; Superfamily: hypothetical protein
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28.2%;
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ilarity 27.4%;
Conservative 14
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Best Local Similarity 28.28
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 SLAD--FDALLDEAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 DKADIEIEGLLLEVL 155
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 37; Conserv
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C: Species: Homo sapiens (man)
C: Saccession: S71090
R: Yahraus, T.: Braverman, N.: Dodt, G.; Kalish, J.E.; Morrell, J.C.; Moser, H.W.; Val
EMBO J. 15, 2314-2923, 1996
A; Title: The peroxisome biogenesis disorder group 4 gene, PXAA1, encodes a cytoplasm
A; Reference number: S71090; MUD: 96272151
A; Accession: S71090
A; Stetus: preliminary
A; Molecule type: DNA
C; Superfamily: FteH/SEC18/CDC48-type ATP-binding domain homology
C; Reywords: ATP; nucleotide-binding motif A (P-loop)
F; 719-928/Domain: FtsH/SEC18/CDC48-type ATP-binding domain homology <VATP>
F; 714-751/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Barody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Loure, 406, 959-964, 2000
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720 TIQLPLEHPELLSLGLRRSGLLLHGPP---GTGKTLLAKAVATECSLTFLSVKGPELINM 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 RIPVE-LRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCG--DGDVHIAPADP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79. QVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 892;
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12;
Cyccession: T29420
RyParkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A; Reference number: 220619
A; Accession: T29420
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-892 < PAR>
A; Cross-references: EMBL:AL031155; PIDN:CAA20065.1
C; Genefics:
A; Note: SC3A7.02c
C; Superfamily: regulatory protein malT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 ETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 78.5; D 34.4%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: |: | | | :: SGVGQRLL----ASLAAELNALDSPVVLVLDEYDRM
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                                                                                                                                                                                                                                                                                                                                                Note: SC3A7.02c
Superfamily: regulatory protein malT
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E

33;

Indels

DB 1;

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C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; metalloprotein;
F;2-260/Product: carbonate dehydratase III #status predicted <MAT>
F;5-259/Domain: carbonic anhydrase homology <CAH>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;94,96,119/Binding site: zinc (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispacesion: 169009
Risalgar, S.K.; Kunz, H.W.; Gill, T.J.
Immunogenetics 42, 244-253, 1995
A;Title: Nucleotide sequence and structural analysis of the rat RT1.Eu and R A; Reference number: 154554; MUID:95402978
A;Accession: 169009
A;Accession: 169009
A;Actus; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-343 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gross_references: GB:L40362; NID:9992571; PIDN:AAC42073.1; PID:9992572 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology F;220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 D---GGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVP 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87. PYRLR-QFHL-----HWGSSDDHGSEHTVDGVKYA---AELHLVHWNPKYNTFKEALKQ 136
                                                                                                                                                                                                                                                                                                                                                                                                      24. PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 SFRIPVELRYET----CDPYAVRLTFH-------LPGDAPVTWAF-GRELLI 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.7%; Score 75; DB 2; Best Local Similarity 24.5%; Pred. No. 7; Matches 35; Conservative 10; Mismatches 36
                                                                                                                                                                                                                                                                     ; Score 75.5; D
; Pred. No. 4.5;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 LGKEQSYTCLVEHEGLPEPLTQR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 LGQERS --- LADFDALLDEALDR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHC class I RT1.C-type protein - rat
                                                                                                                                                                                                                                                                     ch 10.8%;
11 Similarity 28.2%;
31; Conservative 1
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A;Molecule type: DNA
A;Residues: 1-175 <HEI>
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A.Status: not compared with conceptual translation
A.Status: not compared with conceptual translation
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A.Status: not compared
A.Status: not compared
A.Title: Human muscle carbonic anhydrase: gene structure and DNA methylation patterns in
A.Status: not compared with conceptual translation
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A.Status: not not carbonic at not carbonic at nusce fiber
A.Status: not not not carbonic type I muscle fiber
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A.Status: not not carbonic type I muscle fiber
A,Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathd A;Reference number: A82950; MUID:20437337
A;Accession: D83460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <STO>
A;Cross references: GB:AE004577; GB:AE004091; NID:g9947430; PIDN:AAG04872.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: cycH; PA1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Wade, R.; Gunning, P.; Eddy, R.; Shows, T.; Kedes, L. Proc. Natl. Acad. Sci. U.S.A. 83, 9571-9575, 1986
A;Title: Nucleotide sequence, tissue-specific expression, and chromosome location of hum CAII genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c;Date: U5-Feb-1988 #sequence_revision 05-May-1995 #text_change 18-Jun-1999
C;Accession: A26658; A26690; A25850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 TFGEVL-----IRLQVGSDQAMF----RVGTAPLVAFLDRTDKIVPLGQERSLADF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: carbonic anhydrase III; muscle carbonic anhydrase C;Species: Homo sapiens (man)
C;Species: 05-Feb-1988 #sequence_revision 05-May-1995 #text_change 18-Ju
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77.5;
Pred. No. 4.8
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A; Accession: A26658
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27.08;
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Best Local Similarity 27.0%
Matches 34; Conservative
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RT1.Eu and RT1.Aw31

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Length 343;

36;

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Search completed: July 18, 2002, 14:17:37
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C; Species: Homo sapiens (man)
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
C; Date: 28-Oct-1996 #sequence, G; Nicholl, J.K.; Sutherland, G.R.; Simps Eur. J. Biochem. 234, 492-500, 1995
A; Title: Complete nucleotide sequence, expression, and chromosomal localisation of human
A;Cross-references: GB:AE004434; GB:AE003853; NID:g9658531; PIDN:AAE96986.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Spinacia oleracea (spinach)
:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                        47 LLIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVP 106
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S. Superfamily: peroxidase
C; Superfamily: peroxidase
C; Superfamily: peroxidase
C; Superfamily: peroxidase
C; Superfamily: peroxidase
F; 37-118/Disulfide bonds: #status predicted
F; 64/Active site: Arg #status predicted
F; 68.196/Eniding site: heme iron (His) (axial ligands) #status predicted
F; 70-75/Disulfide bonds: #status predicted
F; 124-319/Disulfide bonds: #status predicted
F; 203-228/Disulfide bonds: #status predicted
                                                                                                                                                                                                              28;
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                                                                                                                                                                 Length 175;
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C;Species: Spinacia oleranna احماه العالم الم
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A;Reference number: 216599
A;Accession: T09164
                                                                                                                                                                                                              Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                             Experimental source: subspecies Nobel
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                                                                                                                                                              10.68;
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24.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-723 <SIM>
A; Cross-references: EMBL: Y10465
A; Experimental source: subspecie
C; Genetics:
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R; Simon, P.
                                                                       A; Gene: VCA1094
A; Map position:
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A. Accession: S68178; MUID:96128179
A. Accession: S68178
A. Accession: 13004
A. Accession: 1300
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SUMMARIES	QI	PEX6_YARLI	CAH3_MOUSE	PEX6_RAT	PEX6_HUMAN	CAH3_RAT	CAH3_HUMAN	GLO2_RHOCA	M3KA_HUMAN	CAH3_HORSE	FKB7_WHEAT	DRNE_AERHY	PEX6_SCHPO	PEX6_PICPA	IRF3_MOUSE	LEF4_NPVOP	CHS2_MAIZE	YW84_MYCTU	YME1_SCHMA	NOLA_BRAJA	BCHC_RHOSH	FTZ2_PYRAB	SRYA_DROPS	YJK0_YEAST	ISPE_TREPA	DXR_BACHD	DP3A_VIBCH	FT22_PYRHO	HEMN_BRAJA	HXK1_SCHPO	POL2_BAMMN	GUNC_CELFI	PEX6_YEAST	SYI_TREPA
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oto (Match	12.0	11.2	11.1	11.1	10.9	10.8	10.6	0	10.5	10.4	10.3	10.3	10.3	10.0		6.6	•		7.6	9.7	9.7	7.6	7.	9.6	9.6	9.6		9.6	9.6	9.6	9.6	9.5	9.5
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UCRI_BOVIN MERA_ALCSP PIID_MOUSE BRNF_AERHY VKEQ_YEAST GUNA_BUTFI VP46_YEAST HYSI_SCHPO TRII_STRCO STR6_MOUSE GP21_RAT	ALIGNMENT	PRT;	Created) Last sequence update) Last annotation update) .s protein PAY4 (Peroxin	a lipolyt. a; Saccha: aceae; Ya:	76851; itzen G.A ., Glover peroxisom member o. 1994). EROXISOME	pyright. e of Bioi Institut utions as is not r agreemen @isb-sib.(b. bfam. ATP (PO' MW; C41:		GEVLIR : SVKGPELLN	
9.4 480 1 9.4 1043 1 9.3 237 1 9.3 236 1 9.3 256 1 9.3 577 1 9.3 1067 1 9.2 837 1		STANDARD;	Rel. 29, Creat Rel. 29, Last Rel. 35, Last Synthesis pro	Provide lipolytica (Candida lipolytica). Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetales; Dipodascaceae; Yarrowia. NCBL_TaxID=4952;	N.A. Brade A.M., E Brade A.M., E , Szilard R.K required for rocdes a novel 269:556-566 INVOLVED IN P INVOLVED IN P INCATION: C : BELONGS TO	Tentry is convision of the properties of the pro	AAA16622.1; - 003593; AAA. 003960; AAA_su 003959; AAA_su AAA; 2. 7 AAA; 1. 774; AAA; 1. 774; AAA; 1.	Match 12.0%; Local Similarity 27.8%; Les 25; Conservative	PCGDGDVHIAPADPETF PGTGKTLLAKAIATTFSLNFF	TDKIVPLGQERSLADFDALLDEALDRILAE : : : LDSVAPQRRNGGDSGGVMDRIVSQLLAE
33.4 33.5 34.0 37.0		PEX6_YARLI ID PEX6_YARLI	159596). 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence upo 01-NOV-1997 (Rel. 35, Last annotation of Peroxisome biosynthesis protein PAY4 (Peroxisome biosynthesis protein PAY4 (Peroxisome DayA).	Yarrowia lipol Eukaryota; Fur Saccharomyceta NCBL_TaxID=495	(1) SEQUENCE FROM MEDLINE=94103 Nuttley W.M., Altchison J.D. Altchison J.D. Ipolytica, er J. Biol, Chem : SUNCTION: - : SUNCELLULO.	This SWISS-PRE between the E the European E use by non-F modified and if entities requi	EMBL; L23858; InterPro; IPR(InterPro; IPR(FinesPro; IPR(Ffam; PF00004; SWART; SM0038; PROSITE; PS006 PPEROXISOME; AI NP_BIND 76 SEQUENCE 102	Query Match Best Local Simila Matches 25; CC	55 PCGDGDVHI : 761.PPGTGKTLI	101 TDKIVPLGC : 821 LDSVAPC
ताताता ताता ताच्यच्यच् य		RESUL PEX6_ ID		0000x	RR RR RR R R R R R R R R R R R R R R R	388888888	OR D DR KW B D B R R B B B B B B B B B B B B B B B	Que Bes Mat	oy Db	Oy Db

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16-OCT-2001 (Rel.
                       (Peroxin-6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                  -i- FUNCTION: REVERSIBLE HYDRAFATION OF CARBON DIOXIDE.
-i- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.
                                                                                                                               Mus musculus (Mouse),
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                          Tweedle S., Edwards Y.; "Mouse carbonic anhydrase III: nucleotide sequence and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 78.5; DB 1; Length 259; 28.2%; Pred. No. 0.69; ive 13; Mismatches 33; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
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ZINC (CATALYTIC).
ZINC (CATALYTIC).
E35B5CDDC4A54A93 CRC64;
                                           259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEX6_RAT STANDARD; PRT; 978 AA. P54777; 055097; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000865; Carb_anindrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc. 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:88270; Car3.
InterPro; IPR001148; Carb_anhydrase.
Pfam; PF00194; carb_anhydrase; 1.
                                           PRT;
                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89227981; Pubmed-2496681;
                                                                                                                                                                                                                                          Biochem. Genet. 27:17-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M27796; AAA37355.1; -.
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HSSP; P00918; 1CIM.
SWISS-2DPAGE; P16015; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
29397
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Best Local Similarity 28.29
Matches 31; Conservative
                                           STANDARD;
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93
95
118
259 AA;
                                                                                                                      OR CAR3.
                                           CAH3_MOUSE
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SEQUENCE
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                     RESULT 2
CAH3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        "Peroxisome assembly factor-2, a putative ATPase cloned by functional complementation on a peroxisome-deficient mammalian cell mutant."; Nat. Genet. 11:395-401(1995).
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      718 TIQLPLEHPELLSLGLRRSGLLLHGPP---GTGKTLLAKAVATECSLTFLSVKGPELINM 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 TFHLPGDAPVTWAFGRE---LLIDGGPRPCGDGDVHIAPADPE----TF----GEVLIRL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 QVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
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-1- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN, PEROXISOME.
-1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
16-OCT-2001 (Rel. 40, Last annotation update)
Peroxisome assembly factor-2 (PAF-2) (Peroxisomal-type ATPase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                        Tsukamoto I., Miura S., Nakai T., Yokota S., Shimozawa N.,
Suzuki Y., Orii T., Fujiki Y., Sakai F., Bogaki A., Yasumo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Indels
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K->A: LOSS OF FUNCTION.
D -> G (IN REF. 2).
V -> A (IN REF. 2).
O -> R (IN REF. 2).
R -> C (IN REF. 2).
R -> C (IN REF. 2).
A -> C (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsukamoto T., Hashiguchi N.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL)
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Pred. No. 3
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-FISCHER 344; TISSUE-Liver;
MEDLINE-96083586; Pubmed-7493019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART: SMUJOS, ...., PROSITE; PS00674; AAA; 1.
Peroxisome; ATP-binding; Repeat.
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EMBL; D89657; BAA24931.1; JOINED.
EMBL; D89658; BAA24931.1; JOINED.
EMBL; D89659; BAA24931.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003593; AAA.
Interpro; IPR003960; AAA_sub.
Interpro; IPR003959; AAA_subfam.
Pfam; PP00004; AAA; 2.
SWART; SM00382; AAA: 1.
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28.8%;
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                                                                                                                   Rattus norvegicus (Rat).
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476
748
299
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STRAIN-SPRAGUE-DAWLEY;
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Best Local Similarity
                                                                                                                                                                                                   NCBI_TaxID=10116;
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748
299
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EMBL; AF108097; AAF62564.1; JOINED
                                                                                           MIM; 214100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mutat. 13:487-496(1999).

-1- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS. REQUIRED FOR STABILITY OF THE PTSI RECEPTOR.

-1- SUBCELLULAR LOCATION: CYtOplasmic.
-1- DISEASE: DEFECTS IN PEX6 ARE THE CAUSE OF PEROXISOME BIOGENESIS DISONDER GROUP 4). PED ARE A GROUP OF LETHAL INHERITED DISEASES. THEY ARE CLINICALLY DIVIDED INTO FOUR GROUPS: ZELLWEGER SYNDROME (2S), NEORATAL ADRENOLEUKODYSTROPHY (NALD), INFANTILE REFSUM DISEASE (IRD), AND CLASSICAL RHIZOMELIC CHONDRONYSPRAIS AUGUSTAR (RCDP). ZS IS THE MOST SEVERE PHENOTYPE OF THE PED AND IS CHARACTERIZED BY THE ABSENCE OF PEROXISOMES AND BY MULTIPLE METABOLIC DEFECTS. PATIENTS WITH ZS HAVE SEVERE NEUROLGICAL ABNORMALITIES, DYSMORPHIC FACIAL FEATURES, HEPATOMEGALY, AND MULTIPLE RENAL CYSTS, MOST DIE WITHIN 6 MONTHS OF BIRTH. NALD AND IRD ARE SIMILAR TO 2S, BUT PROGRESSIVELY MILDER, WITH SOME IRD PATIENTS SURVIVING BEYOND THE THIRD DECADE OF LIFE. CLASSICAL RCDP, DISTINCT FROM THE ZS SPECTRRM, IS ASSOCIATED WITH A CHARACTERISTIC FACIAL APPEARANCE, RHIZOMELIA, CHARACTERISTIC FACIAL APPEARANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANTS ZS GLN-812 AND TRP-812.
MEDLINE-9932564; PubMed-10408779;
Zhang Z., Suzuki Y., Shimozawa N., Fukuda S., Imamura A.,
Tsukamoto T., Osumi T., Fujiki Y., Orii T., Wanders R.J.A.,
Barth P.G., Moser H.W., Paton B.C., Besley G.T., Kondo N.;
"Genomic structure and identification of 11 novel mutations of the
PEX6 'peroxisome assembly factor-2' gene in patients with peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-96272151; PubMed-8670792;
Yahraus T., Braverman N., Dodt G., Kalish J.E., Morrell J.C.,
Moser H.W., Valle D., Gould S.J.;
"The peroxisome biogenesis disorder group 4 gene, PXAAA1, encodes a
cytoplasmic ATPase required for stability of the PTSI receptor.";
EMBO J. 15:2914-2923(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97094178; PubMed-8940266;
Fukuda S., Shimozawa N., Suzuki Y., Zhang Z., Tomatsu S.,
Fukuda S., Shimozawa N., Suzuki Y., Zhang Z., Tomatsu S.,
Tsukamoto T., Hashjquchi N., Osumi T., Masuno M., Imaizumi K.,
Kuroki Y., Fujiki Y., Orii T., Kondo N.;
"Human peroxisome assembly factor-2 (PAF-2): a gene responsible for group C peroxisome biogenesis disorder in humans.";
Am. J. Hum. Genet. 59:1210-1220(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             PEX6_HUMAN STANDARD; PRT; 980 AA.
013608; 099476;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Peroxisome assembly factor-2 (PAF-2) (Peroxisomal-type ATPase 1)
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AF108098; ARF62564.1; --
AF108095; AAF62564.1; JOINED.
AF108096; AAF62564.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                     PEX6 OR PXAAA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
EMBL;
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720 TIQLPLEHPELLSLGLRRSGLLLHGPP---GTGKTLLAKAVATECSLTFLSVKGPELINM 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAH3_RAT STANDARD; PRT; 259 AA.
P1411: 054961;
01-JAN-1990 (Rel. 13, Created)
15-JUL.1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 TFHLPGDAPVTWAFGRE---LLIDGGPRPCGDGDVHIAPADPE----TF----GEVLIRL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79. QVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver; Mallis R.J., Jung C.-H., Chatterjee T.K., Fisher R.A., Thomas J.A.; Mallis R.J., Jung C.-H., Chatterjee T.K., Fisher R.A., Thomas J.A.; EDNA sequence of rat liver carbonic anhydrase III."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89166882; PubMed-2852973;
Kelly C.D., Carter N.D., Jeffery S., Edwards Y.H.;
"Characterisation of cDNA clones for rat muscle carbonic anhydrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUE-Liver;
MEDLINE-20361776; PubMed-10900145;
Ikeda M., Ishii Y., Kato H., Akazawa D., Hatsumura M., Ishida T.,
Matsusue K., Yamada H., Oguri K.;
"Suppression of carbonic anhydrase III in rat liver by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dioxin related toxic compound, coplanar polychlorinated biphenyl, 3,3',4,4',5-pentachlorobiphenyl.";
Arch. Biochem. Biophys. 380:159-164(2000).
-!- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%; Score 78; DB 1; Length 980; 28.8%; Pred. No. 3.7; tive 14; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                     812 812 K -> W (IN ZS; ATYPICAL).

/FTIG=VAR_007918.

/FTIG=VAR_007919.

77 77 S -> W (IN REF. 1).

980 AA; 104060 MW; 0ECIC2A75CE0038F CRC64;
                                                                                                                                SMART; SM00382; ALA., -...
PROSITE; PS00674; AAA; 1.
Peroxisome; ATP-binding; Repeat; Disease mutation.
NP_BIND 470 477 ATP (POTENTIAL).
7.44 751 ATP (POTENTIAL).
                                                                       InterPro; IPR003959; AAA_subfam
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InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA_sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.89
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                Pfam; PF00004; AAA; 2.
SMART; SM00382; AAA; 1.
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31; Conservative
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93
95
118
30
259 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                     MIM; 114750;
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                                                                                                                                                                                                                                                                                                                                                                         Lyase; Zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter
                                                                                                                                  FAMILY.
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P96981;
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CONFLICT
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                        PYAVRLIFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
 SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wade R., Gunning P., Eddy R., Shows T., Kedes L.; "Nucleotide sequence, tissue-specific expression, and chromosome location of human carbonic anhydrase III: the human CAIII gene is located on the same chromosome as the closely linked CAI and CAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liloyd J., McMillan S., Hopkinson D., Edwards Y.H.;
"Nuclectide sequence and derived amino acid sequence of a cDNA
encoding human muscle carbonic anhydrase.";
Gene 41:233-239(1986).
                                                                                                                                                                                                                                                                                                                               DB 1; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                               136 PDGIAVVGIFLKIGREKGEFQI-----LLDALDKIKTKGKEAPFNHFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                  -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                              ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
A -> G (IN REF. 1).
FG -> SE (IN REF. 1).
KL -> NV (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes.";
Proc. Natl. Acad. Sci. U.S.A. 83:9571-9575(1986).
                                                                                                                                                                                                                                                                                                                              10.9%; Score 76.5; DE 28.2%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 AA
                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                          InterPro; IPR001148; Carb_anhydrase.
Pfam; PF00194; carb_anhydrase; 1.
ProDon; P0000865; Carb_anhydrase; 1.
PROSITE: PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase: Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                    EMBL; M22413; AAA40846.1; -.
EMBL; AF037072; AAB92558.1; -.
EMBL; AB030829; BAB08111.1; -.
                                                                                                                                                                                                                                                                                  224 KI
29300 MW;
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                              93
95
118
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                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                     HSSP; P00918; 1CIM.
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Best Local Similarity
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223
259 #
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95
118
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P07451;
                                                                                                                                                                                                        Lyase; Zi
INIT_MET
METAL
                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAH3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Probable hydroxyacylglutathione hydrolase (EC 3.1.2.6) (Glyoxalase II) (Glx II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 RDGIAVIGIFLKIGHENGEFQI-----FLDALDKIKTKGKEAPFTKFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 -----IRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
I -> V (IN REF. 2).
W, EFBC56CF7721E4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 75.5; DB 1; 28.2%; Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001148; Carb_anhydrase.
Pfam; PF00194; carb_anhydrase; 1.
ProDom; PD000865; Carb_anhydrase; 1.
PR051TE; PS00162; EOK_CO2_ANHYDRASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M29452; -; NOT_ANNOTATED_CDS. PIR; A25850; A25850. PIR; A26658; A26658. PIR; A26690; A26690. HSSP; P00918; 1CIM. HSC-22PAGE; P07451; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
93
21
95
21
118
30
1
29440 MW;
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Katoh M., Hirai M., Sugimura T., Terada M.; "Cloning and characterization of MST, a novel (putative) serine/threonine kinase with SH3 domain.";
                                      MEDLINE=95249256; PubMed=7731697;
                                                                                                      Oncogene 10:1447-1451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00326; SH3; 1.
SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 31.5
Matches 28; Conservative
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463
464
480
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954 AA;
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
104
125
222
384
                        TISSUE-Brain;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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MEDLINE-98101484; PubMed-9440534;
Borghese R., Crimi M., Fava L., Melandri B.A.;
"The AJP synthase atpHAGDC (F1) operon from Rhodobacter capsulatus.";
J. Bacteriol. 180:416-421(1998).
-i. FUNCTION: THIOLESTERASE THAT CATALYSES THE HYDROLYSIS OF S-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 IAWYLPGAGLLFSGDSLMSWGCGR--LFEGTPAQMFDTLTRLAALPPETRVCSGHEYTAA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIFHLP-----GDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPET------ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 FGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADF----DALLDEAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 NGRFALSLEPGNGRLHDRMDRVTALRLAGEPSLPVTLGEERATNPFLRADDAALRAAL 234
                                                                                 LACTOYL-GLUTATHIONE TO FORM GLUTATHIONE AND D-LACTIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  -!- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M3KA_HUWAN STANDARD, PRT; 954 AA.

Q02779; Q12761; Q14871;
Q01-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)
(Mixed lineage kinase 2) (Protein kinase MST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
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MEDLINE-96128179; PubMed-8536694;
MEDLINE-96128179; PubMed-8536694;
Borow D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
Sutherland G.R., Simpson R.J.;
"Complete nucleotide sequence, expression, and chromosomal localisation of human mixed-lineage kinase 2.";
Eur. J. Biochem. 234:492-500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%; Score 74; DB 1; Length 256; 25.4%; Pred. No. 2;
                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
                                                                                                                              glutathione + a 2-hydroxy acid anion.
-!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
-!- PATHWAY: GLYOXAL PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR001279; Beta_lactam_met. Pfam; PF00753; lactamase_B; 1. Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27342 MW;
                                                                                                                                                                                                                                                                                                                                                      EMBL; X99599; CAA67905.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARG/LYS-RICH (BASIC).
SRL -> AV (IN REF. 2).
LKLREGGSHISLPSGF -> AQAAGRRQPHQPALWL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
              22;
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LEUCINE-ZIPPER (BY SIMILARITY).
LEUCINE-ZIPPER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.6%; Score 74; DB 1; Length 954; 31.5%; Pred. No. 9.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G -> S (IN REF. 2).
G -> R (IN REF. 2).
V -> A (IN REF. 2).
MW; 538F4AAA559BOABA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00108; PROTEIN_KINASE_ST; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR000719; Euk_pkinase. InterPro: IPR001452; SH3.
InterPro: IPR001452; SH3.
InterPro: IPR002040; STY_pkinase. InterPro: IPR001290; Ser_thr_pkinase. InterPro: IPR001245; Tyr_pkinase. Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REF. 3).
G -> S (
G -> R (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X90846; CAA62351.1; -. EMBL, 248615; CAA88531.1; -. PIR; S32468; S32468.
SEQUENCE OF 244-480 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
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P39658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aeromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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DRNE_AERHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
70 Kba peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans isomerase) (Cyclophilin) (Ppiase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 PYAVRLTFHLPGDAPVTWA----FGRELLIDGGPRPCGDGDVHIAPADPE--TFGEVL-- 75
                                                                                                                                           01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum (Wheat).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                  Wendorff K.M., Nishita T., Jabusch J.R., Deutsch H.F.;
"The sequence of equine muscle carbonic anhydrase.";
J. Blol. Chem. 260:6129-6132(1985).
-i.- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-i.- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-i.- SUBCELLULAR LOCATION: Cytoplasmic.
-i. SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE
                       EVPYREIDALAVAYGVAMNKLTLPIPSTCPEPFA---RLL----EECWDPDPHGRP---
   ELRYETCDPYAV-----RLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADP
                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBL_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 PDGIAVVGVFLKIGREKGEFQL-----FLDALDKIKTKGKEAPFTNFD 178
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ZINC (CATALYTIC).
ZINC (CATALYTIC).
B3EECDFF89BFED02 CRC64;
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                                                                                                                        259 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 73.5; DI
Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                             HSSP, P00918, 1803.
InterPro; IPR001148; Carb_anhydrase.
Pfam; PF00194; carb_anhydrase; 1.
Probom, P0000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK.CO2_ANHYDRASE; 1.
Lyase; Zinc; Acetylation.
                                                         - DFGSILKRLEVIEQSALFQM---PLESF 373
                                             69 ETFGEVLIRLQVGSDQAMFRVGTAPLVAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                            MEDLINE=85207593; PubMed=3922970;
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                                                                                                                        STANDARD;
                                                                                                                                                                                                             Eguus caballus (Horse).
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Best Local Simi
Matches 29;
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Q43207;
                                                                                                                        CAH3_HORSE
P07450;
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SEQUENCE
                                                                                                                                                                                                                                                                 SEQUENCE
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MOD_RES
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                                                                                                  RESULT 9
CAH3_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
FKB7_WHEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 ENPKDPDEVFVKYEARLEDGTVVSKSEGVEFTVKDGHLCPALAKAVKTMKKGEKVLLA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 IAPADP-ETFGEVLIRLQVG----SDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLA 114
                                                                                                                                                                                                                                                                                           BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
                                                                                              STRAIN-CV. ATTR: TISSUE-ROOT tip;
Oshra B., Breiman A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPTASE THAT BINDS CALMODULIN.
-!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PERTINE BONDS IN OLIGOPEPTIDES.
-!- INDUCTION: BY HEAT SHOCK.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-ocr-1994 (Rel. 30, Created)
01-ocr-1994 (Rel. 30, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Extracellular deoxyribonuclease precursor (EC 3.1.21.-) (DNase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5C5DAE70D716B541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001179; FKBP_PPHase.
InterPro; IPR001440; TPR.
InterPro; IPR001440; TPR.
InterPro; IPR00154; FKBP, 3.
SMART; SM00028; TPR; 3.
PROSITE; PS00453; FKBP_PPHASE_1; 1.
PROSITE; PS00454; FKBP_PPHASE_2; 3.
ISOMERASE; ROTAMASE; 1.
ISOMERASE; ROTAMASE; HERP_PHASE_3; 3.
ISOMERASE; ROTAMASE; HERP_PRIASE_3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPIASE,
PPIASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPIASE,
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TPR 2.
TPR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62056 MW;
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29.7%;
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Triticum.
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401
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484
559 AA;
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                         NCBI_TaxID=4565;
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PEX6 OR PAS5.
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                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                         Chang M.C., Chang S.Y., Chen S.L., Chuang S.M.; "Cloning and expression in Escherichia coli of the gene encoding an extracellular deoxyribonuclease (DNase) from Aeromonas hydrophila."; gene 122:175-180(1992).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE ENDA/NUCM FAMILY OF NUCLEASES.
                                                                                                                                                                                                                                                                                                                                                                                              41 WAFGRELLI--DGGPRPCG------DGDVH-IAPADPETFGEVLIRLQVGSDQAMFRV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deviin K., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE BIOGENESIS OF PEROXISOMES (BY
                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                       POTENTIAL.
EXTRACELLULAR DEOXYRIBONUCLEASE.
D6C60274CFAE7E29 CRC64;
                                                                                                                                                                                                                                                                                                                                           Score 72.5; DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  948 AA.
                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                         Hydrolase; Endonuclease; Nuclease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 GTAPLVAFLDRTDKIVPLGQERSLADF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----FSDWNGKPNOYGKCOMLVDF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
           MEDLINE-93083980; PubMed=1452026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003593; AAA.
InterPro; IPR003960; AAA_sub.
InterPro; IPR003959; AAA_subfam.
                                                                                                                                                                                                                                                                                                  SEQUENCE 230 AA; 26699 MW;
                                                                                                                                                                                                                                                                                                                                         10.3%;
                                                                                                                                                                                                                               EMBL; M99491; AAA21942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z98849; CAB11501.1; -.
                                                                                                                                                                                                                                                                                                                                                                    28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable peroxin-6. SPAC17A5.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                             PIR; JC1483; JC1483
                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEX6_SCHPO
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               013764;
                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
PEX6_SCHPO
                                                                                                                                                                                                                                                                                                                                                                     Matches
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STRAIN-NRRL 11430;

MEDLINE-94043437; Pubmed-8227124;

Spong A.P., Subramani S.;

"Cloning and characterization of PAS5: a gene required for peroxisome biogenesis in the methylotrophic yeast Pichia pastoris.";

J. Cell Biol. 123:535-548(1993).

-!- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS. NECESSARY FOR MATRIX PEROXISOMAL PROTEINS IMPORT. ESSENTIAL FOR GROWTH ON OLEIC ACID AND METHANOL AS SOLE CARBON SOURCE.

-!- SUBCELLULAR LOCATION: IT MAY BE ASSOCIATED WITH THE CYTOSKELETON OR IT MAY BE CYTOPLASMIC.

-!- SUBLAILY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     667 LRDTLQLPLQFPELFSQGLKPRSGVLLYGPP---GTGKTLLAKAVATELSLEFVSIKGPE 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 LIRLQVGSDQAMFR-----VGTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRIL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 VRLTFHLPGDAPVTWAFGRE----LLIDGGPRPCGDGDVHIAPADPETF------GEV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pichia pastoris (Yeast).
Bukaryota; Mugdi, Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            859 866 ATP (POTENTIAL).
1165 AA; 129137 MW; DEA192C1D5CA46EA CRC64;
                                                                                                                                                                                                                                                                                                                              F41DFD7DE6D391B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Peroxisome biosynthesis protein PAS5 (Peroxin-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                           ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.3%; Score 72.5; Di
25.4%; Pred. No. 13;
Live 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1165 AA
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InterPro; IPR003593; AAA.sub.
InterPro; IPR003959; AAA.sub.
InterPro; IPR003959; AAA.sub.
InterPro; IPR003593; AAA.sub.
SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; 1.
Pfam; PF00004; AAA; 2.
SMART: SM03382; AAA; 1.
PROSITE; PS00674; AAA; FALSE_NEG.
Peroxisome; ATP-binding.
NP_BIND 695 702 ATP
                                                                                                                                                                                                                                                                                                                              SEOUENCE 948 AA; 106505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 222556; CAA80278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches: 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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457 AA.

PRT;

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SEQUENCE FROM N.A. MEDIAGE-9126251; Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rhrans C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.; The sequence of the Orgyla pseudotsugata multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                               Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                          Late, expression factor 4.
                                                                                                                                                                                                                                                                                                                                                                                Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=164623;
                                                                                                                                                    01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                            LEF4_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                              LEF4_NPVOP
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                                RESULT
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                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KDKDG 310
                                                              Gaps
                                                                                                                         TFHLPGDAPVTWAFGRE----LLIDGGPRPCGDGDVHIAPADPETF-----GEVLIR 77
                                                                                                                                                                                                                                                       LQVGSDQAMFRV-----GTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE 130
                                                                                                                                                                                                                                                                                           ::| :| : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | | : ::| | : ::| | | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | :::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                 23;
   DB 1; Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 419;
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7; Mismatches 19; Indels
                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interferon regulatory factor 3 (IRF-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AA.
                                                              Mismatches
Score 72.5; 1
Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
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ProDom; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
10.3%; 23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%;
32.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36925.1; -.
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HSSP; P23906; 2IRF.
MGD; MGI:1859179; IrF3.
InterPro; IPR001346; IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| | | | |:||:
AVFDLRPFVADLIAFME 327
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                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRF3_MOUSE
P70671:
                                Best Local Sim
Matches 28;
   Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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polyhedrosis virus genome.";
Virology 229:381-399(1997).
-!- FUNCTION: REQUIRED FOR LATE AND VERY LATE GENE EXPRESSION (BY
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Q9KK10 vibrio chol
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0941y0 drosophila
Q21029 caenorhabdi
Q9K20 streptomyce
0914y1 streptomyce
06499 mycobacteri
Q931w2 streptomyce
Q95zr0 arabidopsis
Q9ewy7 streptomyce
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03a788 bacillus su
092k21 rhizobium m
09a400 caulobacter
092py5 rhizobium m
09kh05 bradyrhizob
032384 synechococc
09hsm3 halobacteri
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Q31271 rattus norv
O87043 vibrio chol
                            Q9i3m9 pseudomonas
 Q9d1d7 mus musculu
                    Q991c9 mus musculu
          086603 streptomyce
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van Wezel G.P., Rousseau C., Kraal B.;

"Cloning and sequencing of the Streptomyces goldeniensis ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF195770: AAC28481.1; -
SEQUENCE 135 AA; 14843 MW; 32006CC86EDE4ED6 CRC64;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
NCBI_TaxID=121022;
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ive 0; Mismatches 0;
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                    Compugen Ltd
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Copyright (c) 1993 - 2000 Comp
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Result No.

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1 MSFLVSEELSFRIPVELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGD 60
                                                                                                                           Kawamoto S., Ensign J.C.; "Cloning and characterization of a gene involved in regulation of sporulation and cell division of Streptomyces griseus."; Nippon Hosenkin Gakkaishi 9:136-151(1995).
                          Kawamoto S., Ensign J.C.;
"Isolation of mutants of Streptomyces griseus that sporulate in
nutrient rich media.";
                                                                                                                                                                                                                              MEDLINE=97286526; PubMed=9141673; Kawamoto S., Watanabe H., Heeketh A., Ensign J.C., Ochi K.; Kawamoto S., Watanabe H., Heeketh A., Ensign J.C., Ochi K.; Expression and yelsis of a ssgA gene product associated with sporulation and cell division in Streptomyces griseus."; Microbiology 143:1077-1086(1997).

EMBL; D50051; BAA21558 1; SEQUENCE 136 AA: 14783 MW; C6A28A7823AD7C8B CRC64;
                                                                                                                                                                                                                                                                                                                                                            79.3%; Score 556; DB 2; 78.5%; Pred. No. 8.6e-48; iive 12; Mismatches 17;
                                                                    Nippon Hosenkin Gakkaishi 9:124-135(1995)
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Matches 106; Conservative
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SEQUENCE FROM N.A.
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Kinsafi H., Hopwood D.A.;
Mast of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microblol. 21:77-96(1996).
EMBL; A0196823; CAB669641;
SEQUENCE 136 AA: 14920 MW; 4B67CIFIEOBECC88 CRC64;
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                                                                                                                                                         Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                       STRAIN=A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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85.2%; Pred. No. 4.5e-51;
Live 7; Mismatches 13;
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MEDLINE=97000351; PubMed=8843436;
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                                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, PUTATIVE REGULATOR.
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2 MSFLVSEELSFRIPVELRYEVGDPYAIRWIFHLPGDAPVIWAFGRELLLDGLNSPSGDGD 61
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van Wezel G.P., Rousseau C., Kraal B.;
"Cloning and sequencing of the Streptomyces netropsis ssgA gene.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195772; AAG28483.1; -.
SEQUENCE 145 AA; 15838 MW; 92AC0F30DF3D2620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptoverticillium netropsis (Streptoverticillium flavopersicus). Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
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77.8%; Pred. No. 1.5e-46;
tive 12; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 AA.
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Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL137778; CAB70943.1;
       MEDLINE=97000351; PubMed=8843436;
                                                                                                                                  17472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel, 13, 01-MAY-2000 (TrEMBLrel, 13, 01-MAY-2000 (TrEMBLrel, 13,
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                                                                                                                                    159 AA;
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Best Local Similarity
Matches 55, Conserv
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61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                               van Wezel G.P., Rousseau C., Kraal B.;
"Cloning and sequencing of the Streptomyces albus ssgA gene.";
Submitted (oct-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF195771; AAG284821.; -
SEQUENCE 135 AA; 14735 MW; OFCBF4BDB2BA201B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.6%; Score 481; DB 2; Length 135; llarity 71.1%; Pred. No. 2.5e-40; Conservative 14; Mismatches 25; Indels
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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121 DDALNRSLAEEQSAG 135
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Submitted (JAN-2000)
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Best Local Similarity
Matches 96; Conserv
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61 VHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPLGQERSLADFDALL 120
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                                                                                                                                        Gaps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
BMD. Microbiol. 21:77-96(1996).
EMBL; ALO86822; CAB51005.1;
EMBL; ALO86822; CAB51005.1;
SEQUENCE 142 AA, 15364 WW; 857862390AA5ICCB CRC64;
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                                                                                    Length 159;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
BA41013F940D7315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                              33.4%; Score 234; DB 2; L ilarity 42.3%; Pred. No. 1.1e-15; Conservative 13; Mismatches 58;
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Best Local Similarity 38.1%; Pred. No. 7.4e-14;
Matches 48; Conservative 18; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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MEDLINE=97000351; Pubmed=8843436;
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RESULT **Q9X7M8**

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL391041; CAC01575.1;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE REGULATOR.
SC5H1.03.
SC5H1.03.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBL_TaxID-1902;
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                                                                                                                                                                      Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels
                                        STRAIN=A3(2);
Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                  1041; CAC01575.1; -.
156 AA; 17188 MW; 7181972EE7F33FB0 CRC64;
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MEDLINE=97000351; Pubmed=8843436;
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MEDLINE=97000351; PubMed=8843436;
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Submitted (MAY-1999)
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Best Local Similarity
Matches 41; Conserva
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Oliver K., Ha
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Q9X7R1
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STRAIN-3(2);
MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinsahi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049587; CAB40672.1; -.
SEQUENCE 138 AA: 15261 MW; F531BA295144ABA5 CRC64;
77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLGIDDGL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 LIDGGPRPCGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTDKIVPL 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSFLVSEELSFR-----IPVELRYETCDPYAVRLTFHLPG---DAPVTWAFGREL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescae; Streptomyces.
NCBI_TaxID=1902;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                               138 AA.
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                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                   PUTATIVE REGULATOR
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                                          121 DEALDR 126
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                                                 NCBI_TaxID=5076;
                                                                                                                                                              ATP-binding.
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       PEROXIN-6.
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                                                                            Gaps
                                RIPV--ELRYETCDPYAVRLTFHLPGDAPVTWAFGRELLIDGGPRPCGDGDVHIAPADPE 69
                                           13 IPVELRYE-TCDPYAVRLTFHLPG-----DAPVTWAFGRELLIDGGPRPCGDGDVHIAPA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 IPVVLRYDPQLDPSKVCVA--LPGRGGRASGSREWTFSRELLEQGLRAPAGSGEVRVWPC 84
                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Indels
                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                Indels
                                                                                                                                                                                                                                                                             STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 13.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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       Pred. No. 1.7e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 DPETFGEVLIRLQVGSDQ - - AMFRVGTAPLVAFLDRT 101
                                                                                                                                                               126 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%; Score 91.5; D 34.0%; Pred. No. 0.12 ative 10; Mismatches
                Mismatches
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MEDLINE-97000351; PubMed-8843436;
30.5%; PAC.
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               Conservative
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Streptomyces coelicolor.
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Best Local Similarity
       Best Local Similarity
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01-MAR-2001 (
01-DEC-2001 (
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Q9HG03
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Yoon Y.J., Ning S., Mueller R., Hutchinson C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amycolatopsis mediterranei (Nocardia mediterranei).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 LQVGSDQAMFR-----VGTAPLVAFLDRTDKIVPLGQERSLADFDALLDEALDRILAE- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 TFHLPGDAPVTWAFGRE----LLIDGGPRPCGDGDVHIAPADPETF------GEVLIR 77
                                Eukaryota; Fungī; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                      MEDINE-20411849; PubMed=10968639;
Kiel J.A., Hilbrands R.E., Bovenberg R.A., Veenhuis M.;
Kiel J.A., Hilbrands R.E., Bovenberg R.A., Veenhuis M.;
Isolation of Penicillium chrysogenum PEX1 and PEX6 encoding AAA proteins involved in peroxisome biogenesis.";
Appl. Microbiol. Biotechnol. 54:238-242(2000).
EMBL; AF233277; AAG09749.1; -..
InterPro: IPR003595; AAA..
Efam: PF00004; AAA: 1.
Pfam: PF00004; AAA: 1.
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August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Yu T.W.,
Taylor M., Hoffmann D., Kim C.G., Zhang X., Hutchinson C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; Score 85; DB 3; Length 1459; 25.2%; Pred. No. 10; Live 19; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF040570; AAC01740.1; -.
HSSP; Q00441; 10XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1459 AA; 157053 MW; C5219F4DBA6E49B9 CRC64;
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Kim C.G., Yu T.W., Fryhle C., Handa S., Floss H.G.;
J. Biol. Chem. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE CYTOCHROME P450 MONOOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
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Penicillium chrysogenum.
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Chem. Biol. 5:0-0(1998).
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August P.R., Tang L.,
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                                                                                                                                                 39; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 TFHLPGDAPVTWAF----GRELLIDGGPRPCGDGDVHIAPADPETFGEVLIRLQV--GS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Stuter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 291;
                                                                                                               11.8%; Score 82.5; DB 2; Length 351; 24.3%; Pred. No. 3.3;
tive 23; Mismatches 53; Indels 39
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003959; AAA_subfam.
Pfam. PF00004; AAA; 1.0.
Hypothetical protein; Complete proteome.
SEQUENCE 291 AA; 31950 MW; FA611423E14B4DCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 31.9 KDA PROTEIN.
RV2426C OR MTCY428.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 11.6%; Score 81.5; DB 16; Best Local Similarity 27.4%; Pred. No. 3.3; Matches 37; Conservative 14; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                291 AA.
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197 GLGIFVLLQRPAQLATLRDDPSRIADAVEGLL 228
                                                                                                                                                                                                                                                                                                                 PLG-----QERSLADFDALLDEALDRIL 128
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InterPro; IPR001128; Cyt_P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence.";
Nature 393:537-544(1998).
EMBL; Z81451; CAB03770.1; -.
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                                                                                                                                Best Local Similarity 24.3%
Matches 37; Conservative
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                                                                                                                 Query Match
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MEDLINE=21380423; PubMed=11487704;
MEDLINE=21380423; PubMed=11487704;
MEDLINE=21380423; PubMed=11487704;
MEDLINE=21380423; PubMed=11487704;
Menoxisomal Metabolic Function Is Required for Appressorium-Mediated Plant Infection by Colletotritohum lagenarium.";
Plant Cell 13:1945-1957(2001).
EMBL; AF343063; AANLS11; -.
InterPro; IPR003369; AAALsubfam.
InterPro; IPR003959; AAALsubfam.
Pfam; PF00004; AAA: 1.
SMART; SM00382; AAA: 1.
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                                                                                                                                                                                                                 lagenarium).
Eukaryota; Fungi; Ascomycota; Pezižomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1388;
                                                                                                                                                                                                    Glomerella lagenarium (Anthracnose fungus) (Colletotrichum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Indels
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                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                          1388 AA
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25.2%; Pred. No. 34;
Live 18; Mismatches
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                                                                                                                        Created)
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                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.33
Best Local Similarity 25.23
Matches 31; Conservative
141 DKADIEIEGLLLEVL 155
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                                                                                           PRELIMINARY;
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Q9C1E9;
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Q9C1E9
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Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing filamentous microorganisms
Patent: WO 0000613-A 9 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BARRND (NL); LUITEN RUDOLF GIJSBERTUS MARIA (NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
                                             AL096823 Streptomy
AX007222 Sequence
AK195770 Streptomy
AL137778 Streptomy
AL13778 Streptomy
AL096852 Streptomy
AL096852 Streptomy
AL096852 Streptomy
AX083103 S.albus bet
AL391041 Streptomy
AX08419 Sequence
AX084416 Sequence
AX084416 Sequence
AX084416 Streptomy
AX08435 Streptomy
AL035517 Streptomy
AL035517 Streptomy
AL035517 Streptomy
AL035517 Streptomy
AL035517 Streptomy
AL6059 Ralstonia
AR151714 Sequence
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AL021529 Streptomy
AX196078 Sequence
AX195929 Sequence
AL031124 Streptomy
       AF195772 Streptomy
AX007218 Sequence
AX007216 Sequence
D50051 Streptomyce
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AP003825 Oryza sat
U41300 Blastocladi
AL355832 Streptomy
AL139298 Streptomy
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D37878 Streptomyce
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AF124138 Streptomy
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                             (without 2084:582)
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Listing first 45 summaries
                                               - nucleic search, using sw model
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Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Scoring table:

Streptomyce

PAT 06-SEP-2000

Description

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Result

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1. .407
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1 (bases 1 to 438)
van Wezel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces netropsis ssgA gene
Unpublished
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Submitted (18-0CT-1999) Biochemistry, University of Leiden, PO
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                           /gene="ssgA"
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                  /gene="ssgA"
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van Wezel, G.P.
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filamentous microorganisms
Patent: WO 0000613-A 3 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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Streptomyces griseus SsgA; possible cell
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Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Sequence 3 from Patent WO0000613.
AX007218
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BCT 19-MAY-1999
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Streptomyces griseus
Streptomyces griseus
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Isolation of mutants of Streptomyces griseus that sporulate in
nutrient rich media
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                                                                                                                     /gene="ssgA"
/note="strain ATTC of Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 298.2; DB 6;
Pred. No. 6.3e-26;
0; Mismatches 68;
    /organism="Streptomyces griseus"
/db_xref="taxon:1911"
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                                                                                                                                                                                                                                  /protein_id="CAC07384.1"
/db_xref="GI:9995083"
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Kawamoto, S. and Ensign, J.C.
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/product="SsgA"
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Best Local Similarity 83.3%;
Matches 339; Conservative
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/product="Ssga"
/product="Ssga"
/protein_id="CAC07385.1"
/db_xref="GI:9995085"
/translation="MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG
/translation="MSFLVSEELSFRIPVELRYEVGDPYAIRMTFHLPGDAPVTWAFG
/renslation="MSFLVSEED" | NSFLVSEED | NSFLVSEED | NSFLLDGINSPSGDOVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRTD
// TANDEQDETTLGDEPORTEDALGATTA | NSFLVSEED |
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Reducting branching and enhancing fragmentation in culturing
filamentous microorganisms
filamentous microorganisms
Patent: WO 0000613-A 1 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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Streptomyces griseus
Bacteria; Firmicutes; Actinobacteriae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 407;
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/gene="ssgA"
/note="strain ATTC of Streptomyces griseus"
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Pred. No. 6.5e-26;
0; Mismatches 68;
/organism="Streptomyces griseus"
/db_xref="taxon:1911"
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Sequence 1 from Patent W00000613.
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83.3%;
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Matches 339; Conservative
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Juliary Significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22/21:4768-4778(1984)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, etg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the most uppermann initiation codon.
                                           BCT 08-JUL-1999
                                                                                                                                         abaB; bldA regulation; cysA; cystathionine/methionine gamma-synthase/lyase; gntR-family; integrated element; korSA; lysR-family; membrane protein; phosphotyrosine protein phosphatase; psAM2; ptpA; ssgA; thiamine biosynthesis; thiC; transcriptional regulator; traSA.
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                                                                                                                                                                                                                                                                            Streptomyces coelicolor A3(2).
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 1544).
Redenbach,M., Kleser,H.M., Denapaite,D., Elchner,A., Cullum,J., Rinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URE, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrellgeanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.

Cosmid Q11 Cosmid Q11 lies between H24 and D78 on the AseI-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-JUL-1999) Streptomyces coelicolor sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
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                                              linear
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                                   Streptomyces coelicolor cosmid Q11. AL096823
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/clone="cosmid Q11"
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GRELLLLDGLNSPSGDGDVHIGPTEPEGLGDVHIRLQVGADRALFRAGTAPLVAFLDRT
DKLVPLGQEHTLGDFDGNLEDALGRILAEEQNAG"
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                                                                                                                                                                       Shinichi, K. and Ensign, J.
Shinichi, K. and Ensign, J.
Shinichi, K. and Ensign, J.
Cloning and characterization of a gene involved in sporulation and
cell division of Streptomyces griseus
Unpublished (1995)
5 (bases 1 to 1513)
Shinichi, K.
Direct Submission
Submitted (106-APR-1195) Kawamoto Shinichi, National Food Research
Institute, Biomolecular Transfunction Laboratory; Kannondai 2-1-2,
Tsukuba, Ibaraki 305, Japan (Tel:0298-38-8124, Fax:0298-38-7996)
Location/Ouallfiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 ATGAGCTTCCTCGTCTCCGAGGAGCTCTCGTTCCGTATTCCGGTGGAGCTCCGATACGAG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggcgcggaccgcgcctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgaggacagcctg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawamoto,S., Watanabe,H., Hesketh,A., Ensign,J.C. and Ochi,K. Expression analysis of the sagA gene product, associated with sporulation and cell division in Streptomyces griseus Microbiology (Reading, England) 143 (Pt 4), 1077-1086 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 TGGGCGTTCGGCCGCGAGCTGCTGCTGGACGGGCTCAACAGCCCGAGCGGCGACGGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gtccacatcgccccgacccgagcccgaggcctgtcggacgtctccatccggctccaggtg
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Pred. No. 4.5e-26;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Streptomyces griseus"
/strain="B2662"
/db_xref="taxon:1911"
385_.389
392...802
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/protein_id="BAA21558.1"
/db_xref="G1:2281004"
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Best Local Similarity 83.3
Matches 339; Conservative
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                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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REFERENCE
                                                                                                     JOURNAL
                                                                                                                                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcriptional regulator, len: 301 aa; previously transcriptional regulator, len: 301 aa; previously sequenced as TR:Q53869 (EMBL:U37580) S.coelicolor lysR-like protein (301 aa). Highly similar to SW.ARAB_STRAT (EMBL:U3783), araB, Streptomyces antibioticus transcriptional regulatory protein (301 aa), fasta soores; opt: 1581 z-score: 1813.2 E(::0, 80.3% identity in 300 aa overlap. Similar to many other transcriptional regulators. Contains probable helix-turn-helix motif at aa 17.38 (Score 1659, 44.84 SD). Contains Pfam match to PF00126 HTH_1, Bacterial regulatory helix-turn-helix protein, lysR family and PS00044
                                                                                         795 aa; unknown function, previously sequenced as TR:053870 (EMBL:U37580), S.coelicolor hypothetical protein ORF5 downstream of phosphotyrosine protein phosphatase (159 aa). Weak similarity to the N-terminus of TR:069888 (EMBL:AL023797) Streptomyces coelicolor hypothetical protein (172 aa), fasta scores; opt: 158 z-score: 206.4 E(): 0.00036, 46.2% identity in 65 aa overlap. Continues as SCH24.40c in cosmid H24 (EMBL:AL049826)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1518. .2696)
/gene="SCO11.03c"
/note="SCO11.03c, cysA, probable cystathionine/methionine
gamma-synthase/lase, len: 392 as; previously sequenced as SW:CYSA_STRCO (EMBL:037580), cysA, S.coelicolor putative cystathionine gamma-lyase (392 aa). Similar to many e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTVRPVVKRTARAVLLDGDHLILIKRTKPGVDPYWVTPGGGVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDLALLRTFVTVHRAGSFTRAAALLGLSQPAVTSQIRTLERQLG
RPLFLRQARGVTPTTIGDELAHKAAPHLDALVEIAETGLEDDSTLRTLHLAGPPEFTA
ERALPALGELTGEDGQAFALRASFGNAEETLEGLAAGHHDLAIGTTRPRGALHTATPL
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SPATVVAPDLRAVLACAVAGACLAVLPRYLCAEALERGDVVALHDPPVPPLRTYFLVV
RTGTLAMPHTARAHEWLLRAAADWN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative lysR-family transcriptional regulator"
/protein_id="CAB46957.1"
/db_xref="G1:5457269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00044 Bacterial regulatory proteins, lysR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .98
//note="overlap with Streptomyces coelicolor cosmid H24 (GMBL-AL049826) from 41528 to 41625"
//gene="SCQ11.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1. .4279)
/note="sequence corresponding to EMBL:U37580 from 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDTTVVDALHREVYEELGAKISDVVPCFVDTVEHIGEDGGATGVKVQHFFVC"
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/gene="SCQ11.02c"
/note="Match to PF00126 HTH_1, Bacterial regulatory
helix-turn-helix protein, lysR family Score 145.96"
/gene="SCQ11.02c"
                                                                  partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(360. .1265)
/gene="SCQ11.02c"
/note="SCQ11.02c, abaB, probable lysR-family
complement(<1. .289)
/gene="SCQ11.01c"
/note="SCQ11.01c, hypothetical protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="CAB46956.1"
/db_xref="GI:5457268"
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/gene="SCQ11.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                    /label=SCQ11.01c
                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=abaB
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methionine gamma lyase (398 aa), fasta scores; opt: 608 z-score: 653.6 E(): 4.5e-29, 36.98 identity in 404 aa overlap. Highly similar to TR:053668 (EMBL:391393) streptomyces antibioticus hypothetical protein found upstream of the abaB gene (232 aa) (87.1% identity in 232 aa overlap). Contains Pfam match to PF01053 ac overlap. Cys_Met_metabolism plan match to AF01053 and PS00868 Cys_Met_metabolism plan-dependent enzyme attachment site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSDSATTDSAGTGGERSASAPGDGTRAVRAGLPEPVKHEPTLPG
PVFAAHFHLPGDPTGPYTYGRDENPTWTRLESAIGELEAPGEAGVETLVFASGMAAIS
SVLFSQLRAGDTAVLPDDGYQALPLVRAQLEAYGIEVRTAPTGRDAQLDVLDGAKLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IETPSNPGLDVCDVRRLVEAÄHAGGALVÄVDNTLATPLGQRPLELGÄDFSVASGTKÖL
TGHGDVLLGYVAGRDAGAMANTRNRKLYGALPGPMEMULAHRSIATLÖLRVDRQDST
ALKVAEALRTRPETGLRY FGLPDDPSHKVASQQMLRYGCVVSFTLFSRARADRFLDA
IRLVBGATSFGGVRSTAERRGRWGGDAVPEGFFRLSVGAEDPDDLVADLLRALDETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTYRVCFVCTGNICRSPWAEAVFRARVEDAGLGHLVEADSAGTG GWHEGEGADPRTEAVLADHGYGLDHAARQFQQSWFSRLDLVVALDAGHLRALRRLAPT ERDAAKVRLLRSYDPAVAGGDLDVPDPYYGGRDGFEECLEMVEAASTGLLAAVREQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine-phosphatase (164 aa). Contains Pfam me
to PF01451 LMWPc, Low molecular weight phosphotyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5475 ATGAGCTTTCTCGTGTCCGAGGAGCTCTCTTTCCGCATCCCGGTGGAGCTGCGCTACGAG 5534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2693. .3187)
/gene="SCQ11.04c"
/note="SCQ11.04c, ptpA, low molecular weight
protein-tyrosine-phosphatase, len: 164 aa; previously
sequenced as SW:PTPA_STRCO (EMBL.U37580), ptpA,
S.coelicolor low molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 accogggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgacc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atgagetteetegteteegaggageteteetteaagateeeagtegaaetgegataegag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SCQ11.03c"
/note="Match to PF01053 Cys_Met_Meta_PP, Cys/Met
metabolism PLP-dependent enzyme Score 268.52"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative cystathionine/methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00868 Cys/Met metabolism enzymes
pyridoxal-phosphate attachment site"
complement(2693. .3187)
/gene="SCO11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="low molecular weight
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/protein_id="CAB46959.1"
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/db_xref="GI:5457270"
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/gene="SCQ11.03c"
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/transl_table=11
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/transl_table=11
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01-NOV-2000

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RELLIDGGPREGGDGDVHIAPADPETFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
RYVPLGGGRSLADDFALLDBALDFALLAFEQNAG"
135 c 145 g 71 t
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/note="sinilar to Streptomyces griseus SsgA; possible cell
division protein"
/codon_start=1
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Streptomyces goldeniensis
Streptomyces goldeniensis
Bacteria: firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 408)
van Wazel, G.P., Rousseau, C. and Kraal, B.
Cloning and sequencing of the Streptomyces goldeniensis ssgA gene uppublished
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                181 GTCCACATGGGGCGGGGGACGGGGAGGTTCGGGGAGGTCCTGATCGGCGCGCTGCAGGTG
181 giccacategeecegacegaecegagggeetgieggaegietecateeggetecaggig
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/db_xref="ATCC:21386"
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Patent: WO 0000613-A 7 06-JAN-2000;
UNIV LEIDEN (NL); KRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA
(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
VAN (NL)
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RELLIDGGPRPCGGDVHIAPADPEFGEVLIRLQVGSDQAMFRVGTAPLVAFLDRTD
KIVPLGQERSLADFDALLDEALDRILAEEQNAG"
135 c 145 g 77 t
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Streptomyces goldeniensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 407)
Kraal, B., Luiten, R.G. and Van Wezel, G.P.
Reducing branching and enhancing fragmentation in culturing
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 181 giccacategeceegacegaecegagggeetgieggaegieteeateeggeieeggg
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/note="strain ATCC of Streptomyces goldeniensis"
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    .407
    /organism="Streptomyces goldeniensis"
    /db_xref="taxon:121022"

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Pred. No. 3.3e-20;
0; Mismatches 99
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Sequence 7 from Patent WO0000613.
AX007222
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ilarity 75.7%;
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/translation="MSFLVSEELAFRIPVELRYETVDPYAVRLTFHLPGDAPVTWVFG
RELIVEGVEDAAGDGFDVRVCPVGQTATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
QGLSLGSERAHADFDSHLDDALNRSLAEEQSAG"
219 c 192 g 80 t
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van Wezel,G.P., Rousseau,C. and Kraal,B.
Cloning and sequencing of the Streptomyces albus ssgA gene Unpublished
2 (bases 1 to 566)
van Wezel,G.P., Rousseau,C. and Kraal,B.
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241 ggcgcgggccctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc
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Streptomyces albus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Submitted (18-007-1999) Biochemistry, University
9502, Leiden 2300 RA, Netherlands
Location/Qualifiers
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/db_xref="taxon:1888"
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/transl_table=11
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/db_xref="GI:11066161"
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1 (bases 1 to 407)

Kraal, B., Luiten, R.G. and Van Wezel, G.P.

Reducing branching and enhancing fragmentation in culturing
filamentous microorganisms

Patent: WO 0000613-A 5 06-JAN-2000,

UNIV LEIDEN (NL); RRAAL BAREND (NL); LUITEN RUDOLF GIJSBERTUS MARIA

(NL); NL ORGANISATIE VOOR WETENSCHAP (NL); WEZEL GILLES PHILIPPUS
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RELLVEGVLDAAGDGDVRVCPVGQPATREVHTTLQVGSEQALFRVGKAPLLAFLDRTD
QGLSIGSERAHADFDSHLDDALNRSLAFEGSAG"
150 c 150 c 61 t
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Pred. No. 1.9e-17;
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                                                                                                                                                                                                                                                                                                                           DNA
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/protein_id="CAC07386.1"
/db_xref="G1:9995087"
                                                                                                                                                                                                                                                                                                                        AX007220 407 bp
Sequence 5 from Patent WO0000613.
AX007220
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/codon_start=1
/transl_table=11
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1. .>405
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/gene="ssgA"
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72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 29-JAN-2000
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The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elongation factor; endodeoxyribonuclease; GTP pyrophosphokinase; membrane protein; membrane transferase; protein-export membrane protein; regulator; secreted protein; sugar transferase; threonine-tRNA synthetase; transport system inner membrane protein. Streptomyces coelicolor A3(2).
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Actinomycetales; Streptomycineae; Streptomyces.
I (bases 1 to 38640)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
Kinashi,H. and Hopwood,D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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phosphoribosiltransferase; DNA helicase; DNA polymerase III;
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Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
tgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgac
                                                                                                           gtccacatcgccccgaccgacccgagggcctgtcggacgtctccatccggctccaggtg
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Colney, Norwich, Norfolk NR4 7UH, UK
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Streptomyces coelicolor cosmid L2.
AL137778
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Seeger, K.J. and Harris, D.
Unpublished
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SOURCE

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jun/cg1-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg. grg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be the entire insert of the sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein SCL2.01"
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/protein_id="CAB70913.1"
/protein_id="CAB70913.1"
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AVDHLREGVDAHHAYGDLEALRARLDOLVALVETRREERKAGRAKGSPERALA
AVDHLREGVDAHHAYGDLEALRARLSUVTWKGLPRLDRKSDDELMHFSHARSAFSKRRKQH
FAAGLAGAREBARRIKERLVSEALGNSTDWGFTAAARYRDLMSEWKAAGRAGVBHEDD
LWNRFRGAQDVFFAARSSVRARERDAGGSENIKLKEELVTEREKLVPYTDLKGARAAFR
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where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /porce="SCL2.01"
/note="SCL2.01, hypothetical protein, len: >328 aa;
/note="SCL2.01, hypothetical protein, len: >328 aa;
similar to TR:033236 (EMB::298209) Mycobacterium
tuberculoais hypothetical 49.8 kD protein MTCY174.11,
450 aa; fasta scores: opt: 843 z-score: 874.7 E0; 0,
45.9% identity in 296 aa overlap. Contains possible
coiled-coils region"
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1010. .1150
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/note="previous1y sequenced region SW:SCAPTRELA FMBLS 787267 S.coellcolor apt & relA genes" complement(1229. .3772)
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/gene="SCL2.02"
1010. 1150
/gene="SCL2.02"
/note="SCL2.02"
/codon_start=1
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/clone="cosmid L2"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="apt"
/note="SCL2.04c, apt, adenine phosphoribosiltransferase,
/note="SCL2.04c, apt, adenine phosphoribosiltransferase,
Inc. 182 as identical to previously sequenced
SW.APT_STRCO (FWEL:XB7267) Streptomyces coelicolor adenine
phosphoribosyltransferase (EC 2.4.2.7) Apt, 182 as and
highly smilar to SW.APT_ECOLI (FWBL:M14040) Escherichia
coll adenine phosphoribosyltransferase (EC 2.4.2.7) Apt,
183 as, fasta scores: opt: 600 z-score: 682 B E():
1.2e-30; 54.8% identity in 168 as overlap. Contains Pfam
match to entry PF00156 Pribosyltran, phosphoribosyl
aa; fasta scores: opt: 1613 z-score: 1594.3 E(): 0; 58.7% identity in 774 aa overlap. Contains Pfam match to entry PF01842 ACT, ACT domain and match to Prosite entry PS00017 ATP/GTP binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLEARGFILGAPVALRAGLGFIPVRKAGKLPCATLSQAYDLEYGSAEIEVHAEDLTAG
DRVLVVDDVLATGGTAEASLELIRRAGAEVAGLAVLMELGFLGGFRRRLEPALAGAPLE
                                                                                                                                                                                                                                                                                          PVLEPLLRIVRGNDPKIETSTLRQIERAYQVAERWHRGQKRKSGDPYITHPLAYTTIL
AELGMDPATLMAGLLHDTVEDTEYGLEDLRRDFGDVVTLLVDGVTKLDKVKFGERAQA
ETVRKMVVAMAKDPRVLVIKLADRLHNMRTMRYLKREKQEKKARETLEIYAPLAHRLG
                                                                                                                                                                                                                                                                                                                                                                   MNTIKWELEDLAFAILYPKMYDEIVRLYAERAPKRDEYLAVYTDEVOQDLRAARIKAT
YARRKHYYSYVKMIVRRDPAEIYDLYGIRYLYDTVRDCYAALGYYHARWNPYDRR
FKDYIAMPKDNWYQLHTYUIGPGREVDELOIRTFDMHRAEYGIAAHWKYKOEAVAG
ASKVRTDAPKSSGKSKDDHLNDMAWLRQLLDMQKETEDPGEFLESLRPDLSRNEYFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPKGDVIALPAGATPVDFAYAVHTEVGHRTIGARVNGRLVPLESTLDNGDLVEVFTSK
AAGAGPSRDWLGFVKSPRARNKIRAWFSKERRDEAIEQGKDAIVRAMRKQNLPIQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGDSLVTLAHEMRYSDISALYAAIGEGHVSAPNIVQXLVQALGGEEAATEEIDESVPP
SRGRGRKRRANADPGVVVKGVEDVWVKLARCCTPVPGDPIIGFVTRGSGVSVHRSDCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVDSLSREPERILEVEWAPTQSSVFLVAIQVEALDRSRLLSDVTRVLSDQHVNILSAA
VQTSRDRVATSRFTFEMGDPKHLGHVLKAVRGVEGVYDVYRVTSARRPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SW:SCSECAPT EMBL:X85969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MADYPEPGVVFKDITPLLADPGAFAALTDALAEAAGRTGATKVV
                                                                                                                                                                                                                                      /translation="MPDEAQPLTAAKPESASAAAKPAPSAPQAKNDTHGPIQHAPAA
PVDKPAEQQPRPKPLPAERPQNAPVVRAPAGQPARSGSSNRVRARLAKLGVQRANPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to entry PF01842 ACT, ACT domain, score 63.10, E-value 6e-15" complement(2378. .2401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00156 Pribosyltran,
domain, score 150.30, E-value
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Purine/pyrimidine phosphoribosyl transferases signature"
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EMBL:X87267 S.coelicolor apt & relA genes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="adenine phosphoribosiltransferase"
/protein_id="CAB70916.1"
/db_xref="G1:6822210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement(3273. .7460)
/note="previously sequenced region SW S.coolicolor sect, secf a apt genes" complement(3778. .3781)
                                                                                                                                  /transl_table=11
/product="GTP pyrophosphokinase"
/protein_id="CAB70915.1"
/db_xref="G1:682209"
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/note="Pfam match to entry
Phosphoribosyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1256. .1474)
/gene="relA"
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/transl_table=11
                                                                                                               /codon_start=1
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Submitted (16-JUL-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCT 16-JUL-1999
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1 (bases 1 to 35284)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                                                          /gene="sec;"
/note="SC12.05c, secf, protein-export membrane protein,
len: 373 aa; identical to previously sequenced
SW.SECF_STRC0 (EMBL.X85969) Erreptomyces coelicolor
protein-export membrane protein Secf, 373 aa and similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4-hydroxyphenylpyruvate dioxygenase; ABC transporter; amino acid permease; asnC-family; cysteine synthase; nicctinamidase; osmotolerance; oxfdoreductase; permease; phosphoenolpyruvate-dependent; protease; regulator; ribonuclease PH; rph; sugar phosphotransferase system; transcriptional stregulator; transposase; tRNA Leu; zinc metallopeptidase. Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                  35030 TGGCCTCGTTGTGTCGCGAGCGAGTCCTCCCTGCCTGCCCGCGAGGCTGCGGGTACGACA 35089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35090 CGGCCGACCCCTACGCGTGCACGCACCACCACCAGAGACCGAGACCGTCAAGT 35149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35150 GGGTCTTCGCCCGCGACCTGCTCGCCGAAGGTCTCCACCGTCCCACCGGCGACG 35209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35330 CAGACGCCCCCCCCCCCCCCCCCCCCCAACCTCCCATCCGATCAGGAGCTCT 35389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35210 TCCGTGTCTGGCCGTCCCGCAGTCACGGCCAGGGCGTGTGTGCATCGCTCTCAGCTCCC 35269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eggacaagteggtgeegeteggteaggaacagactetgggtgaettegaggaeageetgg 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgacct 121
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tecacategeceegacegaececgagggeetgteggaegtetecateeggetecaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 gegeggacegecetetteegtgeaggegeeeegetggtegeetteetegacegea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacg
                                                                                                                                                                                                                                                  Length 38640;
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                                                                                                                                                                                                                                                                                                                0; Mismatches 172;
                                                                                                                                                                                                                                                  28.2%; Score 114.8; DB 1 55.9%; Pred. No. 2.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 aggccgcgctcggcaagatcctcgccgagg 391
/gene="secf"
complement(4501. .5622)
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Seeger, K. and Harris, D.
Unpublished
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Matches 218; Conserv
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VERSION
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overlap)"

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The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Wholels Acids Research, 22(22):4768-4778(1994) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/

Jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. Way be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlapp between neighbouring submissions.

Cosmid E19A lies between and overlaps cosmids E6 and E56 on the Asel-E genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SCE19A.01"
/gene="SCE19A.01"
/dote="SCE19A.01"
/dote="SCE19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 aa; unknown function, similar to many e.g.
SW:Y03Q_MYCTU (EMBL:Z73902) Mycobacterium tuberculosis
Mypothetical protein (204 aa), fasts acores; opt: 633
z-score: 743.6 E(1): 0, 52.0% identity in 200 aa overlap.
Similar to SW:YGGV_ECOLI (EMBL:U28377), yggv, Escherichia coli hypothetical protein (197 aa) (49.5% identity in 198
                                                                                                                                                                                                                                                                                                                                                                          (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                          sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(243. .845)
/gene="SCE19A.02c"
/note="SCE19A.02c, conserved hypothetical protein, len:
Innes Centre, Norwich Research Park,
                                                                                                                                                              Streptomyces coelicolor sequencing at The Sanger Centre is fu
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="tRNA Leu anticodon TAG, Cove score 69.78"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="IVVDEQGKVERALYNVRATGHVAKIIKDLGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .35284 /organism="Streptomyces coelicolor A3(2)" /strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
/protein_id="CAB50982.1"
/db_xref="GI:5531350"
David A. Hopwood, [3] John Innes Cen
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:100226"
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complement(243. .845)
/gene="SCE19A.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCE19A.01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strand).
                                                                                                           Notes
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gene

FEATURES

CDS

gene

CDS

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/product="hypothetical protein"
/protein_id="cab50983.1"
/db_xref="G1:5531351"
/translation="WTRLILATRNAGKITELRAILADAGLPHDLVGADAYPHIPDVKE
                                                                                                                                                                                                                                                                                                                                                 TGVTFAENALLKAHALAEATGLPAVADDSGLCVDVLNGAPGIFSARWAGRHGDDQANL
DLLLAQIADIADEHRGAHFACAAALALPDGTERVVEGOLKGTLRHAPAGTGGFGYDPI
LQPEGETRTCAELTAEEKNAISHRGKAFRALVPVVRELLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=SCE19A.03c
/product="putalive secreted protein"
/product="putalive secreted protein"
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/db_xxef="G01:531352"
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ADAIADSVTELQAYERADDPTQWEESLNSIDKNLDRIGDQTDNTDVNKAVDDLGKAV
COMPIEMENT[1201..1233]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement(1454. .2191)
/gene="SCE19A.04c"
/note="SCE19A.04c"
/note="S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SCE19A.03c, possible secreted protein, len: 134 aa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative ribonuclease PH"
/protein_id="CABSO981."
/db_xref="g131353"
/translation="MSRIDGRTPQQLRPVIIERGWSKHAEGSVLVSFGDTKVLCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCE19A.05c, hypothetical protein, len: 77 aa;
whornown function, similar to parts of many sugar permeases
e.g. TR:P96159 (EMBL:U65013), malX, Vibrio furnissii PTS
(phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEGVPRWRKGSGEGWVTAEYAMLPRATNTRGDRESVKGRIGGRTHEISRLIGRSLRAV
IDYKALGENTVVLDCDVLQADGGTRTAAITGAYVALADAVAWAQGRKLIKANRKPLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVSAVSVGIVDGTPLLDLRYEEDVRADTDMNVVCTGDGRFVEVOGGTAEAEPFARDELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown function, probable CDS suggested by GC frameplot, positional base preference and amino acid composition. Contains probable N-terminal signal sequence and appropriately positioned PS00013 Prokaryotic membrane lipoprotein lipid attachment site, so may be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /jote="Pfam match to entry PF01138 RNase_PH, 3'
exoribonuclease family, score 266.70, E-value 3.1e-76"
complement(1805 .1843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS01277 Ribonuclease PH signature"
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complement(1511. .2185)
/gene="SCE19A.04c"
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/note="sce19A.05c"
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/gene="SCE19A.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(892. .1296)
/gene="SCE19A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(892. .1296)
/gene="SCE19A.03c"
/codon_start=1
/transl_table=11
/label=SCE19A.02c
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tamase precursor
Biochem. 166, 345-350 (1987)
                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.4%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctgctcgacgggatcaa 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CTGGTCGAGGGAGTCAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 81.0
Matches 111; Conservative
       beta-lactamase
                       Eur. J. B
87275916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
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                                                                                                                                                                                  /translation="MASKAEKVAGLGGIDNIDEIEGCITRLRTEVNDPALVNEAALK AAGAHGVVKMGTAIOVVIGTDADPIAAEIEDDM"
AAGAHGVVKMGTAIOVVIGTDADPIAAEIEDDM"
comptement(2385. 2489)
/gene="Effigue 25219A.052"
/note="Pfam match to entry PF00367 PTS_EIIB,
phosphotransferase system, EIIB, score 43.00, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 26-APR-1993
       scores; opt:
ty in 77 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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behottay, P., Dusart, J., De Meester, F., Joris, B., Van Beeumen, J.,
Erpicum, T., Frere, J.-M. and Ghuysen, J.-M. -M.
Nucleotide sequence of the gene encoding the Streptomyces albus G
                                                                                                                                                                                                                                                                                                                                                                                                                                     (phosphoenolpyruvate-dependent sugar phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system) permease for glucose (523 aa), fasta scores; op 217 z-score: 287.9 E(): 1.1e-08, 48.1% identity in 77 a overlap. Contains Pfam match to entry PF00367 PTS_EIIB, phosphotransferase system, EIIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20142 TCAGGCTCGTCCTGTCGCCCGAGAGCGGCATTCCGGTGCCGGCCCGGCTCGGCTTCGCTACCACA 20201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20442 CCTGCGGGGGGTCGCCGGGGGGCGCGCGCGCGCTCGGGATCGACGGCTGG 20501
                                                                                                                                                                                                                                                                                                                                                            2660. 3955
/gene="SCE19A.06"
/note="SCE19A.06, possible PTS transmembrane component,
len: 431 aa; similar to many PTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20322 TGCGGGTGTGGCCGTCGAAGACGGAGGCCGCAGCGTCGTACTCGTCGTCGGCGGAGCAGCC 20381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tecacategeceegacegacecegagggeetgteggacgtetecateeggetecaggtgg 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgctgtgacct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tgagcttcctcgtctccgaggagctctccttcaagatcccagtcgaactgcgatacgaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10202 CGGACGATCCCTACGCGTGCACTCCACATCGACTCGGCCACCGGTGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gegeggacegecetetteegtgeaggegeeeegeegetggtegeetteetegaeegea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgaggacagcctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 35284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-lactamase.
Streptomyces albus (strain G) DNA, clone pDML6.
Streptomyces albus
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STMLACBG 1410 bp DNA S.albus beta-lactamase gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 108.2; DB 1;
Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 168;
                                                                                                                                 /product="hypothetical protein"
/protein_id="CAB50986.1"
/db_xref="GI:5531354"
                                                                                                                                                                                                                                                                                                          zoo0. .3955
/gene="SCE19A.06"
2660. .3ar=
                                                                                              /transl_table=11
/label=SCE19A.05c
                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20502 CCGAGCTGCTCGCCAGG 20518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.6%;
illarity 55.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 aggccgcgctcggcaag 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M28303.1 GI:153338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                           gene
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STMLACBG
LOCUS
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SOURCE
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/traislation="MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSG
SVSDAERRAGLERASGARLGVYAVDTGSGRTVAYRADELEPMCSVRTLSSAAVLRD
LIDNGEFLSRRILYTQDDVGQAGGAGPETGKPQNLANAQLTVEELCEVSITASDNCAA
NLMLRELGGPAAVTREVRSLGDRVTRLDRWEPELNGAEPGRYTDTTSGRAITYGRL
VLGDALNPRDRRLLTSWLLANTTSGDRFRAGLPDDWTLGDKYTGAGRYGTNNDAGVTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCBA11
Streptcomyces coelicolor cosmid BA11.
AL391041.
AL391041.
AL391041.1 GI:9716211
Amino acid transport integral membran protein; branched amino acid binding secreted protein; branched amino acid transport system thegral membrane protein; polysaccharide blosynthesis protein; requiator; system permease; integral membrane protein; ion transport integral membrane protein; polysaccharide blosynthesis protein; requiator; requiatory protein; secreted amidase; secreted peptidase; secreted peptidase; secreted petidional regulator; transcriptional regulator; transcriptional regulator; transcriptional regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical may for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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0
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomycetaceae;
1 (bases 1 to 32704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGRAPIVLTVLTAKTEQDAARDDGLVADAARVLAETLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 95.4; DB 1;
Pred. No. 0.0095;
0; Mismatches 26;
                                                   /organism="Streptomyces albus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ų
                                                                                                                                                                                                                                                                         /transl_table=11
/product="beta-lactamase"
/protein_id="AAA26775.1"
/db_xref="GI:153339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1204. .1216
/gene="beta-lactamase"
/note="inverted repeat"
1230. .1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="inverted repeat"
540 c 496 g 1
                                                                                                                                                 /gene="beta-lactamase"
243. .1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="beta-lactamase"
                                                                                                                                                                                                                   /gene="beta-lactamase"
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Streptomyces coelicolor A3(2).
                                                                                                 /db_xref="taxon:1888"
243. .1242
Location/Qualifiers
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
correct initiation codon. Where possible we choose an initiation
codon (atg, gtg, ttg or (att)) which is preceded by an upstream
ribosome binding site sequence (optimally 5-13bp before the
initiation codon). If this cannot be identified we choose the most
upstream initiation codon. It may be the entire insert of the
sequenced clone. It may be shorter because we only sequence
overlapping sections once, or longer, because we arrange for a
small overlap between neighbouring submissions.
                                                                                                                                                                  3 (bases 1 to 32704)
Cerdeno,A.M., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
Direct Submission
Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note "nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial regulatory proteins, luxR family and match to rosite entry PSOG621 Bacterial regulatory proteins, luxR family signature. Also contains a possible helix-turn-helix motif at residues 699. 720 (+3.25 SD)"
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//gene="SCBAll.01, possible transcriptional regulator
//note="SCBAll.01, possible transcriptional regulator
//fragment), len: >750 as; similar to TR:095124
(EMBL.ALl09747) Streptomyces coelicolor probable
transcriptional regulator ScJ31.13, 919 as; fasta scores:
opt: 818 z-score: 913.7 E(): 0; 32.6% identity in 775 as
overlap. Contains Pfam match to entry PF00195 gere,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor),
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative transcriptional regulator (fragment)" /protein_id="CAC01573.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                     Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/d_xref="taxon:100226"
/clone="cosmid 8A11"
Mol. Microbiol. 21 (1), 77-96 (1996)
97000351
                                                                                                                                                                                                                                                                                                                                                                                                          Colney, Norwich, Norfolk NR4 7UH, UK
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                                                                                                       Saunders, D.C. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .2254
/gene="SC8A11.01"
<1. .2254
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/gene="SC8A11.01"
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/transl_table=11
                                                                        (bases 1 to 32704)
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                                                                                                                                      Unpublished
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   JOURNAL
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                                                                                                    AUTHORS
JOURNAL
                                                                                                                                                                     REFERENCE
AUTHORS
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                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
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complement(3297.7088)

complement(3297.7088)

/gane="SC8A11.04c, probable secreted peptidase, len: 1253

/gane="SC8A11.04c, probable secreted peptidase, len: 1253

aa: similar to TR:09KL54 (EMBL:AL121566) Streptomyces

coelicolor probable secreted peptidase SCF51A.10 1245 aa;

fasta scores: opt: 1827 z-score: 1848.18 (EMBL:08367)

identity in 1300 aa overlap, to TR:P95684 (EMBL:08367)

streptomyces albogriseolus subtilisin-like protease, 1102

aa; fasta scores: opt: 1365 z-score: 1380.6 E(): 0; 33.4%

identity in 1268 aa overlap and to Streptomyces coelicolor probable secreted peptidase SC8A11.16c, 1239 aa; fasta scores: opt: 1835 z-score: 1467.4 E(): 0; 46.9% identity in 1279 aa overlap. Contains Pfam matches to entries PROMO82 peptidase_288, Subtilase family and PF02225 PA, PA domain and matches to Prosite entries PSO0136 Serine PSO0137 Serine proteases, subtilase family, histidine active site and PSO0138 Serine proteases, subtilase
                               VRARILQRAAGNPLALVELPRAAQGISPPLDDLPLTQRLETAFASRTDSLTRECRTFL
LVLAABPTAPLNQLLDVASRLAGSEVTVYALQBAVDAGLVVLTGRTPEFRHPLMRSAI
                                                                                                                                                                                       ARIMLVSDKAAFEPDEPQRRIQDMIDAAAGAFDVGSTSVÄENLLWRAAARCFFQDGDA
RVRAQAAAELDRWKPDPDAPHVLTVRAYTEPYRRGTDLIARLEKLRPDREDGRLLHYL
                                                                                                                                                                                                                                                                  GSGSMAIGDVGRATRYLAQAASVWRSQGRLGLLARSLAGSWPRLYLGGLAQAREESAE
GIALAERTGRAIVWLGLRATSALTAYLEGRERAARSYNELARHSLEYBYDYDGYDAG
GIVGGLLALFDSRAVBACARAFDKTDPHYHSTSRWLLYPDLYDAAAAARAKEGARE
LLVELPELADRIPSEWMIVARTYSTAVLAPDDTAEDCYDSALSALPDTWPLARARHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCBAll.03"
/gene="SCBAll.03"
/note="SCBAll.03. possible regulator, len: 156 aa; similar
to TR:095277 (EMBL:AL096852) Streptomyces coellcolor
putative regulator SCE19A.24, 142 aa; fasta scores: opt:
272 z-score: 353.0 E(): 3.4e-12; 36.9% identity in 130 aa
                                                                                                                                                       LAAAVPALRQAGELVHDPRRQTGLLVRAAELASEINDRVQAQILLNRADLAEPGPTER
                                                                                                                                                                                                                                                                                                                                                                                                                              OHGRRLRRORRNVDARKPLRLARDEFDRVGAQPWADMAREOLRAAGESDGRRRPSKGE
SLTVQERQIAELASQGLSNREIGQRLFISHRTVGAHLYRIYPRLGITSRGRLSAALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSGDHHGVQAQHSAAQALLPLSLCLSQMTGALEWEDVPAEFRYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDHPLLVTIRFAPEGAPPVTWHVGRDLLHEGLRTTSGLGDVQVWADTPTDRETAWLQV
NAHGDIAIFSLPVPELEEWIDRTYLHVPAGTESSRLGTDAFLSKLFDEPEASSR"
complement(3297. .7058)
                                                                                                               YTRATVADRLSTHRALAETLEGSPGRRLVHLAAATLGPDDELAGQLERFADDAQKRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MASAAATAGTAGALPVMSGQAHADTRGLPSLWDVDRSVVNPENA
YTVTVDQVRAEVAQLMGATEEEFTRPRSAGRLRARPAPRRACRGW"
/translation="IGAARTSSPGTYTLGTHAELVLEPLSPSAAAELLDADAPGLADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2093. .2176
/gene="SC8A11.01"
/note="PS00622 Bacterial regulatory proteins, luxR family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2042. ..2239
/gene="SC8A11.01"
/note="Pfam match to entry PF00196 GerE, Bacterial
regulatory proteins, luxR family, score 49.10, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"hypothetical protein SC8A11.02c"
/protein_id-"CAC01574.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SC8À11.02c"
complement(2184. .2453)
prone="SC8A11.02c"
/note="SC8A11.02c, unknown, len: 89 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"putative regulator"
/protein_id-"CAC01575.1"
/db_xref-"GI:9716214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:9716213"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2787. .3257
/gene="SC8A11.03"
2787. .3257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (2184.
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                        LSDTTAQIGAPDVWSGGNTGEGVGVALLDTGVDAGHDDFAGRIAATASFVPDDDVTDR
WGHGTHAGSTYAGTGAASGGVEKGYAPGASLJIGKVLDNGSGGODGWVAGAGEBWAVED
OHAKIVSMSLGDSPTDGLSEAVNWLSAETGALFVVAAGNSGFDEAYTVGTPAADA
ALTVGSMVGPGKGVDGLDFSSRGPRVGDNAWYPDLTAGTGSFSTAFBEGGRADA
OSLSGTSMATPHYAGAAALLAAEHDDWTGORLKEALVGTTAGTGRESPFDAGSGRVDY
AAAVRSTLLASGDAFAOAHPYTPGGTVRDVTYTNSGPAPVALDILLISPAELDEGLF
TLSEAQVTVPBAGTAASVGYTTHLDAAEDNGSYAATRLVASGAGGAVLARTPVGVNKEGR
RATLALTAKDHHDKFLSGTVITHLDAAEDNGSYAATRLVASGAGGAVLARTPVGVNKEGR
NTGLEPFMDSYAARVRYDSLWYPPPPEVRYGSYTFATRWQIQPPLITESRGYRG
WTGLEPFMDSYAARVRYDSLWYPPPPEVRYGSYTFATRWQIQPPLITESRGSGTFDD
VTVQSRSPOLPEGTRAYRAWAGDGSATEFRGAEVRDRAVAVVRRSDTVAPTDGAAAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAGARQLLILNDGYGKFDPWADLPEAAPLPVASLGTDDSARLLARFRGAGTTTLRVVS
HPVPRYAYDLVRHHDGAVPRDPSYRPAPGELARVDDTFRDTSGGRAVEYRQDISLLGQ
PLGIVPTQVRAQGELTSWYTADDDVRWVSFASRPDLGQRGVARSYEPRSTTRETWFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQHPRLLSDNGTSGQGPFRAGDNISTSVMTAWGDSGGHAGVVWADGDTSRISLYQGGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGEDVNERIVMVGGLSPGPKPYRLVLEGSRNLPDRPYSTRTRTVWDFTSATTDPTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPLPLVQLDYAVAVDLSGRAHRRTELTVTASHLEGAAGAGAIRTATVEVSYDDGATWH
                                                                                                                                                                                                            /translation="MPIPWSRGRGLTVGIAALLVLTATAPAASALPGTVPPAPPAPA
                                                                                                                                                                                                                                           GPTRVLTLITGDRVTVTGEDGAETVLSVTDPHGRSGGAHVMTVGSDTYVYPDAAVPYL
                                                                                                                                                                                                                                                                                                      I RGAA I SAEHSRAADFWT SLTGTGDAAAGGSAARSAT SGGRLAGG I AKVWLDGKVRAT
                                                                                                                                                                                                                                                                       GSGALDERLFNVTELLEDGYDDARADELPLIVTYTDTAARSLGARTPEGARRTRALSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4374. 4613)
/gene="SCBA11.04c"
/note="Pfam match to entry PF02225 PA, PA domain, score
19.00, E-value 0.058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2896 TTCCGGCGGAGTTCCGTTACGATCCCGACCACCCCTCCTCGTCACGATCCGCTTCGCCC 2955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3076 ccecereccriccaegricaacecacacegreacaraeccarcrircaeccreccegecces 3135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 tecceggagaegecetetgtgaeetgggeegtteggeegggagetgetgetegaegggatea 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 acgtctccatccggctccaggtgggggggggggcccgcctcttccgtgcaggcgcccggc 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 teccagtegaactgegataegagaeeeegggateeetaegeggtgeggatgaeetteeace 97
tamily, serine active site. Also contains possible v.terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTALRKSADGWTARLDAPGRARYASLRTTAKDTEGNGVGQTLIRAFGLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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Pred. No. 0.025;
0; Mismatches 146; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                        /product="putative secreted peptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                 /protein_id="CAC01576.1"
/db_xref="GI:9716215"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3196 GCTCGGAACCGACGCTTCCT 3217
                                                                                            /transl_table=11
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54.78;
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correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bentley.S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A. Bentley.S.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A. Direct Submitssion
Submitted (07-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
On May 10, 2000 this sequence version replaced gi:4584464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Substitution in codons is given for each CDS. Granlly the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
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                                                                                                                                                Bacteria: Firmicutes: Actinobacteria; Actinobacteridae;
Bacteria: Firmicutes: Actinobacteria; Actinomycetales: Streptomycetales: Streptomycineae; Streptomycetales: Streptomyceses; Streptomyces; Streptomyceses; Streptomyces; Streptomyces
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requlator; thiolase; transferase.
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                                              Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
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Oliver, K. and Harris, D.
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similar to many egs. TR:086699 (EMBL:AL011515) UvrA-like protein from Streptomyces coelicolor (796 aa) fasta scores; opt: 2047, z-score: 2164.0, E(): 0, (51.9% identity in 776 aa overlap) and SW:UVRA_ECOLI UvrA excinuclease ABC subunit A from Escherichia coli (940 aa) fasta scores; opt: 634, z-score: 669.2, E(): 5.8e-30, fasta scores; opt: 634, z-score: 669.2, E(): 5.8e-30, prosite matches to entry 10.98 aa overlap). Contains two Pram matches to entry 10.98 aa overlap (P-loop). Also contains possible membrane spanning
                                                                                                                                                                                                                                                                                                                                                   GAHGWETLEVDPADDCPDSVFVEDAVVYFRNYALITRPGAESRRAETAGVEEAVARLG
CSVANYWEPGTLDGGDVLKIGDTIYVGRGGRTNAAGVQQLRAAFEPLGARVVAVPVSK
VLHLKSAVTALPDGTVIGHIPLTDVPSLEPRELPVPESGGAHVVLLGGSRLLMAASAP
VTABLLADLGHEPVLDIGEFEKLEGCVTCLSVRLRELYD"
complement (976. .3234)
/gene="SCSF2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MSEFISITGARENNLQDVTLRIPKGRLTVFTGVSGSGKSSVVFD
TIAVESRRQLNETFTWFVRNRLPRYERPHADALEGLIPAIVVDQRPVGGHSRSTVGTM
TDIHSVLRVLFSRHGTPGAGGATAYSFNDPSGMCPGCDGLGRRVQPDWDRILDPARSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADGAVRPPPFAAGTWQCQTYTWTEELDTGKPVCDFTAAERAFLARGRPGSKVTVSGSG
GTWSTEYEGLADRFERLYLKRDLSGWSERTRDLVRGFLVEARPDGGARLNAAALAS
TIDGHSI AADCSRWQITDLIAVLRGIDDVALLPVAGAAVAALERVEAIGHGSYLSIDRET
ATLSGGEGGRIKTYRHGSSLTGMYYTPDESVGLHPVDKRLGDLLLLRLDKGNTVL
VVEHDPDVIALADHVVDMGPRAGADGGRVYFEGTPAGLAASDTLIGRCLGRRTAVKDY
VRAPTGELWYKGAERHHLREVTVAFPTGVLTAVTGVAGSGKSTLVAELTGAHPDAVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQSAIGISARSTPATYLGIMDTVRKVFARETGAEPGFFSFNSAGACGTCEGRGIIHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAFMDPVTTTCHDCEGRRFREEVLRLTVDGRSVADVLAMTAGQALGFFSDPGVRRRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALRDVGLTYLTLGQPLSTLSGGERQRIKLATRLHRTGAVYVLDEPTTGLHMSDVEGLL
ALLDRLVDAGNTVVVVVEHNLDVVAHADRVIDLGPDGGRDGGRVIFEGTPRELLAARGS
                                                                                                                                                                                                                                                                                                                             /translation="MPSKKALVRRPSPRLAEGLVTHVEREKVDHGLALEQWDAYVEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3245. .4879)
/gene="SCSF2A.03c"
/note="SCSF2A.03c, probable ABC transporter, len: 544aa;
similar to many involved in antiblotic resistance egs.
                     NG.NG-dimethylarginine dimethylaminohydrolase from Homo sapiens (285 aa) fasta scores; opt: 323, z-score: 384.7, E(): 4.1e-14, (35.7% identity in 272 aa overlap)."
(experimental). Similar to TR:D1038106 (EMBL:AB001915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
complement(2002. .3162)
/gene="SC5F2A.02c"
/note="Pfam match to entry PF00005 ABC_tran, ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                     /product-"dimethylarginine dimethylaminohydrolase"
/protein_id="CAB4668 1"
/db_xref="G1:4584465"
/db_xref="SWISS-PROT:Q9X7M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transporter, score 35.60, E-value 4e-08." complement(3118. .3141) //gene="SCF2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00005 ABC_tran, ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(976. .3234)
/gene="SC5F2A.02c"
/note="SC5F2A.02c, UvrA-11ke ABC transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1090. .1803)
/gene="SC5F2A.02c"
/note="Pfam match to entry PF00005 ABC_tran
transporter, score 101.40, E-value 1.7e-26.
/gene="SC5F2A.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="UvrA-like ABC transporter"
/protein__d=CAB40669.1"
/db_xref="GI:4584466"
/db_xref="SPTREMBL:Q9X7MS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3245. .4879)
/gene="SC5F2A.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/label=SC5F2A.02c
                                                                                                                                             /transl_table=11
/label=ddah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAEHLRRATRR
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gene

CDS

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/db_xref="Spremal.09x7m6"
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AGDVREBHFETVGDDMDVERRALTAGLEGLGLDHIGLDRTVGEVSGGESVLLRLAALLL
RRPDVLLLLDFPTNNLDYYARRRLYAAYESWPGYMVVYSHDRELLDRYDQIADLRAGSY
TWYGGNLTAYEBALAVEQEAAERWVRVAESDLRRQKRELADAQVVLARRRRYGGKMYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKREPRAVWKLRARTAQOSAGKYRIMHEEKLAGAKERLODAVEAVEDDEIRVÖLPYT
TYREPRAVWELTLEALELAKGARVAGGLDLHGPBRI ALLGKRAGKTTLIKRVAGELAPV
AGEATAHVPLRFLPQRLDVIDA
AGEATUSGGERRRAALADELAKENVABRADGATNNRIRALLARFLFRGARADO
QAATLSGGERRRAALALMALADGLIMLDEPTNNLDMASVROLTGALEAYEGALLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ñ
TR:054381 (EMBL:X79146) from the lincomycin-production gene cluster of Streptomyces lincolnensis 78-11 (578 aa) fasta scores; opt: 1624, z-score: 1696.3, E(): 0, (50.3% identity in 541 aa overlap). Contains two Pfam matches to entry PF00005 ABC_tran, ABC transporter, two Prosite matches to PS00017 ATP/CTP-binding site motif APC prosite match to PS00211 ABC transporters family signature. Also contains a possible coiled-coil region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4739. 4762)
/gene="SC5F2A.03c"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6297 GCGTCTCGTCGCCGCCCCCCCCCTATGCCGAGCATTCCCGCCACCCTGCACTACGACCG 6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ccgggatccctacgcggtgcggatgaccttcc----acctcccggagacgcgcc 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 cgaccgcacggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgagga 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PS00211 ABC transporters family signature."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 gagottoctogtotocogaggagototocttoaagatocoagtogaactgcgatacgagac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6177 GGTCTGCTGGACCTTCTCCCGCGGGGCTGCTCATCGCCGGGATGCAGGACCGAACGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6237 CGCCGACCCGTTCGCCGTCCGCATGACCTTCCCGGCCCCGGCCACCCTCGAGGGCGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 tgtgacctgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 cggcgacgtccacatcgccccgaccgacccgagggcctgtcggacgtctccatccggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6117 CGGCGACGTCCGGGTGCGCCCGTACGCGTACGACCG------CACCGTCCTGGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6066 ccacececeasescacescerearecacerececerescescescesecreces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Pfam match to entry PF00005 ABC_tran, ABC transporter, score 143.80, E-value 3.1e-39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 37245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 74.4; DB 1; Length 37 Pred. No. 1; 0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASHDLPFLESLGITRWLLLEEGELREITPEAVGYSA"
                                                                                                                                                                                                                                                                                                                                                                                     /product="putative ABC transporter"
/protein_id="CAB40670.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3290. .3787)
/gene="SC5F2A.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4403. ../gene="sc5F2A.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4942. .5850
/gene="SC5F2A.04"
4942. .5850
                                                                                                                                                                                                                                                                                                                                                           /label=SC5F2A.03c
                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                around 250aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.3%;
53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.9
Matches 209; Conservative
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Db 6006 CCAGGCCGCCGGCGAGCTGGTGCCGGTGGGTCTCGAGCACCTCCAGCTGGACCTGGACCA 5947

Search completed: July 18, 2002, 11:22:48 Job time: 13778 sec

THIS PACE OF WAR IN THE STORY

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July 18, 2002, 11:37:34; Search time 646.57 Seconds (without alignments) 1080.756 Million cell updates/sec
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SIDSS/gcgdata/geneseq.geneseq.embl.Na1990.bAT:*

SIDSS/gcgdata/geneseq.geneseq.embl.Na1990.bAT:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736436 segs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                       US-09-749-185-8
                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Streptomyces netro	Streptomyces grise	Streptomyces grise	Streptomyces golde	Streptomyces albus	S. spinosa DNA fra	S. spinosa DNA fra	Streptomyces clavu	Streptomyces clavu
SUMMARIES	ΩI	AAZ49731	AAZ49728	AAZ49727	AAZ49730	AAZ49729	AAF88315	AAF88312	AAD14511	AAD14499
	DB	21	21	21	21	21	22	22	22	22
	Query e Match Length DB ID	407	407	438	407	407	45624	50000	1227	15079
dф	Query	100.0	73.3	73.3	61.1	55.2	17.4	17.4	13.9	13.9
	Score	407	298.2	298.2	248.6	224.6	70.8	70.8	56.4	56.4
	Result No.	-	7	m	4	S	و د	7	ω	6

(UYLE-) RIJKSUNIV LEIDEN.

	10	. 56	ω,	38734	20	AAZ32020	Human METH1 relate
	11	26	13.8	38734	22	AAC90077	AL021529 cDNA clon
	12		ω.	109519	22	AAS08693	Micromonospora DNA
	13		ω.	15079	16	AAQ91580	S. clavuligerus cl
	14		2	3241	24	AAS18442	Contig 93 DNA enco
	15.		2	65140	22	AAD17184	Streptomyces nours
	16		ď.	125401	22	AAD17186	Streptomyces nours
υ	17	50.4	2	3957	22	AAA09686	HSV-2 immediate ea
	18	50.4	12.4	80161	20	AAZ21501	DNA fragment of Sa
	19	50.4	12.4	154746	24	AAD25519	Human herpesvirus
υ	20	50.4	12.4	-	24	AAD25519	Human herpesvirus
	21	20	12.3		21	AAA58473	Nucleotide sequenc
	22	6	12.2		16	AAQ99776	Phosphomycin biosy
	23		12.1		21	AAA58471	Nucleotide sequenc
	24	49	12.0		18	AAT74283	Cellulose binding
	25	49	12.0		18	AAT74281	Cellulose binding
	56	49	12.0		18	AAT74282	Cellulose binding
	27	49	7	ന	17	AAT10922	
	28	49	12.0	m	18	AAT63318	Myceliophthora the
	53	49	12.0		21	AA224236	M. thermophila lac
	30	49	12.0	4	22	AAD06345	Sorghum dwarfing g
	31	49	12.0		22	AAD06344	Sorghum full lengt
	32	8	12.0		15	AAQ63295	Consensus sequence
	33	48.8	12.0		23	AAS51481	Pseudomonas aerugi
	34	ω,	11.9		22	AAD14506	S. clavuligerus cl
υ	35	48.6	11.9		12	AAQ13287	P.denitrificans ge
	36		11.9	П	22	AAD14501	Streptomyces clavu
Ö	37		11.9	CA	14	AAQ46806	eryA region of S.
	38	48	11.8	44377	18	AAT78508	Platenolide syntha
	39	48	11.8	4	18	AAT80414	Platenolide syntha
	40		11.7	142	23	AAS54344	Pseudomonas aerugi
	41		11.7	231	14	AAQ35141	srmR coding sequen
	42	47.6	11.7	279	19	AAV49431	Bovine herpesvirus
	43	7.	11.7	3382	14	AAQ48249	Bovine herpesvirus
	44	47.6	11.7	351	16	AAQ94352	BHV1 gI glycoprote
	45	47.4	11.6	3192	18	AAT72106	Myceliophthora the

ALIGNMENTS

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mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23940; bioinsecticide; receptor agonist; antagonist; biomass; ds.
                                                                                                           ssgA; liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                              Location/Qualifiers
1..405
/*tag= a
/label= SsgA_protein
                                                                                     Streptomyces netropsis ssgA gene.
                     BP
                                                                                                                                                                                                                                                                                                                     98EP-0202148.
                   AAZ49731 standard; DNA; 407
                                                                                                                                                                                                                                                                                                99WO-NL00395
                                                                (first entry)
                                                                                                                                                                          Streptomyces netropsis.
                                                                                                                                                                                                                                                    WO200000613-A1
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                                                                18-APR-2000
                                                                                                                                                                                                          mat_peptide
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                                         AAZ49731;
          AAZ49731
                                                                                                                                                                                                Key
RESULT
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121
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                                                                                                                                                                                                                                                                                                                                                             tgggcgttcggccgggagctgctgctcgacggatcaaccgcccgagcggcggacggcgac 180
                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ssgA; liquid culture; filamentous bacteria; secondary metabolite; mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; bioinsecticide; receptor agent; antagonist; biomass; ds.
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                                                                         Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                          Length 407;
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                                                                                                                                                                                                                                         Sequence 407 BP; 63 A; 151 C; 131 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                        100.0%; Score 407; DB 21; 100.0%; Pred. No. 6.9e-67;
WETENSCHAPPELIJK ONDERZO
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                                                                                                                                                                                                                                                                                              Mismatches
                      Luiten RGM;
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                                                                                                          60pp; English.
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                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 407; Conservative
 (NEWE-) NEDERLANDSE ORG
                      В,
                                          2000-147269/13
                                                                                                          Disclosure; Fig 5;
                                                      P-PSDB; AAY44652
                      Van Wezel GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces
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                                                                                                                                                                                                                                                                         Query Match
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The present sequence is a DNA (ATCC 23345) encoding S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entitumour agents ariminating and secondary antipiaristic agents, runninant growth promoters, bioinsecticides, acceptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and enhancing fragmentation in filamentous to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%; Score 298.2; DB 21; Length 407; 83.3%; Pred. No. 8.4e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 407 BP; 60 A; 139 C; 142 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                     (NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                /*tag= a
/label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luiten RGM;
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5; 60pp; English.
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                                                                      1..405
Streptomyces griseus.
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339; Conserv
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                                                                                                                                                                        WO200000613-A1.
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                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                        (UYLE-)
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Matches 33
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151 tgggcgttcggccgcgagctgctgctggacgggctcaacagcccgagcggcgacggcgat 210

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine
                                                                                                                                                                                                                                                                mycellum; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterotaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 23345; biolnsecticide; receptor agontst; antagonist; biomass; ds.
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                                                                                                                                                                                                                                            secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYLE-) RIJKSUNIV LEIDEN.
(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 298.2; DB 2
Pred. No. 8.4e-47;
                                                                                                                                                                                                                                         culture; filamentous bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                           Streptomyces griseus ssgA gene-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 27; 60pp; English.
                                             AAZ49727 standard; DNA; 438 BP
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces griseus.
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                                                                                                                                                                                                                                            liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-1998;
                                                                                                                                           18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-2000
                                                                                             AAZ49727;
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                         4A249727
RESULT
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61 acccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgacc 120

1 atgagetteetegteteegaaggageteteetteaagateecagtegaactgegataegag 60

ó g δλ g ŏ

121 tgggcgttcggccgggagctgctcgacgggatcaaccgcccgagcggcgacggcgac 180

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The present sequence is a DNA (ATCC 21386) encoding S. goldeniensis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, entitumour spents antimigraine agents, herbicides, antiparasitic agents, runniant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                     mycelium; antibiotic, antitumour agent; immunosuppressive agent; hypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; ATCC 21386; bloinsecticide; receptor agonist; antagonist; blomass; AS.
               ggcgcggaccgcgccctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc
                                                                                                  271 ggcgcggaccgtgcgctgttccggggcggggacggcaccgctggtggcgttcctcgaccgg
 gtocacatcgccccgaccgacccgagggcctgtcggacgtctccatccggctccaggtg
                                                                                                                                     acggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgaggacagcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ssgA; liquid culture; filamentous bacteria; secondary metabolite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                        361 gaggeegegeteggeaagateetegeegaggageagaaegeeggetg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/label= SsgA_protein
                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces goldeniensis ssgA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luiten RGM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                         AAZ49730 standard; DNA; 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200000613-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999;
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                                                                  241
                                                                                                                                    301
181
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Page

Matches

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181 181 241 241 301 301 361 361

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The present sequence is a DNA (ATCC 3004) encoding S. albus G SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasiic agents, runninant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acggacaagtcggtgccgctcggtcaggaacagactctgggtgacttcgaggacagcctg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyketide synthase; biosynthesis;
transgenic plant; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 atgagetteetegteteeggaggageteteetteaagateeeagtegaaetgegataegag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 gtccgggtctgcccggtggggcagacggccaccagggaggtgcacatcacctccaggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 accgaccagggettgtcgctcggcagcgagcgggcacacgccgacttcgacagccacctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 atgagetteetegteteegaggagetegeetteegeateeeggtggagetgeggtaegag
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                                  Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
                                                                                                                                                                                                                                                                                                                                                     Score 224.6; DB 21; Length
Pred. No. 3.3e-33;
0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaggccgcgctcggcaagatcctcgccgaggagcagaacgccggctg 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 407 BP; 57 A; 150 C; 139 G; 61 T; 0 other;
                                                                                     5; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                     Query Match 55.2%;
Best Local Similarity 72.0%;
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
 P-PSDB; AAY44650
                                                                                     Disclosure; Fig
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                                                                                                                                                                                              accegggatecetaegeggtgeggatgaeetteeaeeteeeeggagaegeeetgtgaee 120
                                                                                                                                                                                                                                                                                     acctgtgatccctacgccgtgcggctgacctttcatctgcccggagatgccccggtgacc 120
                                                                                                                                                                                                                                                                                                                                                                                                            ggcgcggaccgcgccctcttccgtgcaggcgccccgccgctggtcgccttcctcgaccgc 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                         1 atgagetteetegteteggaagaacteteetteegtatteeggtggagetgegttaegag 60
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                                                                                                                                                                                                                                                                                                                                                                          gtccacatcgcgcccgccgacccggagacgttcggcgaggtcctgatccgcctgcaggtg
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                                                                                                                          atgagetteetegteteegaggageteteetteaagateeeagtegaaetgegataegag
                                                                                                                                                                                                                                                                   tgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgac
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                                                                                       ;
0
                                                      Length 407;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 T; 0 other;
                                                     21;
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                                                   Score 248.6; DB
Pred. No. 1.2e-37
                                                                                       Mismatches
C; 145 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
SsgA_protein
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1..405
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                                                   61.18;
75.78;
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A; 135
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                                                                                       Conservative
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces albus G.
 96
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                                                                     Similarity
 BP;
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Sequence 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000
                                                                                     308;
                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ49729
                                                                       Local
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AAZ49729 RESULT

360

240

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Gaps

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Length 407;

9 9 polyketide synthase; biosynthesis; transgenic plant; insect resistance;

(first entry)

Salas JA;

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Velten

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Froede

Moehrle V,

99DE-1057268 99DE-1040596

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S. spinosa DNA fragment SEQ ID 1.
                                                                                                   spinosyn; polyketide aglycone; macrolide; insecticidal; ds.
                                                                                  Forosamine; trimethylrhamnose;
                                                                                                                                                                Saccharopolyspora spinosa.
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                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                          27-AUG-1999;
                                                                                                                                                                                                                                                                                    29-NOV-1999;
    28-AUG-2001
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      contractive, and contracted by the corresponding of the corresponding definition to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylrhamnose to a spinosyn or polyketide aglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of titheir precursors or derivatives, including production of transgenic plants that express (II) and thus have increased resistance to insects. (i) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are macrolides with insecticidal, but not antibacterial, activity, and can ascolides with insecticidal, but not antibacterial, activity, and can expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of common which contains the coding regions for proteins involved in consamine and trimethylrhamnose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ή;
                                                                                                                                                                                                                                                                                                                        This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (I) to identify, inactivate or modulate genes involved in the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20799 AGCTIGCGGACTICTIGAACGACGACCTAGGTCGAACCTGGTGATGAACACGGT 20740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21036 TCGGCGTGGAGCTGCGGTACGACACCCCCAATCCGTACGAGATCTCCATGAAGCTCAACG 20977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20859 TGGTCGTGATCGAGATGAGCTCGCCGTCGGGGCAGGCCTCCTTCGAGGTGAATGCTGACC 20800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20976 TAGGCACGGACGGACAGGACTGGGTGATCGCCCGCGACCTGCTGGCCGACGGCTGA 20917
                                                                                                                                                                                                    enzymes for spinosyn biosynthesis, useful for insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20916 TCGCCGAGGCAGGCGAAGGCGATGTGCGGATCGGCC---CTCGACGGGGTTTTCCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggtcaggaacagactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 45624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45624 BP; 7933 A; 14913 C; 14940 G; 7838 T; 0 other;
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                                                                                                                        Salas JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70.8; DB 22;
Pred. No. 6.3e-05;
0; Mismatches 162;
                                                                                                                        Velten R,
                                                                                                                                                                                                                                                                                  Claim 7; Page 58-74; 354pp; German.
                                                                                                                        ĸ,
                                                                                                                        Froede
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.4%;
Best Local Similarity 52.3%;
Matches 181; Conservative
99DE-1057268
                                          99DE-1040596
                                                                                                                                                                                                      New nucleic acid encoding recombinant production of
                                                                                                                        Moehrle V,
                                                                                                                                                              WPI; 2001-267102/28.
                                                                                  (FARB ) BAYER AG.
  29-NOV-1999;
                                        27-AUG-1999;
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This invention describes a novel method nucleic acid (I) and its encoded polypeptide (II) containing at least one region that encodes an enzymatic activity involved in biosynthesis of spinosyns. (I) are used (i) to identify, inactivate or modulate genes involved in the biosynthesis of (II); (ii) to generate a library of polyketide synthases; (iii) for adding forosamine or trimethylihamnose to a spinosyn or polyketide anglycone; and (iv) for recombinant production of the corresponding enzymes, which are used for production of (II), their precursors or derivatives, including production of (II), their precursors or and thus have increased resistance to insects. (I) are also useful as markers for sequencing of the Saccharopolyspora spinosa genome. (II) are also be used to raise specific antibodies, useful for identifying expression clones in a gene bank. Cells transformed with (I) may produce (II) at significantly increased levels or produce new derivatives of (II). This sequence represents a genomic DNA fragment of the S. spinosa genome which contains the coding regions for proteins involved in forcesamine, trimethylrhamnose and polyketide synthase biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24589 tcggcgtggagctgcggtacgacagccgcaatccgtacgagatctccatgaagctcaacg 24648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24766 tggtcgtgatcgagatgagctcgccgtcgggggcaggcctccttcgaggtgaatgctgacc 24825
enzymes for spinosyn biosynthesis, useful for insecticidal spinosyns and their derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 cgctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggtcaggaacagactc 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     teceagtegaactgegataegagaeeeggggateeetaegeggtgeggatgaeetteeace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     teceeggagaegeetgtgaeetgggegtteggeegggagetgetgetegaegggatea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24649 taggcacggacggtcaggtggactgggtgatcgcccgcgacctgctggccgacgggctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218. acgtctccatccggctccaggtgggcgcggaccgccctcttccgtgcaggcgcccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 50000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50000 BP; 8484 A; 16290 C; 16535 G; 8691 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70.8; DB 22;
Pred. No. 6.3e-05;
0; Mismatches 162;
                                                                                                                                                           7; Page 14-31; 354pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4%;
ilarity 52.3%;
Conservative
New nucleic acid encoding recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 181; Conserv
                                                                                                                                                               Claim
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AAF88312 standard; DNA; 50000 BP

AAF88312 RESULT

AAF88312

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338 tgggtgacttcgaggacagcctggaggccgcgctcggcaagatcct 383

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AAD14511

Key

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/trag= g //product= "Clavulanic acid biosynthesis enzyme, CLA" //product= "Clavulanic acid biosynthesis enzyme, CLA" //transl_except= (pos:6590..6592, aa:Leu-Clx) //ote= "The CDS corresponds to ORF4 and does not include
                                                                                                                                         969 ggcgggcaaccgggacgagacggtcttccccgacccggaccgggtggacgtggaccgcga 1028
                                                                                                                                                                                                                                                       1029 egecegeceatetegeetteggecaeggeatgeaceagtgeetgggecagtggetgge 1088
                                                                                                                                                                                                                                                                                                                                                                    1089 ccgggtggagctggaggagatcctcgccggggtgctgcgctggatgcccggtgcccggtt
                                                                                                                                                                                                314
  Clavulanic acid biosynthesis enzyme; antibiotic; infectious disease; broad spectrum beta-lactamase inhibitor; ds.
                                                                                      gaccgaccccgagggcctgtcggacgtctccatccggctccaggtgggcgcggaccgcgc
                                                                                                                                                                                                   cctcttccgtgcaggcgcccgccgctggtcgccttcctcgaccgcacggacaagtcggt
                                                                                                                                                                                                                                                                                                             315 gccgctcggtcaggaacagactctgggtgacttcgaggacagcctggaggccgcgctcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product- "Clavulanic acid biosynthesis enzyme"
/transl_except- (pos:5476..5478, aa:Ala-Glx)
/note- "Corresponds to ORF3"
5482..5653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Clavaminate synthase isozyme (cs2)"
/transl_except= (pos:7583..7585, aa:Arg-Glx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Open reading frame (ORF)1 protein"
/bransl_except= (pos:112..114, aa:Gly-Glx)
1765..2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces clavuligerus 15 Kb genomic DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= d
/note= "Intergenic region"
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/note= "Intergenic region"
5654..6595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/note= "Intergenic region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 caagatcctcgccgaggagcagaacgccgg 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
complement (109..1764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΒÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD14499 standard; DNA; 15079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..7588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD14499;
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                                                                                      195
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CONSTRUCTION OF THE SET OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
24826 agcttgcggacttcttgaacgacacctacgacgtggtcgaacctggtgatgaacacccggt 24885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vel enzyme required for clavulanic acid biosynthesis which is useful
broad spectrum beta-lactamase inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgcggtgcggatgaccttccacctcccggagacgcgcctgtgacctgggcgttcggccg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgaggagctgctgcgcttccactccatcgtgcagaacgggctggcccgtgccgcggtgga 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgacgtccacatcgcccc 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clavulanic acid biosynthesis enzyme; antibiotic; infectious disease; broad spectrum beta-lactamase inhibitor; open reading frame; ORF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Open reading frame (ORF)10 protein"
/transl_except= (pos:1222..1224, aa:Trp-Glx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces clavuligerus ORF10 DNA downstream to pcbC gene.
                                                                                                                                         24886 ggatgaacgtcgacgaggtgctgagccagctgctctcgcacaacct 24931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1227 BP; 161 A; 439 C; 451 G; 176 T; 0 other;
                                                                                      tgggtgacttcgaggacagcctggaggccgcgctcggcaagatcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56.4; DB 22;
Pred. No. 0.035;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 75-76; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paradkar AS;
                                                                                                                                                                                                                                                                                   BP,
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                                                                                                                                                                                                                                                                              AAD14511 standard; DNA; 1227
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93US-0134018.
95US-0567801.
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ilarity 48.2%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0385028
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aidoo KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-342772/36.
P-PSDB; AAE07915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pcbC gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6232106-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1993;
06-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-1997;
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Best Local Simi
Matches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2001
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Length 15079;

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The present invention relates to DNA sequences encoding enzymes required for clavulanic acid biosynthesis. Clavulanic acid is a broad spectrum beta-lactamase inhibitor and is an important antibiotic for the treatment of infectious diseases. The present sequence is Streptomyces clavuligerus 15 Kb genomic DNA fragment comperising 10 open reading frames (ORFs), eight of which are involved in clavulanic acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel enzyme required for clavulanic acid biosynthesis which is useful as broad spectrum beta-lactamase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-342772/36.
P-PSDB; AAE07906, AAE07907, AAE07908, AAE07909, AAE07910, AAE07911,
AAE07912, AAE07913, AAE07914, AAE07915.
                                                         /product= "Clavulanic acid biosynthesis enzyme"
/transl_except= (pos:9071..9073, aa:Thr-Glx)
/note= "Corresponds to ORF6"
9077..9240
                                                                                                                                                                                                                                                            /product= "Clavulanic acid biosynthesis enzyme"
//transl_except= (pos:11001..11003, aa:Gly-Glx)
//transl_except= (pos:1207..12027..12621
                                                                                                                                                                       product= "Clavulanic acid biosynthesis enzyme"
                                                                                                                                                                                                                                                                                                                                                                          /product= "Clavulanic acid biosynthesis enzyme"
/transl_except= (pos:12625.12627, aa:Val-Glx)
/transl_except= "Corresponds to ORF9"
13366..13768
                                                                                                                                                                                    'transl_except= (pos:10903..10905, aa:Lys-Glx)
note= "Corresponds to ORF7"
0909..10997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "ORF10 protein"
/transl_except= (pos:14990..14992, aa:Trp-Glx)
"Corresponds to ORF5"
                                                                                                                                                                                                                                                                                                                          /*tag= p
/note= "Intergenic region"
complement (12622..13365)
                                                                                                                                                                                                                                 /note= "Intergenic region"
complement (10998..12296)
                                                                                                                                 'note= "Intergenic region"
                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= r
/note= "Intergenic region"
13769..14995
                      .uy- )
/note= "Intergenic region'
895..9076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paradkar AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 2; 75pp; English.
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93US-0134018.
95US-0567801.
                                                                                                                                               241..10908
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'589..7894
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06-DEC-1995;
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Sequence 15079 BP; 2105 A; 5475 C; 5331 G; 2168 T; 0 other;

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                                                                           14737 ggcgggcaaccgggacgagacggtcttccccgacccggaccgggtggacgtggaccgcga 14796
                                                                                                                                                                                                                                                                                                                            14857 ccgggtggagctggaggagatcctcgccgcggtgctgcgctggatgcccggtgcccggct 14916
                                                                                                                                               14677 ggacgtccagctcgacgatgtgctcatccgggcgggcgagggcgtggtgctgtcgctgtc 14736
                                                                                                                                                                                                                                                                   14797 egecegeceatetegeetteggeeaeggeatgeaecagtgeetgggeeagtggetgge 14856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, METH1; METH2; anti-angiogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis inhibitor; abnormal wound healing; inflammation; rheumation rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection;
                                                         75 cgcggtgcggatgaccttccacctcccggagacgcgctgtgacctgggggtttcggccg 134
                                                                                                                                                                                                                                                                                                374
                             Gaps
                                                                                                                  gaccgaccccgagggcctgtcggacgtctccatccggctccaggtgggcgcgggccgcgc
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                             Indels
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Score 56.4; DB 22;
Pred. No. 0.031;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 296-321; 457pp; English.
                                                                                                                                                                                                                                                                                                                                                           375 caagateetegeegaggageagaaegeegg 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human METH1 related EST AL021529.
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13.9%;
48.2%;
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             Best Local Similarity 48.2
Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HASTINGS G A.
RUBEN S M.
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28-AUG-1998;
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 Query Match
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Crohn's disease; atherosclerosis; birth control;

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respectively. METHI and METHI there been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rhemmatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arthritis promitions. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoinmune disorders, acquired (e.g. by chemotherapy or toxins), or infections and acute conditions. The products can also be used for detection and diagnosis. AA323002 to AA323080, and AA44503 to AA43211 represent sequences given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cggcgccgaggcgttcgcccggctgacctccgacgagggcgccgtcgacgacttcggctt 2575
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  metalloprotease thrombospondin (METH) proteins METH1 and METH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 56; DB 20; Length 38734; 46.4%; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38734 BP; 6142 A; 13140 C; 13585 G; 5867 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2876 gcggttgctcggctccggcgaactggtcggcg 2907
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Matches 182;
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The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). The present sequence is an expressed sequence type (EST) for METH. METH can be used for inhibiting anglospensis in an individual, and for treating cancer, benign tumours, an ocular anglospensic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculospensis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial anglospensis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb anglospensis, Osler Webber syndrome, plaque neovascularisation, telangiectasis, haemophiliac joints, anglofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 ccgggagctgctgctcgacgggatcaaccgcccgagcggcgacgtccacatcgc 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Trulli SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHI and METH2 polynucleotides and encoded polypeptides, used inhibit anglogensis in the treatment of disorders such as cance rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.8%; Score 56; DB 22; Length 38734; 46.4%; Pred. No. 0.034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210; Indels
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BETH ISRAEL DEACONESS MEDICAL CENT.
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Terrett JA;
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99US-0147823.
99US-0373658.
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JONAK Z L.
TRULLI S H.
FORNWALD J A.
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                                                           WO200071577-A1
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                              Unidentified
                                                                                                                       25-MAY-2000;
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22-FEB-2000;
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	ggcg 2907 nthetic enzymes for Everninomycin. -neck gene; orthomicin; ricana.	EvdA" (1382) (13891381) (14902611) (14902611) (26182622) (26223860) (28673870)	/*tag
192 2696 252 2756 312 312 372	28/6 geggttgete 308693 AAS08693; 26-SEP-2001 (f Micromonospora Everninomicin; fermentation; c Micromonospora	CDS RBS CDS RBS CDS RBS RBS	FT CDS FT RBS FT RBS

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complement (47156..49234)
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51627..52715
/*tag= bi
/product= "EvsB"
51629.51629.51629.51629
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complement (41679..42707)
/*tag= ay
/product="EvrV"
complement (42714..42717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= bm
/product= "EvbB"
complement (55125..55128)
/*tag= aq
/product= "EvrO"
complement (36235..36963)
                                                                                                                                                                                                                                                               /product= "Evrw"
complement (43807..43811)
/*tag= bb
                                                                                                                                                                                                                                                                                                   /*tag= bc
/product= "EvrX"
complement (45014..45760)
/*tag= bd
                                                                                                                                                                                                                                                                                                                                   /product="Evry"
complement (45767..45770)
/*tag= be
                                                                                                                                                                                                                                                                                                                                                                                 /product="Evr2"
complement (45952..45956)
/*tag= bg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (54362..55117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= bo
/product= "EvbC"
complement (56100..56103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (56184..56813)
                                                                                                            /*tag= au
/product= "Evrs"
complement (40216..40890)
                                                                                                                                                                                                                                                                                                                                                              complement (45962..46714)
/*tag= bf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (55135..56094)
                                                              /product= "EvrQ"
complement (38072..38566)
                                                                                                                                             /product= "EvrT"
complement (40899..40902)
                                                                                                                                                                                                                                                                                        complement (43799..44866)
                                                                                                                                                                                                                                             complement (42810..43799)
                                             complement (36998..38026)
                                                                                                 complement (38892..40163)
                                                                                                                                                                       complement (40887..41576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= bk
/product= "EvsC"
53554..54207
/*tag= bl
/product= "EvbA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= bq
/product= "EvbC2"
56961..58709
                                                                                /*tag= at
/product= "EvrR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..53557
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52889..
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                                        94541 gccaccgggtacgcgctggacgccgccgccgatcgggcccgccggctggcccggctggaa 94600
                                                                                                                   85 atgacettecacetececeggagaegegeetgigaeetgggegtteggeegggagetgetg 144
                Gaps
                                                                                                                                                                                                                                                             Clavulinic acid; clavulinate; antibiotic; beta-lactamase-inhibitor;
Score 55.8; DB 22; Length 109519;
Pred. No. 0.035;
0; Mismatches 147; Indels 0;
                                                                                                                                                /*tag= h
/label= ORF8
complement (12662..13365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (10998..12296)
                                                                                                                                                                                                                                                                                                Location/Qualifiers
complement (49..1745)
                                                                                                                                                                                                                                                                                                                                                         /*tag= c
Jabel- ORF3
554. 6595
/*tag= d
/label- ORF4
/note= "cla gene"
6611..7588
                                                                                                                                                                                                    AAQ91580 standard; DNA; 15079 BP
                                                                                                                                                                                                                                                S. clavuligerus cla gene region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= 1
/label= ORF9
13769..14995
/*tag= j
/label= ORF10
                                                                                                                                                                                                                                                                                                               /*tag= a
/label= ORF1
2216..3937
/*tag= b
/label= ORF2
3940..5481
                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= e
//abbl= ORF5
7895..9076
/*tag= //tabel= ORF6
9241..10908
/*tag= //tag= ORF7
13.7%;
Best Local Similarity 49.5%;
Matches 144; Conservative C
                                                                                                                                                                                                                                 13-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                  Streptomyces clavuligerus.
                                                                                                                                                                                                                                                                     cla gene; ds.
                                                                                                                                                                                                                   AAQ91580;
                                                                                                                                                                                       RESULT 13
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AAD17184 standard; DNA; 65140.BP.
  agriculture;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Narbonolide polyketide synthase; PKS; narbomycin modification enzyme; erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethymycin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 14617 cgaggagctgctgcgcttccactccatcgtgcagaacgggctggccgtgccgcggtgga 14676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14857 ccgggtggagctggaggagatcctcgccgggtgctgcgctggatgcccggtgcccggtt 14916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14737 ggcgggcaaccgggacgagacggtcttgcccgacccggaccgggtggacgtggaccgcga 14796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 ggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgacgtccacatcgcccc 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaccgaccccgaggcctgtcggacgtctccatccggctccaggtgggcgcggaccgcgc 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cctcttccgtgcaggcgcccgccgctggtcgccttcctcgaccgcacggacaagtcggt 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gccgctcggtcaggaacagactctgggtgacttcgaggacagcctggaggccgcgctcgg 374
                                                                                                                                                                                                                                                                                                                                                                                                                           75 cgcggtgcggatgaccttccacctccccggagacgcgcctgtgacctgggcgttcggccg 134
                                                                                                                                                                                                                                                                    A library of S. clavuligerus NRRL 5741 genomic DNA fragments (15-22 kb) constructed in cosmid pLART3 was screened for the cla gene using a probe based on a partial N-terminal sequence from the CLA enzyme. Isolated clone K6L1 included a 15kb fragment having the sequence given in AAQ91580 that included the cla gene (ORF4).
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                              P-PSDB; AAR77858; AAR77859; AAR77860; AAR77861; AAR77862; AAR77863;
AAR77864; AAR77865; AAR77866; AAR77867.
                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                  Clavulanic acid biosynthesis enzymes and corresp. DNA - useful biosynthesis of the antibiotic in Streptomyces hosts which do naturally produce clavulanate
                                                                                                                                                                                                                                                                                                                                                                               Length 15079;
                                                                                                                                                                                                                                                                                                                                          Sequence 15079 BP; 2097 A; 5488 C; 5324 G; 2170 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contig 93 DNA encoding S. narbonensis polyketide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                               DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 caagatectegeegaggageagaacgeegg 404
                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                              Paradkar AS;
                                                                                                                                                                                                                                               Disclosure; Fig.2; 41pp; English.
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                                                                                                                                                                                                                                                                                                                                                                              13.5%;
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                                                        93CA-2108113
                                                                               93CA-2108113
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches 158; Conservative
                                                                                                                              Aidoo KA, Jensen SE,
                                                                                                       (UYAL-) UNIV ALBERTA
                                                                                                                                                  WPI; 1995-207301/28
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                              08-OCT-1993;
                                                        08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-2002
           CA2108113-A.
                                  09-APR-1995
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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The present invention relates to recombinant DNA vectors (cosmids) that encode for the narbonolide polyketide synthase (PKS) enzyme and various narbonnycin modification enzymes from Streptonyces narbonnesis. The recombinant DNA vectors can be used to produce recombinant ketide synthases and a variety of different polyketides (e.g. erythromycin, rapamycin, tylosin, narbomycin, picromycin, methylmycin and neomethymycin) for use in agriculture, medicine and health. The recombinant vectors may be used to produce polyketides in relatively high yields. AAS18432-AAS18443 represent contig DNA sequences that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1826 teggtetgetectegegaetecggegeceeggegeeegagegtgaeaaggeggegeeeagg 1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1886 cggtgtcccgcaaggtcgccgagaacggcgcggtgctcctgcgaaacgaggccaggccc 1945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 tcgaactgcgatacgagacccgggatccctacgcggtgcggatgaccttccacctccccg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding narbonolide polyketide synthases from Streptomyces narbonensis, useful for the recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gagacgegectgtgaeetggggegtteggeegggagetgetgetegaeggggateaaeegee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3241 BP; 520 A; 1174 C; 1125 G; 422 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.7%; Score 51.8; DB 24; 47.4%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encode for S. narbonensis PKS enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 20-22; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2126 cettegggacgeggateceggeggege 2152
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                                                                                                                                                                                                                                                                                                                                                                                   (KOSA-) KOSAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyketides, e.g. narbomycin
                                                                                                                                                                                                          99US-0434288
                                                                                                                                                                                                                                                                          98US-107093P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 155; Conservative
Streptomyces narbonensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDaniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                          05-NOV-1999;
                                                                                                                                                                                                                                                                          05-NOV-1998;
27-MAY-1999;
                                                                US6303767-B1
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                                     Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster; antifungal; antibiotic; nysl; ds.
                      Streptomyces noursei nys1 DNA of nystatin PKS gene cluster.
                                                                                                                                                                                                                                                                                protein"
not include start codon"
                                                                                                                                                                                                                                                                                                                                     product= "NysR4 (short) protein"
note= "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                             /note= "CDS does not include start codon"
complement (62551..63615)
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "CDS does not include start codon" (21755..64961
                                                                                                  /product= "NysD2 partial protein"
/note= "CDS does not include stop codon"
complement (1056..2576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
(SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
(ALPH-) ALPHARMA AS.
                                                                                                                                                                                                                                                       product "NysR1 protein"
                                                                                                                                                                                                                                                                                                                                                                      /product= "NysR5 protein"
                                                                                                                                                                                                                                                                                                               product= "NysR3 protein"
                                                                                                                                /product= "NysD1 protein'
2806..6906
                                                                                                                                                                          /*tag= d
/product= "NysB protein"
16550.49840
                                                                                                                                                                                                       /product= "NysC protein"
50260..51015
                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= m
/product= "ORF1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                     /product= "ORF2 protein"
                                                                                                                                                         /product= "NysA protein"
6952..16530
                                                                                                                                                                                                                                 product= "NysE protein"
                                                                            Location/Qualifiers
complement (1..1035)
                                                                                                                                                                                                                                                                                        "CDS does
                                                                                                                                                                                                                                                                                product= "NysR2
                                                                                                                                                                                                                                                                                                7180..59963
                                                                                                                                                                                                                                                                                                                                               /note= "CDS c
61736..62497
                                                                                                                                                                                                                                        1405..54305
                                                                                                                                                                                                                                                                4329..57190
                                                                                                                                                                                                                                                                                                                        0415..61047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-2000; 2000GB-0002840.
10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38-FEB-2001; 2001WO-GB00509
       (first entry)
                                                                                                                                                     /*tag= c
                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                                                                                                                         note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINVENT AS.
DZIEGLEWSKA H.
ZOTCHEV S B.
SEKUROVA O N.
                                                                                                                                                                                                                           *tag=
                                                             Streptomyces noursei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SINTEF STIFTE
ALPHARMA AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200159126-A2.
      29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SINV-)
(DZIE/)
(ZOTC/)
(SEKU/)
                                                                                                                                            CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the cloning and sequencing of the gene cluster encoding a modular type I polyketide synthase (PKS) enzyme in the blosynthesis of the macrolide antiblotic nystatin. The nystatin PKS is useful as antifugal antiblocics. The present sequence is a Streptomyces noursel nysl DNA of nystatin PKS gene cluster.
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                                                                                                                                                                                                                                                                                                                           New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 gctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggtcaggaacagactct
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                                                                                                                    Strom AR;
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                                                                                                                    Brautaset T,
                                                                                                                 3, Sekurova ON, Fjaervik E, Brautase
Ellingsen TE, Sletta H, Gulliksen O;
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 116-151; 266pp; English
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Job time: 11367 sec
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Matches 119; Conservative
FJAERVIK E.
BRAUTASET T.
                                                                                                                                                                                                          WPI; 2001-557614/62
                                                          (STRO/) STROM A R.
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Appl Appl Appl Appl Appl

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APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: AShish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS PIICE
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEFAX: (202 39305350
TELEFAX: (202) 39305350
TELEX: RCA-248593 IDEA UR
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                  US-07-951-715A-6
US-08-459-448A-6
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HOLECULE TYPE: DNA (genomic)
US-09-385-028-23
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STRANDEDNESS: single
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COUNTRY: U.S.A.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-510-6468-17

US-08-310-6468-11

US-08-387-942C-7

US-09-036-987A-1

US-09-036-987A-1

US-08-814-052-17

US-08-814-052-17

US-08-814-052-18

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US-08-814-052-18

US-08-814-052-18

US-09-081-485-1

US-09-083-485-1

US-09-083-485-1

US-09-385-028-13

US-09-385-028-13

US-08-804-227C-7

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length
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TITLE OF INVENTION: Polypeptides Involved in The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide E
TITLE OF INVENTION:
Office Sequences: 45
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0
                                                                                                                                     13.9%; Score 56.4; DB 4; Length 15079;
48.2%; Pred. No. 0.0028;
tive 0; Mismatches 171; Indels 0;
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
**TI,ING DATE: 03-AUG-1995
**TI,ING DATE: 03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14917 CGCGGTGCCCTTCGAGGAGCTGGACTTCCG 14946
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                                                            Streptomyces clavuligerus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08510646B Patent No. 6077699 GENERAL INFORMATION:
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Debussche, Laurent
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Lacroix, Patricia
    DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thibaut,
                                                                                                                                                            Similarity
                    8
; MOLECULE TYPE: D
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Stre;
US-09-385-028-1
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US-08-510-646B-17
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                                                          cgcggtgcggatgaccttccacctcccggagacgcgcctgtgacctgggcgttcggccg 134
                                                                                               849 CGAGGAGCTGCTGCGCTTCCACTCCATCGTGCAGAACGGGCTGGCCCGTGCCGCGGGGA 908
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                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Acid Blosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
STATE: D.C.
                    0; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILLING DATE: 29-740-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 538-666
TELEPAX: (202) 3930530
TELEFAX: RCA 248593 IDDA UR
    Pred. No. 0.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1149 CGCGGTGCCCTTCGAGGAGCTGGACTTCCG 1178
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  48.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 15079 base pairs
TYPE: nucleic acid
Best Local Similarity 48.2
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US, FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                  LENGTH: 3241
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US-08-387_942C-7
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STATE: VI
COUNTRY:
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APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
ITTLE OF INVENTION: POSTKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
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               APPLICATION NUMBER: PCT/FR 93/00923 FILING DATE: 25-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 92/11441 FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 CGGACTCGCCGAGATGCTGGCCGAGG 423
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                                                                                                                         NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 408-4400
INFORMATION FOR SED ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
TYPE: nucleic acid
STRANDENNESS: double
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Best Local Similarity 50.3%;
Matches 194; Conservative
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MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
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PRIOR APPLICATION DATA:
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; OTHER INFORMATION:
US-08-510-646B-17
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       12.7%; Score 51.8; DB 4; Length 3241; 47.4%; Pred. No. 0.022; Live 0; Mismatches 172; Indels 0.
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APPLICANT: VALLA, SVEIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATA:
FILING DATE: 05-May-1995
CURRENT APPLICATION NUMBER: US/09/434,288 . USRENT FILING DATE: 1999-11-05 PRIOR APPLICATION NUMBER: 60,107,093 PRIOR FILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2126 ccttcgggacgcggatcccggcggcgc 2152
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                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-09-434-288-11
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                                                                                                                       NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
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85 atgacettecacetececegaagaegegeetgtgaeettgggegtteggeegggagetgetg 144
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Tradway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Tribe OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1998-08-09
EARLIER FILING DATE: 1998-03-09
                                                                                                                                                                                                                                                                                                                                                                    Length 80161;
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                                                                                                                                                                                                                                                                                                                                                                    Score 50.4; DB 3;
Pred. No. 0.039;
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                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                    12.4%;
51.4%;
LENGTH: 80161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDCS: linear
MOLECULE TYPE: DNA (genomic
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
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APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Maddurl, Krishnamurthy
APPLICANT: Maddurl, Krishnamurthy
APPLICANT: Maddurl, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Turner, Jansynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow AgroSciences LLC Patent Department
STREET: 9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                     REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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....ER: US/09/036,987A
09-MAR-1998
171: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentTn Policy
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NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09036987A Patent No. 6143526 GENERAL INFORMATION:
         REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-7
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.00.
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CITY: Indianapolis
STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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APPLICANT:
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                   237. ggtgggcgcgggaccgcgccctcttccgtgcaggcgccccgccgctggtcgccttcctcga
                                                                                                                                                                                                                             Sequence 17, Application US/08814052 Patent No. 6015783
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
:ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.0%;
Best Local Similarity 53.1%;
Matches 128; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 2279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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STATE: New YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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US-08-814-052-17
                                                                                                                                1969 C 1969
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                                                                                            297 c 297
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405 Lexington Avenue, Suite 6400
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265 gcaggcgcccgccgctggtcgccttcctcgaccgcacggacaagtcggtgccgctcggt 324
                                                                               cgacgtccacatcgccccgaccgacccgaggcctgtcggacgtctccatccggctcca
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cherry, Joel R.
APPLICANT: Cherry, Joel R.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Brown Seperal Dolberg
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
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                                                                                                                              325 caggaacagactctgggtgacttcgaggacagcctg 360
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MEDIUM TYPE: Diskette
COMPUTER: IS COMPOUTER: DOS
SOFTWARE: FASTSO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE: 06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 3
Pred. No. 0.077
0; Mismatches
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Patent No. 6015783
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 3,728
REFERENCE/DOCKET NUMBER: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
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INFORMATION FOR SEQ ID NO: 19:
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ilarity 53.1%;
Conservative (
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TYPE: nucleic acid
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CITY: NC.
STATE: New YC..
COUNTRY: U.S.A.
TP: 10174-6401
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Best Local Similarity
Matches 128; Conserv
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US-08-814-052-19
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CORRESPONDENCE ADDRESS:
- ADDRESSEE: No. 60157830 No. 6015783disk of No. 6015783th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
1909 GACGACCACCTCCGGGGCCGTCTCGGACGCCGACGCCCTCTGCGC 1968
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0.077;
                                                                                                                                                                                                                                                                                                                    APPLICANT: Von der Osten, Claus
APPLICANT: Cherry, Joel R.
APPLICANT: Bornvad, Mads E.
APPLICANT: Wind, Jesper
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF STAILS OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 3; Length 227
Pred. No. 0.077;
0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/814,052
FILING DATE: 06-MAR-1997
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
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3: No. 5981243o No. 5981243disk of No. 5981243th America, Inc.
405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2692 esceceseacecesecraerraneceseccharecrareceseseseseseaceranear 2751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 gacccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgac 119
                                                                                                                                                                                                                                                                                                                                    APPLICANT: OXENB LL, Karen M.
APPLICANT: AASLYNG, Dorrit A.
TITLE OF INVENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCFODING SAME
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(586..831, 917..994, 1079..1090, 1193..1264,
1337..2308, 2456..2524, 2618..3028)
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Pred. No. 0.076;
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COMPUTER READABLE FORM:
COMPUTER: ID174-6401
COMPUTER: ID Floppy disk
COMPUTER: ID FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,218A
FILING DATE: 29-SEPT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4184.120-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
                                                                                                                                                                           ; Sequence 1, Application US/08939218A; Patent No. 5981243
; GENERAL INFORMATION:
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NAME: ROZEK, Carol E.
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET UNBERS: 4184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                            APPLICANT: BERKA, Randy Michael
APPLICANT: BROWN, Stephen H.
APPLICANT: XU, Feng
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                                                                                                                                                                                                                                                                                          XU, Feng
SCHNEIDER, Palle
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53.1%;
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INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 3183 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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Matches 128; Conserv
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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LOCATION:
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US-08-939-218A-1
                                                                1969 C 1969
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                    297 c 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1849 CCACTGCCACATCGCCTGGCACGTCTCGGGCGCCTGGGCGTCGTCTACCTCGAGCGCGC 1908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 gacccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgac 119
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                                                                                                                                                                                                                Sequence 18, Application US/08814052
Patent No. 6015783
GENERAL INFORMATION:
APPLICANT: Cherry, Joel R.
APPLICANT: Cherry, Joel R.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Vind, Jesper
APPLICANT: Vind, Jesper
APPLICANT: Vind, Jesper
APPLICANT: TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
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Pred. No. 0.077;
0; Mismatches 110; Indels
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFFWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,052
CLASSIFICATION: 510
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REFERENCE/DOCKET NUMBER: 466
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53.1%;
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NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,7
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Best Local Similarity 53.1;
Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PRO-
TITLE OF INVENTION: OR
UNDER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 601578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-878-9655
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EDNESS: single
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MEDIUM TYPE: Diskett
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US-08-814-052-18
                                                                                                          2075 C 2075
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US-08-814-052-18
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Best Local Similarity
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PCT-US95-06815-1
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                                  2872 CGACGACCTGCGCGGGCCGTCTCGGACGCCGACGACCTCTGCGC 2931
237 ggtggggggggggggggggcgtttcgtgcagggggcgccgccgctggtcgccttcctcga 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCFODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
join (587..832, 918..995, 1078..1089, 1189..1260,
1333..2304, 2452..2520, 2614..3024)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06815
FILING DATE: 31-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, Suite 6400 COUNTY: U.S.A. ZIP: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,781
FILING DATE: 03-June-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9506815 GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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996...1077
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CORRESPONDENCE ADDRESS:
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NAME/KEY:
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LOCATION:
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LOCATION:
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PCT-US95-06815-1
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APPLICANT:
                                                                                                                                297 c 297
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                                                                                                                                                                                                2688 GGGGGGGACGCGGGCCTGCTGAGCGGGGCCAACCCTGTGCGGCGGGGACGTGTCGATGCT 2747
                                                                                                   60 gacccgggatccctacgcggtgcggatgaccttccacctccccggagacgcctgtgac 119
                                                     3; Gaps
                                                                                                                                                                                                                                                                                                      177 cgacgtccacatcgccccgaccgacccgagggcctgtcggacgtctccatccggctcca
                                                                                                                                                                                                                                                                                                                                237 ggtgggcgcgcgcgcgcctcttccgtgcaggcgcccggcgctggtcgcctcga
     Length 3187;
Score 49; DB 5; Length 318
Pred. No. 0.076;
0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08706037
Patent No. 5770419
GENERAL INFORMATION:
APPLICANT: Xu, Feng
APPLICANT: Wahleithner, Jill A.
TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
TITLE OF INVENTION: ENHANCED ACTIVITY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4526.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/08/706,037
FILING DATE: 30-AUG-1996
CLASSIEFCATION: 435
PRIOR APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY APERICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY APERICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
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TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
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  Query Match 12.0%;
Best Local Similarity 53.1%;
Matches 128; Conservative
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ADDRESSEE: No. 59481210 No. 5948121disk of No. 5948121th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2812 CCACTGCCACATCGCCTGGCACGTCTCGGGCGCCTGGGCGTCGTCTACCTCGAGCGCG 2871
                                                                                                                                                                                                                                                                                                                                                                                                             60. gacccggggatccctacgcggtgcggatgaccttccacctccccggagacgcgctgtgac 119
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     2752 GCCGGCGTTCGGGTGGTGGTGCTTCCGGGCCGAACCCGGGCGCCTGTT
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                                                                                                                                       CCATION: Join(586..831, 917..994, 1079..1090, 1193..1264, LOCATION: 1337..2308, 2456..2524, 2618..3028)
                                                                                                                                                                                                                                              Query Match 12.0%; Score 49; DB 1; Length 3192; Best Local Similarity 53.1%; Pred. No. 0.076; Matches 128; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dorrit Aaslyng
APPLICANT: Sorensen, Niels H.
TITLE OF INVENTION: Laccases with Improved Dyeing
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,485
FILING DATE: 20-MAY-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORREX.7AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFREENCE/POCKET NUMBER: 4639.204-US
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/09083485
; Patent No. 5948121
                                                                                 DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGIH: 3192 base pairs
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                                           single
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                   TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                      NAME/KEY:
                                                            TOPOLOGY:
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New York
                                                                                                                                                                                                                                              2693 GGCGCGGGACGCGGGCCTGCTGAGCGGGGCCAACCCTGTGCGGCGGGACGTGTCGATGCT 2752
                                                                                                                                                                                                                                                                                                                              2753 GCCGGCGTTCGGGTGGTGCTGTCCTTCCGGGCCGACAACCCGGGCGCCTGGCTGTT 2812
                                                                                                                                                                                                                                                                                                                                                                                                120 ctgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcg---gcgacgg 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: XU, Feng
APPLICANT: SCHNEIDER, Palle
APPLICANT: OXENB LL, Karen M.
APPLICANT: AASLYNG, DOITIL A.
TITLE OF INVENTION: PURIFIED MYCELIOPHTHORA LACCASES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCFODING SAME
                                                                                                                                                                 3;
               join(587..832, 918..995, 1080..1091, 1194..1265, 1338..2309, 2457..2525, 2619..3029)
                                                                                                                      Length 3192;
                                                                                                                 Score 49; DB 1; Length 319
Pred. No. 0.076;
0; Mismatches 110; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,661A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4184.010-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,146
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08940661A Patent No. 5795760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BERKA, Randy Michael
APPLICANT: BROWN, Stephen H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                    Query Match 12.0%;
Best Local Similarity 53.1%;
Matches 128; Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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               ; LOCATION:
; LOCATION:
US-08-706-037-26
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                                                                                                                                            3; Gaps
                                                         join(586..831, 917..994, 1079..1090, 1193..1264, 1337..2308, 2456..2524, 2618..3028)
                                                                                                                  Query Match 12.0%; Score 49; DB 2; Length 3192; Best Local Similarity 53.1%; Pred. No. 0.076; Matches 128; Conservative 0; Mismatches 110; Indels
STRANDEDNESS: single
TOPOLOGX: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                             ) NAME/KEY: CDS
; LOCATION: join
; LOCATION: 1337
US-09-083-485-1
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Search completed: July 18, 2002, 11:34:28 Job time: 11458 sec

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1139.217 Million cell updates/sec
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                                                                                                                                    July 18, 2002, 10:12:53; Search time 4821.96 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                     13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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gb_gss:* em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* 1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estin:*
5: em_estpo:*
6: em_estpl:*
7: em_estpl:*
10: gb_est2:*
11: gb_htc:* EST:* Database:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AL053013 Drosophil AL053013 Drosophil BL717260 103101861 BC8158938 1024060E0 BC843065 1024001D0 AL066051 Drosophil AC075896 Pan trog1 AC077010 Pan trog1 AC05464 Pan trog1 BC274193 WHE2230_F BE360790 DG1_67_C1 AC058290 Pan trog1 AC066051 Drosophil AC066051 Drosophil BE360790 DG1_67_C1 AC058290 Pan trog1 BE360790 HE2230_F BE360790 HE2230_F BE360790 HE2230_F BE222743 WHE220_C Description CNS0091P BI717260 BG858938 BG843065 CNS006XK AG075896 AG077010 AU183257 AG054664 BG274193 BE366790 AG058290 AG058290 AG058290 AG058290 AG058290 AG058290 П Query Match Length DB 61.8 60.4 Score Result 132 100 111 112 113 114 116 116 No. O Oυ O O

/organism="brosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCI-98"

OCTNBD011	Drosophil	HVSMED001	HVSMEC001	SP_1032_A	WHE0902_E	WHE2952_D	HVSMEn001	PSR6697 I	Pan trogl	WHE2622_B	WHE0332_A	AV403894	HVSMED001	Drosophil	HVSMEf000	HVSMED001	UI-R-CZ0-	AL508912		PSR6874 I	LMAJFV1_1		ENTLG55TF	nbeb0003C	Drosophil	Pan trogl	L2031k.d_
97131579	AT.106054	R1958982	BG310059	AZ196424	BE606915	BI479101	BI958084	BE427747	AG060835	BM135627	\sim	AV403894	BF629308	AL098882	BF255377	BF629131	B1278791	AL508912	AL098882	BE427870	AQ852043	AG130935	AZ672521	AQ856496	AL066742	AG042970	BH018881
A7131579	NOTO TAKE	R1958982	BG310059	AZ196424	BE606915	B1479101	BI958084	BE427747	AG060835	BM135627	BE426827	AV403894	BF629308	CNS010EW	BF255377	BF629131	BI278791	AL508912	CNSOIOEW	BE427870	AQ852043	AG130935	AZ672521	AQ856496	CNS0072Q	AG042970	BH018881
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ALIGNMENTS

	GSS. fruit fly. M Drosophila melanogaster Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkely Drosphila Genome Project (BDCP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Canoer Genetics at the Roswell Park Canoer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDCP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for upbridization from the BACPAC Resource Center can be found at http://hacnac.made buffalo.edu/drosophila hac.htm.	
0 2	KEYWORDS SOURCE ORGANISM REFERENCE	AUTHORS TITLE JOURNAL	COMMENT	FEATURES SOURCE

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Local Similarity
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BI717260
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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- Web: www.genoscope.cns.fr.

- Obtermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                             57 cgagacccgggatccctacgcggtgcggatgaccttccacctccccggagacgcctgt 116
                                                                                                                                                                                                                                         620 CCSSKSVCGTSCSSSSSCSSSSSTSSSSTSKSSSSGSSSSSSSYTTSKSTSASG 679
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                                                                                                                                                                          Gaps
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Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
I (bases 1 to 925)
                                                                                                                                                                                                                                                                                              117 gacctgggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacgg
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                                           511 others
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                                                                                                                          Query Match 15.2%; Score 61.8; DB 12; Best Local Similarity 11.7%; Pred. No. 0.59; Matches 41; Conservative 177; Mismatches 133;
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                                           172
/clone="BACR19D16"
/note="end : TET3"
61 c 61 g
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Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii

Chlamydomonas reinharde:

Chlamydomonadaceae; Chlamydomonas.

I (bases 1 to 684)

S Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.

Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031

L Unpublished (2001)

Contact: Charles Hauser

DCMB Box 91000
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BI717260.1 GI:15692955
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/strain="CC-1690 wild type mt+ 21gr"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda 2ap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II ilbrary, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 cccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgacct 121
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                                                                                                                                                                                                    Length 925;
                                                                                                      511 others
                                                                                                                                                                                                       Score 60.4; DB 12;
Pred. No. 0.99;
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                                                                                                                                                                                                                                                      43; Conservative 162; Mismatches
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/db_xref="taxon:7227"
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/clone="BACR19D16"
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61 9
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Durham, NC 27708-1000
                                                                         /note="end
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Fax: 919 613 8177
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122
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cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H2C2 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda 2AP II (Stratagene) in the Ecoki (5') and Xhori (all sites: pBluescript II SK- plasmids were excised from the lambda a ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806.
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Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 704)
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Contact: Charles Hauser
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                                                                                                                                                                                                                                                                                                                         Length 684;
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Pred. No. 4.9;
0; Mismatches 140; Indels
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Location/Qualifiers
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Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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illarity 50.0%;
Conservative
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/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAPP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in the light, TAP medium in the dark, HS (minimal) medium in the poly mRNA was purified from each sample, pooled and cDNA synthesized. The CDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRN [6', and XhoI [3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
Andryses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Unpublished (2000)
Contact: Charles Hauser

DCMB Box 91000
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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BG843065.1 GI:14224249
EST.
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Pred. No. 8.1;
0; Mismatches 134; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; 50.2%; I
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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Matches 135; Conservative
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ORIGIN
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                                                                                            /note="Vector: pBluescript II SK-; Site_I: ECORI; Site_2:
XhO1; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAPP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in the light, TAP medium in the dark, HS (minimal) medium in the plup. TAP medium in the dark, HS (minimal) medium in the poly mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the Ecork (5') and XhO1 (3') sites. pBluescript II SK-plasmids were exclsed from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit ALO66051
                                                   /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information places see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggaccgcgccctcttccgtgcaggcgcccggctggtcgccttcctcgaccgcacgga 305
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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/strain="CC-1690 wild type mt+ 21gr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 cgcgctcggcaagatcctcgccgaggagcagaacgccggc 405
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                           /db_xref="taxon:3055
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Drosophila melanogaster
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AG075896.1 GI:16627698 GSS; GSS (genome survey sequence).
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-068024.R.
Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG075896 816 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-068024.R, genomic survey sequence.
AG075896
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Direct Submission
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                                                                                                                                                                                                                                                                  melanogaster"
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N09"
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit
            Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRP.
Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
                                                                                                                                                                                                                                                                                                                                                                                                                           122 gggcgttcggccgggagctgctgctcgacgggatcaaccgcccgagcggcgacggcgacg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 844)
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9 g 66 t 29 others
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rel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                 1. 816
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-068024.R"
                                                                                                                                                                                                                                                                                                                                       Score 53.4; l
Pred. No. 12;
                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanze
276 c 418 g 66
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                                                                                                                 R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
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                                                                         Sequencing: M13Rev
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-071G05.R.
Pan troglodytes
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Pan troglodytes DNA, clone: PTB-071G05.R, genomic survey sequence.
AG077010
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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ilarity 14.5%; Pred. No. 19;
Conservative 147; Mismatches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila me
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR11216"
/note="BaCR11216"
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45; Conserv
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/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="1560487"
/clone_lib="Rice cDNA from immature leaf including apical
meristem (under short day condition)"
/dev_stage="immature leaf including apical
a 236 c 125 g 48 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG054664.1 GI:16592107
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-040G15.R.
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                     264 tgcaggcgccccgccgctggtcgccttcctcgaccgcacggacaagtcggtgccgctcgg 323
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                       Length 447;
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                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                     ; Score 51.8; DB
; Pred. No. 23;
0; Mismatches
                                                                          /organism="Oryza sativa"
                                       Location/Qualifiers
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R.Site 1 : SacI
R.Site 2 : SacI.
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Best Local Similarity 54.9%;
Matches 101; Conservative
 PROJECT - 'RGP'.
                 E60487_97A.
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Spermatophyta: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Ehrhartoideae; Oryzeae; Sasaki,T. and Yamamoto,K.

Rice cDNA from immature leaf including apical meristem (2001) Context: Takuji Sasaki
Unpublished (2001)
Context: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-860. Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7441
Fax: 81-298-38-74458
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehirro-chou, Tsurumi *ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 gacgcgcctgtgacctggggcgttcggccgggagctgctgctcgacgggatcaaccgcccg 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 agcg---gcgacggcgacgtccacatcgccccgaccgacccagaggcctgtcggacgtc 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 957;
                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
| 437 c 412 g 28 t 41 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                             Location Qualifiers
1. 957
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-071G05.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52.2; I
Pred. No. 19;
                                                                                                                                                                                                                          Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                       Sequencing: M13Rev
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AU183257.1 GI:13896921
                                                                                                                                                   tracking errors.
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53.1%;
                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 127; Conservative
 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Fax: 706 542 1805
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BE360790.1
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Best Local S
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aegilops speltoides.
Aegilops speltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akhunov, E., Anderson, O.D., Chao, S., Chin, A., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Kianian, P., Lazo, G.R., Miller, R., Otto, C., Rausch, C.J., Seaton, C.L., Simons, K., Tong, J.C. and Zhang, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG274193 469 bp mRNA linear EST 21-FEB-2001
WHE2230_F05_K10ZS Aegilops speltoides anther cDNA library Aegilops
speltoides cDNA clone WHE2230_F05_K10, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 aacagactctgggtgacttcgaggacagcctggaggccgcgctcggcaagatcctcgccg 388
                                                                                                                                                                                                                                       gectgicggacgictecaiceggetecaggigggegegggacegeecteteegigeag 268
                                                                                                                                                                                                                                                                                                                                                                                                  269 gegeceegeegetggtegeetteetegaeegeaeggaeaagteggtgeegeteggteagg 328
                                                                                                                                                                                                                       cottocacotococogagacgogoctgtgacotgggcgttcggccgggagotgctgctcg 148
                                                                                                                                                                                             Gaps
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                                                                                                                                                             Length 770;
                                                                                      BAC Library"
34 others
                                                                                                                                                                                            Indels
                                                                                                                                                                                        0; Mismatches 169;
                                                                                                                                                              DB 12;
                                                                                   /clone_lib="PTB Chimpanzee Male
428 c 226 g 21 t
1. .770
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-040G15.R"
                                                                                                                                                             Score 51.4; I
Pred. No. 26;
                                                         /sex="male"
/cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Email: oandersn@pw.usda.gov
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                                                                                                                                                             12.6%;
ilarity 46.7%;
Conservative
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DG1_67_C10.b2_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA
sequence.
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/organism="Aegilops speltoides"
/cultivar="F2 from 2-12-4-8-1-1-(1) x P136909-12-811-(1
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The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Pred. No. 35;
0; Mismatches 150;
                                                                                                                                                                /db_xref="taxon:4573
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Contact: Cordonnier-Pratt MM
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ORIGIN

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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRx cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr ) Determination of this BAC-end sequence was carried out as part of a
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
tel.181-45-503-911, Fax:81-45-503-9110)
Clones are derived from the chimpanzee BAC library PTB This BAC en
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSOO6XK
Drosophila melanogaster genome survey sequence 77 end of BAC #
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 ccacctccccggagacgcgcctgtgacctgggcgttcggccgggagctgctgctcgacgg 152
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 gtcggacgtctccatccggctccaggtgggcgcggaccgcgccctcttccgtgcaggcgc
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                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
509 c 521 g 14 t 58 others
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Pred. No. 34;
0; Mismatches 161;
                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-045C04.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fly), genomic survey sequence. AL066051
                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                            : pKS145
                                                                                                                                   Sequencing: Ml3Rev
                                                                                        clone tracking errors.
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ilarity 48.2%;
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R.Site 2
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-045C04.R.
                                                                                                                                                                       1. .504
//crganism="Sorghum bicolor"
//db_xref="taxon:4558"
//db_cref="taxon:4558"
//clone_lib="Dark Grown 1 (DG1)"
//clone_lib="Dark Grown 1 (DG1)"
//cote="Corgan: 5-day-old dark-grown seedlings; Vector:
Lambda Zap: Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."
- 216 c 133 g 64 t
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                  to exclude PolyA, vector and regions threshold for highest quality sequence
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Pan troglodytes DNA, clone: PTB-045C04.R, genomic survey sequence.
AG058290
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50.6; DB 10;
Pred. No. 35;
0; Mismatches 169;
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                                                                                                        High quality sequence stop: 477 POLYA-No.
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                    Sequences have been trimmed
below Phred quality 16. The
Email: mmpratt@uga.edu
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                                                                                   Seq primer: JEN REV
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pateter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 gacccgggatccctacgcggtgcggatgaccttccacctccccggagacgcgcctgtgac 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI4N09"
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Murine Mphi type I C glutamicum prote C. glutamicum SRT S. epidermidis ope Human carbonic anh

Human secreted pro

Polypeptide sequen Rat RC-9 implicate Rat allograft infl Rabbit beta 2 inte Rabbit beta-integr Rabbit beta-integr Rabbit alpha-d prot Rabbit alpha-d prot Human polypeptide MEAV vaccine. Syn Arabidopsis thalia

HSV-2 strain SB5 C Arabidopsis thalia Cellulomonas fimi

Minimum DB s Maximum DB s

Database

Result

Searched:

Sequence:

Title:

Run on:

Neisseria meningit Human ORFX ORF2258 Human glutamate re

Propionibacterium

S. epidermiuis orc Neisseria gonorrhe

epidermidis ope

Drosophila melanog

Human glutamate Protein encoded

HSV-2 strain SB5 C HSV-2 strain SB5 C Arabidopsis thalla

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SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosuppressive agent; mypocholesterolaemic agent; enzyme inhibitor; antimigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; blomass.
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
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AAW72840
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AAU02198
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                                                                                                                       Streptomyces netropsis.
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N-PSDB; AAZ49731.
WO200000613-A1.
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 RESULT
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Streptomyces golde
Streptomyces albus
Propionibacterium
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Arabidopsis thalia
Arabidopsis thalia
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Novel human diagno
Novel human diagno
                                                                                         (without alignments)
115.010 Million cell updates/sec
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2. (SIDSS/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3. (SIDSS/gcgdata/geneseqp-embl/AA1981.DAT:*
4. (SIDSS/gcgdata/geneseqp-embl/AA1981.DAT:*
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1 MSFLVSEELSFKIPVELRYE.......FEDSLEAALGKILAEEQNAG 135
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                                                                            July 18, 2002, 14:15:03; Search time 130.38 Seconds
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                                                      747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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AAY77574
ABG05279
ABG20257
                                                       OM protein - protein search, using sw model
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AAY44650
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606
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446
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77
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WPI; 2000-147269/13.
                                                                                                                                                                                                 Similarity
                                                                                                                                            135 AA;
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Matches 116;
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                                                                                                                                                                                    Query Match
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                                                             The present sequence is S. netropsis SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycelium in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents,
                                                                                                                                                                                                                                                                                                                                                          VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
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                                                                                                                                                                                                                                                                                           1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
                                                                                                                                            hypocholesterolaemic agents, enzyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                                                                                                          SsgA; liquid culture; filamentous bacteria; secondary metabolite; mycellum; antibiotic, antitumour agent; immunosupressive agent; hyporholesterolaemic agent; enzyme inhibitor; antihigraine agent; herbicide; antiparasitic agent; ruminant growth promoter; bioinsecticide; receptor agonist; antagonist; biomass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
Reducing branching and enhancing fragmentation in filamentous microorganisms used to improve their liquid culturing properties
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Pred. No. 1.5e-72;
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(NEWE-) NEDERLANDSE ORG WETENSCHAPPELIJK ONDERZO.
                                                                                                                                                                                                                                                                  Mismatches
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                                       English.
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100.0%;
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                                      Fig 5; 60pp;
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                   135 AA;
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The present sequence is S. griseus SsgA protein. SsgA reduces branching and fragment septation and enhances fragmentation of mycellum in liquid culture resulting in lower viscosity of culture broths. Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, enzyme inhibitors, antimigralne agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  culture; filamentous bacteria; secondary metabolite;
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Pred. No. 1.5e-62;
7; Mismatches 12; Indels (
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85.98;
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Filamentous bacteria can be transformed with ssgA gene-containing plasmid to enhance the production of secondary metabolites such as, antibiotics, antitumour agents, immunosuppressive agents, hypocholesterolaemic agents, nazyme inhibitors, antimigraine agents, herbicides, antiparasitic agents, ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                                                                                                                                     1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD
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                                                                                                                                                        78.6%; Score 544; DB 21; 77.8%; Pred. No. 2.5e-55;
                                                                                                                                                                                       12; Mismatches
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121 dealdrilaeegnag 135
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Matches 105; Conserv
                                                                                                          135 AA;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                             61 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
                                                                                                                                                  Gaps
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ruminant growth promoters, bioinsecticides, receptor agonists and antagonists and biomass.
                                                                                                            Length 135;
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                                                                                                                                                30; Indels
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                                                                                                            64.5%; Score 446; DB 21;
63.0%; Pred. No. 6.4e-44;
ive 20; Mismatches 30
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Jen S, Carter
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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e J, Zhang Y,
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                                                                                                          Query Match
Best Local Similarity 63.09
Matches 85; Conservative
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                                                        135 AA;
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
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06-APR-1999;
08-APR-1999;
16-APR-1999;
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25-MAR-1999;
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         and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthtalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                           119 vrftggeplirpslenlvaatstirrtngtppitalttngigldrrvdglveagldrvni 178
                                                                                                                                                                                                                                             ----- LDRTDK 103
                                                                                                                                                                                                                              12 KIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLD------GINRPSGDGDVH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                 Length 400;
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                                                                                                                                                                                                                                                                                                                           SV------PLGQEQTLGDFEDSLEAALGKILAEEQNA 134
                                                                                                                                                                              11.6%; Score 80.5; DB 22; 24.4%; Pred. No. 0.99; iive 19; Mismatches 61;
                                                                                                                                                                                                                                                                            63 IAPTDPEGLSDVSIRLQVGADRALFRA-GAPPLVAF------
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, Jen S, Carter D;
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L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                        Local Similarity 24.4% tes 39; Conservative
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                                                                                                                                             400 AA;
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Matches
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by constant and constant and sequences are used in the treatment, prevention and diagnosis of medical conditions caused by constant and the disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

December 18 also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with ache vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies contacting therefore treat P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed presence of the connectors of th
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Pred. No. 1.9;
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99US-0123548.
99US-0125788.
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18 - JUN - 1999;
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15-JUL-1999;
16-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
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29-JUN-1999;
30-JUN-1999;
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20-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                               Indels 24; Gaps
                                                                                                                                                                                                                                                                    4 LVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGR-----ELLLDGINRPSG 57
                                                                                                                                                                                                                                10.7%; Score 74; DB 21; Length 456; 25.7%; Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 32224.
                                                                                                                                                                                                                                                                                                                  58 DGDVHIAP----TDPEGLSDVSIRLQVGADRALFRAGAPPL 94
                                                                                                                                                                                                                                                  16; Mismatches 35;
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990S-0159330.
990S-0159331.
990S-0159637.
990S-0159584.
990S-0160747.
99US-0160767.
                                                                        9908-0160770
9908-0160814
9908-0160816
9908-0160980
9908-0160981
9908-0161405
9908-0161360
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9908-0161360
9908-0161361
9908-0161361
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990S-0123180.
990S-0123548.
990S-0125788.
990S-0126785.
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99US-0130449.
99US-0130510.
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99US-0128714.
99US-0129845.
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                                                                                                                                                                                                                                         Best Local Similarity 25.79
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
14 - OCT - 1999;
21 - OCT - 1999;
22 - OCT - 1999;
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28-OCT-1999;
29-OCT-1999;
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26-OCT-1999;
28-OCT-1999;
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08-APR-1999;
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21-APR-1999;
23-APR-1999;
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25-MAR-1999
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Human cytoskeletal protein, HCYT; cell proliferation; immunological; reproductive; nervous disorder; cytostatic; immunosuppressive; anti-HLV; anti-diabetic; antiarteriosclerotic; dermatological; anti-inflammatory; anti-infertility; vasotropic; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cytoskeletal proteins useful for diagnosing, treating preventing cell.proliferative, immunological, reproductive, developmental and nervous disorders
                                                                                                                                                                                                                                                    4 LVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGR-----ELLLDGINRPSG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Azimzai Y;
                                                                                                                                                                                                                        24;
                                                                                                                                                                                                     DB 21; Length 456;
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                                                                                                                                                                                                                                                                                      Human cytoskeletal protein (HCYT) (clone 3768043).
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                                                                                                                                                                                                    10.7%; Score 74; 25.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                           AAY77574 standard; Protein; 806 AA.
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Baughn MR;
          990S - 0159584 .
99US - 0160741 .
99US - 0160768 .
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99US - 0160981 .
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98US-0155228
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Matches 26; Conservative
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Patterson C, Lal P,
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N-PSDB; AAZ58979.
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         18-0CT-1999;
21-0CT-1999;
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21-0CT-1999;
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25-0CT-1999;
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26-0CT-1999;
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26-OCT-1999;
28-OCT-1999;
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19-AUG-1998;
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99US-0151930.
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99US-0153070.
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990S-0148341.
990S-0148684.
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990S-0149368.
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99US-0150566.
99US-0150884.
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99US-0154039.
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99US-0156596.
99US-0157117.
          99US-0144814.
99US-0145086.
99US-0145088.
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99US-0145087.
99US-0145089.
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99US-0145218.
99US-0145224.
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990S-0146386.
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990S-0147038.
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99US-0155139.
99US-0155486.
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99US-0145913.
99US-0145918.
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99US-0147260.
99US-0147303.
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990S-0149929.
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 99US-0144884
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Claim 20; SEQ ID No 35638; 103pp; English.
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                                                                                                                  The invention provides human cytoskeletal proteins (HCYT) and nucleic acids encoding the proteins. The HCYT polypeptides can be expressed by standard recombinant methodology. The HCYT polypeptides, modulators and antibodies are useful for treating or preventing a disorder associated with decreased and increased expression or activity of HCYT in mammals. The polypeptides are also useful for diagnosing HCYT activity disorders such as cell proliferative, immunological, reproductive, developmental and nervous disorders. Sequences AAY77569-576 represent HCYT
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494 elkfellekdpyal-----dvpnt-afgrehspygpsplgwpssetraflspptlle 544
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19;
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Pred. No. 19;
3; Mismatches
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                                         84pp; English.
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23-AUG-2000; 2000US-0649167.
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                                         Page 69-70;
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N-PSDB; AAS69466.
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Best Local Similarity
Matches 47; Conserv
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (Cr identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving cuprissed applied in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. ABG00010-ABG30377 represent movel human cand sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat fip. wipo.int/pub/published_pct_sequences.
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507 elkfellekdpyal-----dvpnt-afgrgsrgpgnpldhqitnergesscdrltdp 557
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23-AUG-2000; 2000US-0649167
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The present invention describes human secreted proteins obtained from human fetal brain, fetal kidney or adult blood contains the present sequence represents a human secreted protein. The human secreted proteins, and polynucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, issue growth activity, activity, the human sectivity is the production of the property of the property of the property of the property of the production activity, activity, activity, the production of the production of the production activity, activity, activity, activity, the production of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding secreted human proteins potentially useful as, e.g. immunostimulators
                                                                                                                                                                                                                                                                                                           Agostino MJ, Clark HF, Collins-Racie LA, Evans C;
Fechtel K, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
Steininger RJ, Treacy M, Wong GG;
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                                           98WO-US27140.
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97US-0068379
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20-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 ELRYE--TRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDG-----DV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 HIAPTDPEGLS---DVSIRL-----QVGADRAL------FRAGAPPLVAF-- 97
                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferation; differentiation; immune stimulating; vaccine; suppression; haematopoiesis regulation; tissue growth; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; cadherin; tumour invasion suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; immunostimulator; nutrition; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 72.5; Di
; Pred. No. 21;
13; Mismatches
                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 50616; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY24788 standard; Protein; 1369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 -- LDRTDKSVPLGQEQTLGDFEDSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 psldkmdgsmpsemessrndtkddl 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein am728_60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5%;
29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777 AA;
N-PSDB; AAS84444
                                                                                                                                                                                           biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1999
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6
                                                                                                                                                                                          1100 elkfellekdpyal-----dvpnt-afgrgsrgpgnpldhqitnergesscdr1tdp 1150
                                                                                                                                                                                                                                                                                                 Human; secreted protein; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimulant; dermatological; antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; cytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour;
                                                                                                                                                                                                                                                                97
                                                                         Gaps
                                                                                                                              16 ELRYE--TRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDG-----DV 61
                                                                                                                                                                                                                                                                ---FRAGAPPLVAF--
      Length 1369;
                                                                  41; Indels
10.5%; Score 72.5; DB 20; 29.0%; Pred. No. 44; tive 13; Mismatches 41;
                                                                                                                                                                                                                                                            62 HIAPTDPEGLS---DVSIRL----QVGADRAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU39009 standard; Protein; 1369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            1211 psldkmdgsmpsemessrndtkddl 1235
                                                                                                                                                                                                                                                                                                                                                                                    98 -- LDRTDKSVPLGQEQTLGDFEDSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein am728_60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                     Conservative
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tumour inhibition; gene therapy.

AAY24788 RESULT

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Homo sapiens W09932614-A1 01-JUL-1999. us-09-749-185-9.rag

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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation activity or may induce production of other or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune deficiencies and disorders e.g. severe combined cornium to disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, in the treatment of burns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and ulcers; as well as in treatment of purns, incisions and solved in sease, diseases, diseases (Huntington's disease, and Shy Drager syndrome, infections, and of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory powel disease, ulcers, bone regeneration. The protein, having activin or inhibins related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The proteins and nucleic acids are also useful as food supplements. The proteins and nucleic acids are also useful as food supplements. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٠.
ن
                          graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; Huntington's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||::| |||||
| 1100 elkfellekdpyal-----dvpnt-afgrgsrgpgnpldhqitnergesscdrltdp 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELRYE--TRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDG-----DV 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans C;
Wong GG;
autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1369;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lavallie E, Collins-racie LA, F
7, Steininger RJ, Spaulding V,
Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%; Score 72.5; D
29.0%; Pred. No. 44;
:ive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system disorders (e.g. stroke) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 482-487; 619pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2000; 2000US-0539330
04-DEC-2000; 2000US-0729674
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Best Local Similarity 29.00.
Best Local Similarity 29.00.
The 42; Conservative
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                                                                                                                                                                                     food supplement; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCoy JM, La
Agostino MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639363/73.
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                                                                                                                                                                                                                                                                                                                              WO200175068-A2
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                         11-0CT-2001
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Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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   NAMES OF COLUMN 
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The present invention provides a number of murine and human Ibal derivatives, which are capable of inhibiting the function of cells with monocyte or macrophage activity. These can be used as immunomdulators to prevent and treat diseases caused by a decrease or increase in the activity or the function of macrophages or an activator or an inhibitor of the function of cells of macrophage type. The present sequence is one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK------ILAEEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 slkrmleklgvpkthlelkrlirevssgseetf-sysdflrmmlgkrsallrmilmyeek 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 AFG-----RELLLDGINRP-----SGDGD------VHIAPTDPEGLSDVSIRLQV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A macrophage function modifier useful for preventing and treating diseases caused by the increase or decrease in macrophage activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 afgllkaggeerleginkgflddpkysndedlpskleafkvkymefdlngngdidi---m
                                                                                                                                                                                                                    Human; mouse; immunomodulatory; monocyte; macrophage; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                             (KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
(IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
(MOCH ) MOCHIDA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 71.5; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 2.9; 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the function of cells of macropha of the derivatives of the invention.
             AAG90040 standard; Protein; 129 AA.
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98 -- LDRTDKSVPLGQEQTLGDFEDSL 120
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                                                                                                   AAB98959 standard; Protein; 147
                                                                                                                                                                                                                                                                                                                                         99JP-0260793.
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                                                                                                                                                               20-AUG-2001 (first entry)
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                                                                                                                                                                                            Murine Mphi type IbaI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-313369/33.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH25799
                                                                                                                                                                                                                                                                              JP2001078775-A.
                                                                                                                                                                                                                                                                                                                                         14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1999;
                                                                                                                                                                                                                                                                                                             27-MAR-2001.
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                                                                                                                                AAB98959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function
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                                                                                    AAB98959
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26-SEP-2001 (first entry)

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteriu are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yokoi H;
                                                                                                                                                                                        Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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Senoh A, Ikeda M, Ozaki A;
                                                                                                                 C glutamicum protein fragment SEQ ID NO: 3794.
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum.
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Best Local Similarity 27.68
Matches 29; Conservative 90 35 g οχ ò

Search completed: July 18, 2002, 14:15:04 Job time: 10334 sec

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US-09-413-814-80
Sequence 80, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
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US-08-171-385-5
US-08-485-618-103
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APPLICANT: Cloo, Paul M
APPLICANT: Cloo, Paul M
APPLICANT: Cloo, Paul M
APPLICANT: Cloodberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Meller, Joachin
APPLICANT: Meller, Joachin
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA Sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA Sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA Sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: Hans
TITLE OF INVENTION: HANS
FILER APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
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Best Local Similarity 31.5%; Pred. No. 4.2;
Matches 35; Conservative 8; Mismatches
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44; Indels

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635 PFGNGE---RMYHSGDLALVRGDGQ--VAFLGRRDHQIKIRGQRVELGEIESHLRGLEGI 689
                                                                                                                    68 PEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPL-GQEQTLGDFEDSLEA--- 122
                                                                                       15 VELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDG-----INRPSGDGDVHIAPTD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-GAMMA
NUMBER OF SCHENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                     Pred. No. 2.6; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,986A
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08015986A Patent No. 5532123
18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 76 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
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24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 amino acids
                     Best Local Similarity 29.0%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                              123 ALGKILAEEQN 133
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690 AAAVVQAESQH 700
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York COUNTRY: U.S.A.
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US-08-015-986A-10
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m
                                                                                                                                                                                                                         APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/21535
CURRENT APPLICATION NUMBER: US/09/413,814
EARLIER FILING DATE: 1999-10-07
EARLIER PILING DATE: 1999-10-07
BARLIER FILING DATE: 1999-10-07
SOFTWARE: PATON NUMBER: DE 198 46 493.2
SOFTWARE: PATON NOS: 107
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APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              875 MOVLGRIESSLGIRTTLRTLFEHPTLAQLASHLSSGAASTSAAAATALERGLTRPDGPSS 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 3079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VHIA-PTDP----EGLSDVSIRLQVGADRALF-----RAGAPPLVAFLDR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 PRVATPEEPFALTEGORAMWLECQKSADGALYNLGRTVRLGAGVDVAALRR 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Besellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Beyer, Stefan
APPLICANT: Babecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Petra
APPLICANT: Cino, Paul M
APPLICANT: Goldberty, Steven L
APPLICANT: Goldberty, Steven L
APPLICANT: Hofle, Gerhard
                   Gesellschaft fuer Biotechnologische Forschung mbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79.5; DB
Pred. No. 4.2;
8; Mismatches
                                             Bristol-Myers Squibb, Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44, Application US/09413814 Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Sorangium cellulosum
US-09-413-814-80
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US-09-413-814-44
                                                                                  APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 31.5%;
Matches 35; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 881
                                                                                                                                                                                                             APPLICANT: Hofle, Gerhard
                                                                   Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 80
LENGTH: 3079
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9:
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                                      Gaps
                                      33;
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 Length 259;
                                      34; Indels
                                                                         24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP--
 DB 1;
; Score 70.5; D
; Pred. No. 1.7;
18; Mismatches
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DB 4; Length 881;

10.8%; Score 75;

Query Match

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 08/015,986
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leeslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-028
TELEPHONE: 212-790-9090
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-8864/9741
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
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STREET: 1155 Avenue of the Americas
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
"NAUTER: IBM PC COMPATIBLE
"NEW P
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/015,973
                                                                                                                               US/08/446,363
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FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%;
24.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 24.19
Matches 27; Conservative
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                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-446-363-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: sir
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                                                                                                                                                                FILING DATE:
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                                                                                        GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-GAMMA
NUMBER OF SECHENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: U.S.A.
2 ID: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,973
FILING DATE: 10-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
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; Pred. No. 1.7;
18; Mismatches
                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: 8
STREET: 1155 Avenue of the Americas CITY: New York
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STREET: 1155 Avenue of the Americas
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Sequence 10, Application US/08446363
Patent No. 5891700
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEFAX: (212)790-9090
TELEFAX: (212)869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
                             Sequence 6, Application US/08015973 Patent No. 5604094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.19
Matches 27; Conservative
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unknown
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; MOLECULE TYPE: protein
US-08-015-973-6
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US-08-015-973-6
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69 - EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
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; Pred. No. 1.7;
18; Mismatches 34; Indels 3
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; Sequence 6, Application US/08448164
; Patent No. 522536
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP--
PatentIn Release #1.0, Version #1.25
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Length 259;

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-792-013-7
                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|::: | |::| : |: | 1::| 11 | 1 | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,929
FILING DATE: 23-JUN-1993
CLASSIFICATION NUMBER: 314
ATTORNEY/AGENT INFORMATION:
NAME: COTULZI, LAUTA A.
REGISTRATION NUMBER: 30742
REGISTRATION NUMBER: 30742
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
TELEPKS: 212 869-8864/9741
TELES: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
TEMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Patent No. 6160090
GENEAL INFORMATION:
GENEAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Grumet, Martin H.
APPLICANT: Marcol, Martin H.
APPLICANT: Marcol, Martin H.
APPLICANT: Marcol, S. Richard U.
TITLE OF INVENTION: A NEW CLASS OF RPTPASSES: THEIR
MINDER OF INVENTION: STRUCTURAL DOMAINS AND LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
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; Pred. No. 1.7;
18; Mismatches 34;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
CUNTRY: U.S.A.
ZIP: 10036
                                TELEPHONE: (212)790-9090
TELEFAX: (212)869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.1%;
Matches 27; Conservative 18
                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-448-164-6
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STRANDEDNESS: single
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; MOLECULE TYPE: protein
US-08-081-929-6
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US-08-081-929-6
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                                      33;
                                                                                                                                                  69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
                                                                                                                                                                        Length 146;
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                                      Indels
                                                                           24 PYAVRMTFHLPGDAPVTWA - - - FGRELLLDGINRPSGDGDVHIAPTDP - -
                                      34;
10.2%; Score 70.5; DB 4; 24.1%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastER to Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,013 FILING DATE: Filed Herewith CLASSIFICATION: 435
                                      18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Murry, Lynn E.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYTOKINES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
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Pred. No. 1;
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                                                                                                                                                                                                                                                                                Sequence 7, Application US/08792013 Patent No. 6204021
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRACE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
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nilarity 27.3%;
Conservative 1:
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IBM Compatible
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                                      27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
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IMMEDIATE SOURCE:
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81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK------ILAEEQ 132
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Patent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                 APPLICANT: Russell, Mary E.
APPLICANT: Utans, Ulrike
APPLICANT: Utans, Ulrike
TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Indels
                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COREATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,441B
FILING DATE: 21-DEC-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0:
TELECOMMUNICATION INFORMATION
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.3%;
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COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
Matches 33; Conserva
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02110-2804
GENERAL INFORMATION:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                          Sequence 5, Application US/08171385
Patent No. 5527884
GENERAL INFORMATION:
APPLICANT: MATY E. Russell
APPLICANT: Ulrike Utans
TITLE OF INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%; Score 69.5; DE illarity 27.3%; Pred. No. 1; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/Z Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AFG----RELLLDGINRP-----SGDGDVH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05433/006001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/171,385 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-361-441B-5; Sequence 5, Application US/08361441B; Patent No. 6077948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INPORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0543:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-171-385-5
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Best Local Similarity
Matches 33; Conserv
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                   133 N 133
                                                          127 N 127
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APPLICATION NUMBER: US/08/605,672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 103, Application US/08605672
Patent No. 5817515
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 581751561 Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: 111inois STATE: 111inois COUNTRY: United States
              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 10.0%; Score 69.5; DB Best Local Similarity 23.4%; Pred. No. 5.3; Matches 33; Conservative 17; Mismatches
                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27866/32797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2786
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                        38,659
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Floppy disk
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-485-618-103
MEDIUM TYPE:
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US-08-605-672-103
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170 WQRPLHLACEAVPTESEGLRSTS----CSVNHPIFQGGAQG--TFVVKFDVS----SKAS 219
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Patent No. 5831029
RAPELICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.25
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                                                                                    FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATONNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                              27866/32684
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FILING DATE: 530
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
TIME DATE: 23-DEC-1993
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APPLICATION NUMBER: US 08/173,497
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                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-4...
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: Patentin Release #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 LGD-----RLLMGASASSENN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LGDFEDSLEAALGKILAEEQN 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-605-672-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Search completed: July 18, 2002, 14:16:09 Job time: 9699 sec
                                FILING DATE: 21-DEC-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-943-363-103
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Patent No. 5337478

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION:
CORRESPONDENCE: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STAFE: Illinois
CONTYR: United States
COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ----VHIA,----PIDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32684

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECAX: 312-474-0448

TELECAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:

LENGTH: 494 anino acids

TYPE: ANION acids

TYPE: ANION acids

TYPE: ANION acids
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Pred. No. 5.3
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 LGD----RLLMGASASSENN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 LGDFEDSLEAALGKILAEEQN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 23.4%;
Matches 33; Conservative 1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-482-293A-103
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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123 TLLVGLSLELTVTVTVTVRNEGEDSYGTAITLYYPAGL------SYRRVSGQTQP 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 WQRPLHLACEAVPTESEGLRSTS----CSVNHPIFQGGAGG--TFVVKFDVS----SKAS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 37; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.0%; Score 69.5; DE Best Local Similarity 23.4%; Pred. No. 5.3; Matches 33; Conservative 17; Mismatches
US 08/362,652
                                                                                                                                       REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-474-6300
TELEFAX: 312-474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 animo acids
TYPE: amino acid
                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 LGD-----RLLMGASASSENN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 LGDFEDSLEAALGKILAEEQN 133
      APPLICATION NUMBER:
```

THIS PAGE BLANK USPION

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2002, 14:17:37; Search time 73.98 Seconds (without alignments) 175.345 Million cell updates/sec Run on:

US-09-749-185-9

Title: Perfect score:

692 1 MSFLVSEELSFKIPVELRYE......FEDSLEAALGKILAEEQNAG 135 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable regulator	probable requlator	probable regulator	probable regulator	amidophosphoribosy	carbonate dehydrat	endoglucanase C (E	hypothetical prote	amidophosphoribosy	conserved hypothet	probable ClpA/B-ty	translation initia	carbonate dehydrat	hypothetical prote	conserved hypothet	penicillin-binding	penicillin binding	conserved hypothet	carbonate dehydrat	probable alcohol d	hypothetical prote		ご		hypothetical prote	probable membrane	hypothetical prote	MHC class I RT1.C-	glycosyl hydrolase
SUMMARIES	Π	T37179	T36147	T35247	T35319	G81935	A22612	S15271	H84169	A81170	F87327	G83635	S12566	152551	H70678	AD3237	G97472	AC2691	B87500	A43641	Н69789	B90668	E85518	AE0358	C70963	B64993	G91017	A85862	σ	E75484
	BB	7	7	7	7	7	7	7	7	7	7	7	Н	7	7	~	~	7	7	N	_	7	7	N	N	7	ď	~	N	7
	Query Match Length DB	136	142	138	142	514	259	1101	313	514	818	902	611	260	291	408	757	757	347	260	346	732	732	891	265	1337	1534	1534	343	657
dР	Query	79.2	34.2	23.0	19.1	11.6	11.5	11.4	11.1	11.0	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.6	10.6	10.6	10.6	10.6	10.5	10.5	10.5	10.5	10.5	10.5
	Score	548	237	159	132.5	80	79.5	79	76.5	97	75.5	75.5	75	74.5	74.5	74.5	74.5	74.5	74	3	E,	73.5	3	3	73	73	73	73	72.5	72.5
	Result No.	-	7	ო	4	Ŋ	9	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

	probable oxidoredu	probable secreted	transcription regu	hypothetical prote	carbonate dehydrat	probable secreted	laminin alpha 5 ch	UDP-N-acetylmuramo	v-type ATP synthas	ionized calcium bi	allograft inflamma	hexokinase (EC 2.7	hypothetical prote	pyruvate dehydroge	hypothetical cytos	aldehyde dehydroge
	D64754	T36609	B90719	: C85569	CRHU3	T44873	: T10053	: AD0068	: D75487	JC4902	155617	S68694	: E70747	: F83676	: AE3254	: AC3043
	732 2	433 2	225 2	225 2	260 1	387 2	3635 2	458 2	690 2	146 2	147 2	484 2	626 2	328 2	389 2	505 2
	10.5	10.3	10.2	10.2	10.2	10.2	10.2	10.1	10.1	10.0	10.0	10.0	10.0	10.0	10.0	10.0
-	72.5	7.1	70.5	70.5	70.5	70.5	70.5	7.0	7.0	69.5	69.5	69.5	69.5	69	69	69
	30	31	32	33	34	35	36	37	38	39.	40	41	42	43	44	45

ALIGNMENTS

RESULT

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probable regulator - Streptomyces coelicolor (5) Species: Streptomyces coelicolor (5) Species: Streptomyces coelicolor (5) Species: Streptomyces coelicolor (5) Species: Older-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 (5) Accession: T37179 (5) Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, July 1999 (5) Accession: T37179 (6) A. Reference number: Z21598 (7) A. Reference number: Z21598 (7) A. Steule type: DNA (7) CSEE> A. CTOSS references: EMBL. AL096823; PIDN: CAB46964.1; GSPDB: GN00070; SCOEDB: SCOIl.09 A. Experimental source: strain A3(2) (5) Genetics: A. Genetics: A. SCOEDB: SCOIl.09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.2%; Score 548; DB 2; La Best Local Similarity 77.8%; Pred. No. 1.1e-46; Matches 105; Conservative 14; Mismatches 16;
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121 EAALGKILAEEQNAG 135 ò

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RESULT

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A;Gene: SCOEDB:SC5H1.03
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                                                       Query Match
Best Local Similarity 30.69
Matches, 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSFLVSEELSFKIPV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: OS-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Accession: T35247
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: 221573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Molecule type: DNA
A. Residues: 1-138 <OLI>
A. Residues: 1-138 <OLI>
A. Cross-references: EMBL:AL049587; PIDN:CAB40672.1; GSPDB:GN00070; SCOEDB:SC5F2A.05c
A. Experimental source: strain A3(2)
C. Genetics:
A. Genetics:
A. Genetics: Company company of the comp
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Accession: T33319
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A;Reference number: 221575
A;Reference number: 221575
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DDL
A; Residues: 1-142 < OLL>
A; Residues: 1-142 < OLL>
A; Residues: EMBL: AL049863; PIDN: CAB42928.1; GSPDB: GN00070; SCOEDB: SC5H1.03
A; Experimental source: strain A3(2)
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A;Gene: SCOEDB:SCE19A.24
C;Superfamily: Streptomyces coelicolor probable regulator SCE19A.24
                                                                                                                                                         Length 142;
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                                                                                                                                                                                                                             26;
                                                                                                                                                  34.2%; Score 237; DB 2;
39.7%; Pred. No. 4.1e-16;
iive 20; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.0%; Score 159; DB 2; Best Local Similarity 33.1%; Pred. No. 1.8e-08; Matches 40; Conservative 13; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T35247
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-138 <OLL>
                                                                                                                                                  Query Match 34.2%
Best Local Similarity 39.7%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 AELLAR 142
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amidophosphoribosyltransferase (EC 2.4.2.14) NMA0892 [similarity] - Neisseria meningil C; Species: Neisseria meningitidis
C; Species: OS-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C; Accession: G81935
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo i Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491 A; Reference number: A81775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-514 <-PAR>
A;Coss-references: GB:ALL62754; GB:AL157959; NID:g7379424; PIDN:CAB84172.1; PID:g737
A;Experimental source: serogroup A, strain 22491
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::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::
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                                                                                                                                                                                                                                                                    11 FKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ELRYETRDPYA-----VRMTFHLP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: purF; NMAO892
C;Superfamily: amidophosphoribosyltransferase
C;Keywords: glycosyltransferase; pentosyltransferase
F;2-514/Product: amidophosphoribosyltransferase #status predicted <MAT>
F;2/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                       GLSDVSIRLQVGAD-----RALFRAGAPPLVAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 GDA------PVTWAF-GRELLL--DGI------NRPSGDGDVHIAPTDP
                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 514;
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Indels
19.1%; Score 132.5; DB 2; 30.6%; Pred. No. 7.6e-06; ive 21; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 DRTDKSVPLGQEQTLGDFEDSLEAALGKILAEEQNAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 --- DSSCFNGIYQT-GDIDD---AYLDRLSAEKSGCG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 80; DB 23.0%; Pred. No. 5.1; ive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A22612
carbonate dehydratase (EC 4.2.1.1) III - horse
Alternate names: carbonate dehydratase III
C;Species: Equus caballus (domestic horse)
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T.M.

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QY g

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C;Species: Neisseria meningitid;
C;Species: Neisseria meningitid;
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: A81170
C;Accession: A81170
C;Accession: A017 H; Sauders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Olin, H; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignanl, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Accession: A81170
A;Accession: A81170
A;Accession: A81170
A;Residues: 1-514 <- TET>
A;Cross-references: GB:AE002423; GB:AE002098; NID:g7225913; PIDN:AAF41108.1; PID:g722
A;Cross-references: GB:AE002423; GB:AE002098; NID:g7225913; PIDN:AAF41108.1; PID:g722
A;Gene: NMB0690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amidophosphoribosyltransferase (EC 2.4.2.14) NMB0690 [similarity] – Neisseria meningi
                                                                                  Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium species NRC-1
Cispecies: Halobacterium species: Halobacterium species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE004437; NID: 910579744; PIDN: AAG18724.1; GSPDB: GN00138 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 FKIPVELRYET------RDPYAVRMTFHLPGDAPVTWAFGRELLLD--GINRPS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LSDVSIRLQVGADRALFRAGAPPLVAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ELRYETRDPYA------VRMTFHLP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: amidophosphoribosyltransferase
C;Keywoods: glytosyltransferase; pentosyltransferase
F;2-514/Product: amidophosphoribosyltransferase #status predicted <WAT>
F;2/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%; Score 76; DB 2; Length 514; llarity 23.0%; Pred. No. 13; Conservative 23; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | | : | : | | : | 224 -DRVREQVEAGSEEVGEDAYNLAELGIGTNVAVTELVGSVLLDEKAAG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 LDRTDKSVPLGQEQTLGDFEDSLEAAL------GKILAEEQNAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%; Score 76.5; 24.4%; Pred. No. 6.2
                                                     hypothetical protein Vng0096c [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 GD-----GDVHIAPTDPEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSFLVSEELSFKIPV--
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les. 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-313 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: VNG0096C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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C: Species: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change Ol-Dec-2000
C: Accession: S15271; A43636
R: Coutinho, J.B.; Moser, B.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Mol. Microbiol. 5, 1221-1233, 1991
A: Title: Nucleotide sequence of the endoglucanase C gene (cenC) of Cellulomonas fimi, it
A: Accession: S15271
A: Accession: S15271
A: Molecule type: DNA
A: Residues: I-1101 < COU>
A: Coustrain arry
A: Molecule type: DNA
A: Residues: 1-1101 < COU>
A: Coustrain arranalated the codon GAC for residues 361, 380, 400, 550, 670, and 8
A: Moser, B.; Gilkes, N.R.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Appl. Environ. Microbiol. 55, 2480-2487, 1989
A: Title: Purification and characterization of endoglucanase C of Cellulomonas fimi, clon
A: Reference number: A43636
A: Accession: A43636
A: Courter and A43636
A: Courter and A43636
A: Courter and A43636
A: Courter A43636
A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
    22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAP-----TDPEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 YETRDPYAV--RMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSI 76
                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-259 <WEN>
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Superfamily: carbonate dehydratase; carbon-oxygen lyase; hydro-lyase; zinc
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; zinc
F;4-258/Domain: carbonic anhydrase homology <CAH>
F;1/Modified site: acetylated amino end (Ala) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1.64,'W' <MOS>
:Cross-references: GB:M29707; NID:9144417; PIDN:AAA23087.1; PID:9144420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
C; Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_c
C; Accession: A22612
K; Wendorff, K.M.; Nishita, T.; Jabusch, J.R.; Deutsch, H.F.
J. Biol. Chem. 260, 6132, 1985
A; Title: The sequence of equine muscle carbonic anhydrase.
A; Reference number: A22612; MUID:85207593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 79.5; DE; DE; Pred. No. 2.5; 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: cenC
A;Start codon: GTG
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%; 26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%;
30.5%;
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                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-259 <WEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 29; Conserv
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
                                                                                                                                                                                                                                                                                   A; Accession: A22612
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Genetics:

256

q δ g

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RESULT

11;

90;

OY 35 GDA	Query Match Best Local Similarity 24.6%; Pred. No. 28; Matches 35; Conservative 18; Mismatches 46; Indels 43; Gaps 6; Qy 7 EELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPT 66
RESULT 10 F87327 conserved hypothetical protein CC0633 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: F87327 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647 A;Accession: F87327 A;Accession: F87327 A;Molecule type: DNA A;Residues: 1-818 <sto> A;Residues: 1-818 <sto> A;Cross-references: GB:AE005673; NID:q13421844; PIDN:AAK22618.1; GSPDB:GN00148</sto></sto>	<pre>Qy 105 VPLGGEQTLGDFEDSLEAALGK 126 b 315 VGAGGAAGTGDAANLKFALAR 336 RESULT 12 \$12566 translation initiation factor eIF-4B - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: \$12566 R;Milburn, S.C.; Hershey, J.W.B.; Davies, M.V.; Kelleher, K.; Kaufman, R.J. BMD J. 9, 2783-2790, 1990 A;Title: Cloning and expression of eukaryotic initiation factor 4B cDNA: sequence det A;Reference number: \$12566; MuID:90360989 A;Accession: \$12566 B;Milburn, B</pre>
C;Genetics: A;Gene CC0633 Query Match Best Local Similarity 27.2%; Pred. No. 25; Matches 41; Conservative 17; Mismatches 50; Indels 43; Gaps 8; Qy 22 RDPYANFMTFHLPGDAPVTWAFGRELLLOG-INRPSGDGDVHIAPTDFBGL 71	A.Residues: 1-611 cMLA A.Residues: 1-611 cMLA A.Cross-references: EMBL:X55733; NID:q288099; PIDN:CAA39265.1; PID:g288100 A.Cross-references: EMBL:X55733; NID:q288099; PIDN:CAA39265.1; PID:g288100 A.Cross-references: EMBL:X55733; NID:q288099; PIDN:CAA39265.1; PID:g288100 C.Genetics: A.Gene: GDB:EIF44B A.Cross-references: GDB:126410; OMIM:603928 A.Cross-references: GDB:126410; OMIM:603928 C.Superfamily: human translation initiation factor eIF-4B; ribonucleoprotein repeat hackeywords: blocked amino end; protein biosynthesis; RNA binding C.Keywords: blocked amino end; protein repeat homology <rrm2> C.Keywords: blocked amino end; protein repeat homology <rrm2> C.Keywords: blocked amino end; protein repeat homology <rrm2> C.Keywords: blocked amino end; protein biosynthesis; RNA binding C.Keywords: blocked amino end; brotein biosynthesis; RNA binding C.Keywords: blocked amino end; brotein biosynthesis; RNA binding C.Keywords: blocked amino end; blocked amino</rrm2></rrm2></rrm2>
Db 195 A-VSRNLRSPHYAAPITAPPITL-PAEAPKVVAFYLPQFHPFDENDTWMGKGFTEWTNVSK 252 QY 108 GQEQTLGDFEDSLEAALGKILAEE 131 QY 108 GQEQTLGDFEDSLEAALGKILAEE 131 Db 253 AQPQFLGHYQPRLPADLGFYDLRQREVLAQQ 283 RESULT 11 G83635 Probable ClpA/B-type chaperone PA0090 [imported] - Pseudomonas aeruginosa (strain PAO1) C.Species: Pseudomonas aeruginosa C.Species: Pseudomonas aeruginosa (strain PAO1) C.Species: Pseudomonas aeruginosa (strain PAO1)	Oy 14 PVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAP 65
C. Accession: G83635 R;Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 Nature 406, 969-964, 969-964	dehydratase (EC 4.2.1.1) III - rat e names: carbonic anhydrase III Rattus norvegicus (Norway rat) -Aug-1996 #sequence_revision 12-Aug-1 nn: 152551, A48856; B61530; S13896 -ID.; Carter, N.D.; Jeffery, S.; Edwar p. 8, 401-406, 1988 haracterization of cDNA clones for ra e number: 152551; MUID:89166882 preliminary; translated from GB/EMBL/ ; type: mRNA

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conserved hypothetical protein Atu6078 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: 11-3n-2002 #text_change 11-Jan-2002 C;Accession: AD3237 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl. Science 294, 2317-2332; 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Afrite: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A.Reference number: AB2577; PMID:11743193
A.Reference number: AB2577; PMID:11743193
A.Reference number: AB2577; PMID:11743193
A.Reference number: AB2577; PMID:11743193
A.Reference number: AR2678
A.Residues: 1-408 <KUR>
A.Residues: 1-408 <KUR>
A.Residues: 1-408 <KUR>
A.Resperimental source: Strain C58 (Dupont)
A.Reperimental source: Strain C58 (Dupont)
A.Genetics:
A.Genetics:
                                                                                                                                                              ----PPLVAFLDRTDKSVPLGQEQ 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSG-----DGDVHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLG 108
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                                                               24, TGYLPDTATATAVFLADRLGKPLLVEG - - - PAGVGKTELARAVAQATGSGLVRLQCYEGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 74.5; Ilarity 25.5%; Pred. No. 13; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12. KIPVELRYETRDPYAVRMTFHLPGDAPVTWA----
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he: 9548 sec
                                                                                                                           83 D--RALF------RAGA----
                                                                                                                                                                                                                                                   112 TLGDFEDSLEAALGKILAE 130
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nes 38; Conserv
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Best Local S:
Matches 38
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Job time: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 19-28, 'X', 30-33 <NAG>
A; Residues: 19-28, 'X', 30-33 <NAG>
A; Experimental source: Long-Evens Cinnamon
B; Chai, Y. C.; Jung, C.H.; Lii, C.K.; Ashraf, S.S.; Hendrich, S.; Wolf, B.; Sies, H.; Thc
Arch. Blochem. Blophys. 284, 270-278, 1991
A; Title: Identification of an abundant S-thiolated rat liver protein as carbonic anhydra
A; Reference number: $13896; MUID:91112820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: profein
A; Molecule type: profein
A; Residues: 25, X',27-34,38,'T',40-42,'XX',45-46,'S',48-51,'X',53-56,'RVV',74,'XXTFX',86
C; Superfamily: carbonate dehydratase; carbonic anhydrase homology
C; Keywords: blocked amino end; carbon-oxygen lyase; hydro-lyase
F;5-259/Domain: carbonic anhydrase homology <CAH>
                                                                                                                                                                          A; Molecule type: protein
A; Residues: 19-45;120-128, 'XFG', 132-142 <LYN>
A; Residues: 19-45;120-128, 'XFG', 132-142 <LYN>
A; Experimental source: Zucker, adipocytes
A; Note: sequence extracted from NCBI backbone (NCBIP:129636, NCBIP:129637)
R; Nagase, T.; Sugiyama, T.; Kawata, S.; Tarui, S.; Deutsch, H.F.; Taniguchi, N.
Comp. Biochem. Physiol. B 99, 199-201, 1991
A; Title: Analyses of polypeptides in the liver of a novel mutant (LEC rats) to hereditar
e III and triosephosphate isomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C) Accession: H70678
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Raiandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Ahuthors: Sqraes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID: 98295987
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-291 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:Z81451; GB:AL123456; NID:93261662; PIDN:CAB03770.1; PID:91666159
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTSEEALKQPDG 139
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A;Cross-references: GB:M22413; NID:g203224; PIDN:AAA40846.1; PID:g203225 R;Lynch, C.J.; Brennan, W.A.J.; Vary, T.C.; Carter, N.; Dodgson, S.J. Mm. J. Physiol. 264, EG21-EG30, 1993 A;Title: Carbonic anhydrase III in obese Zucker rats. A;Reference number: A48856; MUID:93236031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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Superfamily: hypothetical protein MTH1814
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A61530; MUID: 92070082
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26.6%;
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Best Local Similarity 25.99
Matches 36; Conservative
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GenCore version 4.5
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OM protein - protein search, using sw model

July 18, 2002, 14:31:56; Search time 45.63 Seconds (without alignments) 114.555 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-749-185-9 692 1 MSFLVSEELSFKIPVELRYE......FEDSLEAALGKILAEEQNAG 135

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	tion	equus cabal	cellulomona	homo sapien	rattus norv	mus musculu	mycobacteri	escherichia	rhodobacter	homo sapien	mus musculu	deinococcus	rattus norv	phormidium	schizosacch	mycobacteri	herpes simp	halobacteri	streptomyce	haemophilus	mns mnscnln	drosophila	mycobacteri	escherichia	homo sapien	mycobacteri	mycobacteri	mus musculu	buchnera ap	newcastle d	mycobacteri	pseudomonas	neurospora	Saccharomyo
	Description	P07450	P14090	P23588 1	P14141	P16015 p		P77489			_	_		_		_		-		_		_	_	-	_	_	_	_	_	_	_		869	20050
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SUMMAKIES	ID	CAH3_HORSE	GUNC_CELFI	IF4B_HUMAN	CAH3_RAT	CAH3_MOUSE	YQ31_MYCTU	YAGR_ECOLI	SECD_RHOCA	CAH3_HUMAN	LMA5_MOUSE	VATI_DEIRA	AIF1_RAT	CYF_PHOLA	HXK1_SCHPO	YT17_MYCTU	EXON_HSV2	ENDA_HALVO	GLN1_STRVR	RF3_HAEIN	E2K3_MOUSE	PS73_DROME	YW84_MYCTU	KDPE_ECOLI	2261_HUMAN	SYH_MYCLE	GYRA_MYCKA	EPB4_MOUSE	RPOC_BUCAI	RRPL_NDVB	UNG_MYCTU	YW40_PSEAE	GYS_NEUCR	ADG2 VEACH
	DB	<u>:</u> –	-	-	-	7	-	П	٦	٦	Н	П	-	7	-	-	Н	-	-	-4	Н	н	-	-	-		Н	П	П	-	Ч	7	-	,-
	Length	259	1101	611	259	259	432	732	554	259	3718	069	147	338	484	602	620	339	469	527	1114	252	143	225	1370	427	549	987	1407	2204	227	285	206	761
ď	Query Match	11.5	11.4	10.8	10.8	10.6		10.5	10.3	10.2	10.2	10.1	10.0	10.0	10.0	•								9.6		•	9.5		٠	•		9.5	9.5	6
	Score	79.5	79	75	74.5	73.5	73	72.5	71	70.5	70.5	70	69.5	69.5	69.5	69.5	69	68.5	68.5	68	67.5	67	66.5	66.5	66.5	99	99	99	99	99	65.5	65.5	65.5	55
	Result No.	7	2	m	4	D.	9	7	6 0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

. Q8ywh5 anabaena sp	P51537 nordotis ma	P14432 mus musculu	P34536 caenorhabdi	O53189 mycobacteri	P20013 trametes ve			-	005118 methylobact	Q49467 mycobacteri	P27002 thermus agu
MOAE_ANASP	MYG_NORMA	HA1T_MOUSE	YNC3_CAEEL	TIG_MYCTU	LIGC_TRAVE	GLY1_ASHGO	GLO2_RHOCA	ACCD_PORPU	KPYK_METEX	GYRA_MYCGO	SYFB_THETH
-	-	~4	7	٦	П	٦	٦	7	٦	-	-
165	377	384	421	466	372	382	256	288	483	550	785
9.4	9.4	9.4	9.4	9.4	9.3	9.3	9.5	9.5	9.5	9.5	9.5
65	65	. 65	65	65	64.5	64.5	64	64	64	, 64	64
34	32	36	37	38	39.	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1 CAH3_HORSE ID CAH3_HORSE STANDARD; PRT; 259 AA.		RN [1] RP SEQUENCE. RX MEDLINE-85207593; PubMed=3922970; RA Wendorff K.M., Nishita T., Jabusch J.R., Deutsch H.F.; RT "The sequence of equine muscle carbonic anhydrase.";	J. Biol. Chem. 260:6129-6132(1985)!- FUNCTION: REVERSIBLE HYDRATATION OF -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) -!- SUBCELLULAR LOCATION: CYtoplasmic!- SIMILARITY: BELONGS TO THE EUKARYOTI	FAMILY. PIR; A22612; HSSP; HSSP; InterPro; IPF Pfam; PF00194 ProDom; PD000 PROSITE; PS00	KW Lyase: Zinc; Acetylation. FT MOD_RES FT METAL FT <	Query Match 11.5%; Score 79.5; DB 1; Length 259; Best Local Similarity 26.6%; Pred. No. 0.9; Matches 29; Conservative 16; Mismatches 37; Indels 27; Gaps	Qy 24 PYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEG 70 1 1 1 1 1 1 1 1 1	Qy 71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119 : : : : : Db 139.IAVVGVFLKIGREKGEFQLFLDALDKIKTKGKEAPFTNFDPS 180	RESULT. 2 GUNC_CELFI ID GUNC_CELFI STANDARD; PRT; 1101 AA. AC P14090;

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EMBL; M29708; AAA23088.1; ALT_SEQ
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                                                                                                                                                                                                                                                                                                                                                                                               Coutinho J.B., Moser B., Kilburn D.G., Warren R.A.J., Miller R.C. Jr.; "Nucleotide sequence of the endoglucanase C gene (cenc) of Cellulomonas fini, its high-level expression in Escherichia coli, and characterization of its products."; Mol. Microbiol. 5:1221-1233(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2] SEQUENCE OF 1-64 FROM N.A., AND SEQUENCE OF 625-641.
MEDLINE-90103465; PubMed-2604391; Marren R.A.J., Miller R.C. Jr.;
Moser B., Gilkes N.R., Kilburn D.G., Warren R.A.J., Miller R.C. Jr.;
"Purification and characterization of endoglucanase C of Cellulomonas fimi, cloning of the gene, and analysis of in vivo transcripts of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92269585; PubMed-1375311; Coutinho J.B., Gilkes N.R., Warren R.A.J., Kilburn D.G., Miller R.C., Jr.; Liburn D.G., miller R.C., Jr.; Coutinho J.B., Gilkes N.R., Warren B.A.J., Kilburn D.G., and sephadex is mediated by the N-terminal repeats."; Mol. Microbiol. 6:1243-1252(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97074498; PubMed-8916925;
Johnson P.E., Joshi M.D., Tomme P., Kilburn D.G., McIntosh L.P.;
"Structure of the N-terminal cellulose-binding domain of Cellulomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fimi cenc determined by nuclear magnetic resonance spectroscopy.";
Biochemistry 35:14381-14394(1996).
-!- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
(1) ENDOCLUCANASES WHICH CUT INTERNAL BETA-1, 4-GLUCOSIDIC BONDS;
(2) EXOCELLOBIOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE
FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linkages in cellulose.
                                01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Endoglucanase C precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase C)
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SIMILARITY: CONTAINS 2 CELLULOSE-BINDING DOMAIN (CBD) REMOTELY
                                                                                                                                                                                                            Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas. NCSI_TaxID=1708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION OF IG-LIKE DOMAINS.
MEDLINE-97035265; PubMed-8860921;
Bateman A., Eddy S.R., Chothia C.;
"Members of the immunoglobulin superfamily in bacteria.";
Protein Sci. 5:1939-1942(1996).
                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appl. Environ. Microbiol. 55:2480-2487(1989).
                                                                                                                                                                                                                                                                                                             FROM N.A., AND SEQUENCE OF 33-42.
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                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 484;
MEDLINE=92065819; PubMed=1956299;
     Created)
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CELLULOSE-BINDING DOMAINS.
01-JAN-1990 (Rel. 13,
01-MAR-1992 (Rel. 21,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                      Cellulomonas fimi
                                                                                                                    (Cellulase C).
                                                                                                                                                                                                                                                                                                                SEQUENCE
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EMBL; X57858; CAA40993.1; -. EMBL; M29707; AAA23087.1; ALT_TERM.

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200 YGTSEPVFADGRMCVDLPGGQGNPWDAG--LVYNGV--PVGEGESYVLSFTASATPDMPV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milburn S.C., Hershey J.W.B., Davies M.V., Kelleher K., Kaufman R.J.; "Cloning and expression of eukaryotic initiation factor 4B cDNA: sequence determination identifies a common RNA recognition motif."; EMBO J. 9:2783-2790(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 YETRDPYAV--RMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methot N., Pause A., Hershey J.W., Sonenberg N., "The translation initiation factor eIF-4B contains an RNA-binding region that is distinct and independent from its ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; FALSE_NEG.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Signal; Repeat; Immunoglobulin domain; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1FBAD189CC5F8B5D CRC64;
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EIF4B.
                                                                                                                                                                                                                                                                                      ENDOGLUCANASE C.
CELLULOSE-BINDING 1.
                                                                                                                                                                                                                                                                                                                              CELLULOSE-BINDING 2
CATALYTIC.
CATALYTIC.
IG-LIKE DOMAIN 1.
IG-LIKE DOMAIN 2.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%; Score 79; DB 130.5%; Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM: N.A., AND PARTIAL SEQUENCE.
MEDLINE-90360989; PubMed-2330971;
PIR; $15271; $15271.
PBB; 1ULO; 01 ARR-97.
PBB; 1ULO; 01 ARR-97.
INTERPO; 1PR0013015; CBD_6.
INTERPO; 1PR001701, Glyco_hydro_9.
INTERPO; 1PR001701, Glyco_hydro_9.
INTERPO; 1PR001509; Ig_MHC.
INTERPO; 1PR001906; Ig_MHC.
PFam: PP022018; CBD_6; 2.
Pfam: PP022018; CBD_6; 2.
Pfam: PP02927; CelD_N; 1.
Pfam: PP02927; CelD_N; 1.
Pfam: PP00197; Ig; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE-94187701; PubMed-8139536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   115216 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 RLQV----GADRALFRAGAPPL 94
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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173
318
880
1006
1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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64
212
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SEQUENCE
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Best Local 5
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IF4B_HUMAN
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                                                                                                                                                                                                                                                                                                     STRAIN=Wistar; TISSUE=Liver;

X MEDLINE=20361776; PubMed=10900145;

MEDLINE=20361776; PubMed=10900145;

A Ikeda M., Ishii Y., Kato H., Akazawa D., Hatsumura M., Ishida T.,

A Matsusue K., Yamada H., Oguri K.;

T. Suppression of carbonic anhydrase III in rat liver by a dioxin-related toxic compound, coplanar polychlorinated biphenyl, T. 3,3,4,4,4,5-pentachlorobiphenyl.";

L Arch. Biochem. Biochem. Biophys. 380:159-164(2000).

C -: FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.

C -: SUBCELLULAR LOCATION: Cytoplasmic.

C -: SUBCELLULAR LOCATION: Cytoplasmic.

PAMILY.

FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTFGEALKQPDG 138
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01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-III).
                                                                                                                                                Mallis R.J., Jung C.-H., Chatterjee T.K., Fisher R.A., Thomas J.A.; "cDNA sequence of rat liver carbonic anhydrase III."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 74.5; DB 1; Length 259; 26.6%; Pred. No. 2.8;
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ZINC (CATALYTIC).
ZINC (CATALYTIC).
A -> G (IN REF. 1).
FG -> SE (IN REF. 1).
KL -> NV (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR001148; Carb_anhydrase. Pfam; PF00194; carb_anhydrase; 1. Probom; PD000865; Carb_anhydrase; 1. PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1. Lyase; 2inc.
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                             Biosci. Rep. 8:401-406(1988).
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259 AA;
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                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                         IISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAH3_MOUSE
P16015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                 Methot N., Song M.S., Sonenberg N.;

"A region rich in aspartic acid, arginine, tyrosine, and glycine (DRVG) mediates eukaryotic initiation factor 4B (eIF4B) self-association and interaction with eIF3.";

Mol. Cell. Biol. 16:5328-5334(1996).

-! FUNCTION: REQUIRED FOR THE BINDING OF MRNA TO RIBOSOMES. FUNCTIONS IN CLOSE ASSOCIATION WITH EIF4-F AND EIF4-A. BINDS NEAR THE 5'-TERMINAL CAP OF MRNA IN PRESENCE OF EIF4-A. BINDS ATP. PROMOTES THE ATPASE ACTIVITY AND THE ATP-DEPENDENT RNA UNWINDING ACTIVITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 TAPRAAREPNI-----DRSRL-PKSPPYTAFLGNLPYDVTEESIKEFFRGLNISAVRLP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 PVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVH-----IAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 PVSWADETDD------LEGDVSTTW------HSNDDDVYRAPPIDRSILP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAH3_RAT STANDARD; PRT; 259 AA. P141. 054961; 01-3An-1990 (Rel. 13, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

BEDLINE-SB166882. PubMed-2852973;
Kelly C.D., Carter N.D., Jeffery S., Edwards Y.H.;
"Characterisation of cDNA clones for rat muscle carbonic anhydrase
                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: SELF-ASSOCIATES AND INTERACTS WITH EIF3 P170 SUBUNIT. SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 75; DB 1; Length 611; 25.0%; Pred. No. 7; tive 15; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5EAD0891694D00D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 TOPEGLSDVSIRLQVGADRALFRAGAPPLVAFL----DRTDKSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein biosynthesis; Initiation factor; RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PLGQEQTLG----DFEDSLEAALGKILAEEQNAG 135
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                          MEDLINE-96413282; PubMed-8816444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X55733; CAA39265.1; -. PIR; S12566; S12566.
MIM; 603928; -.
                                                                                                                                                                                                                                                                                                                                               BOTH EIF4-A AND EIF4-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000504; RRM. Pfam; PF00076; rrm; 1. SMART; SMO0360; RRM; 1.
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nes 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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Best Local Si
Matches 39;
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NCBI_TaxID=562;
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P77489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAAELHLVHWNPRYNTFGEALKOPDG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAP-----TDPEG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                        Biochem. Genet. 27:17-30(1989).
-!- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
-!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
-!- SUBCELLULAR LOCATION: CYLOplasmic.
-!- SIMILARITY: BELONGS TO THE BUKARYOTIC-TYPE CARBONIC ANHYDRASE
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                         Tweedie S., Edwards Y.; "Mouse carbonic anhydrase III: nucleotide sequence and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 LSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E35B5CDDC4A54A93 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
19-CCT-2001 (Rel. 40, Last annotation update)
RV2631 OR MT2707 OR MTCY441.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%; Score 73.5; DE llarity 26.6%; Pred. No. 3.5; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 AA
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00194; Carb_anhydrase.
Probom; PD000865; Carb_anhydrase; 1.
PROSITE; PS00162; Cdr_co2_anhydrase; 1.
Lyase; Zinc. 0 0
                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001148; Carb_anhydrase.
                                                                             MEDLINE-89227981; PubMed-2496681;
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MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29397 MW;
                                                                                                                                                                                                                                                                                                 EMBL; M27796; AAA37355.1; -. PIR; A43641.
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SWISS-2DPAGE; P16015; MOUSE.
MGD; MGI:88270; Car3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 AA;
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hes 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                 SEQUENCE FROM N.A.
                                            NCBI_TaxID=10090;
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                                                                                                                                                                                   FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQ31_MYCTU
P71930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                studies.
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       Ω.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 PYAVRMTFHLPGDAPVTWAFG-----RELLLDGINRPSGDGDVHIAPTDPEGLSDVS 75
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                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and
       Harris
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Hamlin N., Holroyd Coliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Cutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5%; Score 73; DB 1; Length 432; 28.9%; Pred. No. 7.3; ive 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propriet is a series of the proteome. Convenior 393 and 200 cm, 20175CalD9BEED4 CRC64; SEGUENCE 432 AA; 45586 MW; 2F1175CalD9BEED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 -- IRLQV--GADRALFRAGAPPLVAFLDRTDKSVPLG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
116-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yagR.
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55 CGVRLLVGEGLDREELQ---PRLPAVMDRLDRAIPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 280225; CAB02365.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMESHIFT IN POSITION 257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MT2707; -.
TubercuList; Rv2631; -.
InterPro; IPR001233; UPF0027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01139; UPF0027; 1.
PROSITE; PS01288; UPF0027; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE007103; AAK47022.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.59
Best Local Similarity 28.99
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLSDVSIRLQVGADRAL--FRAG--APPLVAFLDRTDKSVPLGQEQTLG------DF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 GAPAVSFRFNVSGARAFGDYTAGHIGEPFAIVLDGKVISAPTIQAHIAGGSGIITGRFSI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 KLTFHPVLSTTSNPNAPV--ASGNELLPDAERQGLYHLLDEVPVVTGDDLTDARPTTDDN 294
FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).
SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
WHICH COMPRISE SECA, SECB, SECB, SECE, SECF, SECG AND SECY
                                                                   (BY SIMILARITY).
SUBCELULAR LOCATION: Integral membrane protein (By similarity).
SIMILARITY: BELONGS TO THE SECD/SECF FAMILY. SECD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.RMTFH-----LPGDAPVTWAFGREL------LLDGINRPSGDGDVHIAP-TDPE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=87092290; PubMed=3099285; Wade:R., Gunning.P., Eddy R., Shows T., Kedes L.; Wade:R., Gunning.P., Eddy R., Shows T., Kedes L.; Mucleotide sequence, tissue-specific expression, and chromosome location of human carbonic anhydrase III: the human CAIII gene is located on the same chromosome as the closely linked CAI and CAII genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo, sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86221704; PubMed-3086182;
Lloyd J., McMillan S., Hopkinson D., Edwards Y.H.;
"Nucleotide sequence and derived amino acid sequence of a cDNA
encoding human muscle carbonic anhydrase.";
Gene.41:233-239(1986).
                                                                                                                                                                                                                                                                                                                                                                                                         Protein transport; Translocation; Transmembrane; Membrane.
TRANSMEM 10 30 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 554;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DF2CBEEBA9F69EDF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.3%; Score 71; 27.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEATDLALLLRAGALPAGMTFLEERTIG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                        EMBL; U69979; AAB62801.1; -. InterPro; IPR003335; Secb_SecF. Pfam; PF02355; Secb_SecF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58943 MW;
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455
511
536
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435
491
516
554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAH3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
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Best Local (
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CAH3_HUMAN
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D
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                                                                                                                                                                                                                                                       K.,
Lin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular and immunological analysis of an ABC transporter complex
    SEQUENCE FROM N.A.

STAIN-KIZ / MGI555;

MEDLINE=97426617; Pubmed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.;
                                                                                                                                                                                                                                                Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: YAGR, YAGS AND YAGT COULD BE THREE SUBUNITS OF A DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldman B.S., Beckman D.L., Bali A., Monika E.M., Gabbert K.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                        ΙO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 732;
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO VERTEBRATE XANTHINE DEHYDROGENASES AND TC
R.PALUSTRIS 4-HYDROXYBENZOYL-COA REDUCTASE SUBUNIT HBAC.
                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01315; Ald_Xan_dh_C; 1.
Pfam; PF02738; Ald_Xan_dh_C2; 1.
Hypothetical protein; Oxidoreductase; Complete proteome.
SEQUENCE 732 AA; 78088 MW; AF198715794F0138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72.5; DB Pred. No. 15; US Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      required for cytochrome c biogenesis.";
J. Mol. Biol. 268:724-738(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein-export membrane protein secD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U73857; AAB18013.1; -.
EcoGene; EG13557; yagR.
InterPro; IPR000674; Aldxan_dh_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97318920; PubMed=9175857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000136; AAC73387.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELAEKAGIDPV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 DRALFRAGAPPL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECD_RHOCA
033517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Local Best Loc Matches

SECD_RHOCA

RESULT

366

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8

Gaps

42;

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'Completion of the N-terminal sequence of the murine Laminin alpha
                                                                                                         REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                9
                                86 PYRLRQ-FHL-----HWGSSDDHGSEHTVDGVKYAA---ELHLVHWNPKYNTFKEALKQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                24 PYAVRMTFHLPGDAPVTWA----FGRELLLDGINRPSGDGDVHIAPTDP------- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 -EGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%; Score 70.5; DB 1; Length 259; 24.1%; Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                               ZINC (CATALYTIC).
ZINC (CATALYTIC).
ZINC (CATALYTIC).
I -> V (IN REF. 2).
W; EFBC56CF7F721E4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                34;
Proc. Natl. Acad. Sci. U.S.A. 83:9571-9575(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMAS_MOUSE STANDARD; PRT; 3718 AA. Q61001; Q9JHQ6; 01-NOY-1997 (Rel. 35, Created) 01-NAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Laminin alpha-5 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                Pfam; PF00194; carb_anhydrase.
Probom: P0000865; Carb_anhydrase; 1.
PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
Lyase; Zinc.
                                                                                                                                                                                                      PIR; A22850; A25850.
PIR; A26850; A25850.
PIR; A26658; A26658.
PIR; A26690; A26690.
HSCP: POPPR: PIR; A26690.
                                                                                                                                                                                                                                                                            interPro; IPR001148; Carb_anhydrase.
                          MEDLINE=88056301; PubMed=2824285;
                                                                                                                                                                                                                                                                                                                                                           30 I
29440 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-92 FROM N.A. Timpl R., Sasaki T.;
                                                                                                                                                                                                                                                           HSC-2DPAGE; P07451; HUMAN. MIM; 114750; -.
                 PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                        0
93
95
118
30
259 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                 FAMILY
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                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                   METAL
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A Miner J.H., Lewis R.M., Sanes J.R.;

A Miner J.H., Lewis R.M., Sanes J.R.;

A Lobalited (NOV-1997) to the EMBL/GenBank/DDBJ databases.

LEDNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, 6 ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACRELLIAR MATRIX. COMPONENTS.

LISTORIAL ALPHA-5 CHAIN MAY BE THE MAJON LAMINA ALPHA CHAIN OF ADULT EPITHELIAL AND/OR ENDOTHELIAL BASAL LAMINAS.

LOBULES AND CONNESTING OF THREE DIFFERENT POLYPERTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISTING OF THREE SHORT ARMS WITH GLOBULES AT EACH END.

COMPRISTING ONE LONG E THREE SHORT ARMS WITH GLOBULES AT EACH END.

COMPRISTING SPECIFICITY: IN ADULT, HIGH LEVELS IN HEART, LUNG, AND KIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.

AND SKIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.

AND SKIN. EXPRESSED IN MANY TISSUES IN EMBRYONIC DAY 11.

MITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

MITH OTHER LAMININ 21.5 LAMININ GAIRE DOMAINS.

LISTURARITY: CONTAINS 21.5 LAMININ G-LIKE DOMAINS.

LISTURDARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
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R Pfam; PF0005; laminin_G; 2.

R Pfam; PF0005; laminin_Nterm; 1.

R PRINTS; PR00011: EGFLaNIN.

R Probom; PD003031; Laminin_B; 1.

R SMART; SM0018; EGF_Lam; 17.

R SMART; SM00281; Lams; 1.

R SMART; SM00281; Lams; 1.

R SMART; SM00181; Lams; 1.

R SMART; SM00181; Lams; 1.

R SMART; SM00182; LamG; 5.

R SMART; SM00182; LamG; 5.

R PROSITE; PS001186; EGF_1; 19.

R PROSITE; PS01186; EGF_2; 3.

R PROSITE; PS0025; Lam_GDOMAIN; 5.

R PROSITE; PS0025; Lam_GDOMAIN; 5.

R QIYCOPICIEIN; Basement membrane; Extracellular matrix; Coiled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                    5, and widespread
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases,
                                                                                                             MEDLINE-657BL/6 X CBA; TISSUE-Lung; MEDLINE-96081906; PubMed-7499364; Miner J.H., Lewis R.M., Sanes J.R.; Molecular cloning of a novel laminin chain, alpha expression in adult mouse tissues."; J. Biol. Chem. 270:28523-28526(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:105382; Lama5.
InterPro; IPR000561; EGF-like.
InterPro; IPR001086; LamNT.
InterPro; IPR001034; Laminin_B.
InterPro; IPR002049; Laminin_G.
InterPro; IPR001791; Laminin_G.
Pfan; Pf00052; Laminin_B: 1.
Pfan; PF00053; Laminin_B: 1.
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                                                                          SEQUENCE OF 84-3718 FROM N.A.
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3129 MTFHGHGFLPLALPDVAPIT----EVVYSGFGFRGTQDNNLLYYRTSPDGPYQVSLREG 3183
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09RWH3.
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
ATPI OR DR0695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 MTFH-----LPGDAPVTWAFGRELLLDGIN-RPSGDGDVHIAPTDPEGLSDVSIR-- 77
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Mite O., Bisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Woffat K.S., Qln H., Jiang L., Pemphile W., Crosby M., Shen M.,
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Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
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Matches 28; Conserv
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                LAMININ ALPHA-5 CHAIN,
LAMININ N-TERMINAL (DOMAIN VI).
LAMININ EGF-LIKE 1.
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CELL ATTACHMENT SITE (POTENTIAL).
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Gaps

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Biophys. Res. Commun. 224:855-862(1996).
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CONFLICT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             34 PGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVG-ADRALFRAGAP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WISTAR; TISSUE-Testis; MEDLINE-96311378; PubMed-8713135; Imai Y., Ibata I., Ito D., Ohsawa K., Kohsaka S.; Ima I. To D., Ohsawa K., Kohsaka S.; Ima I wovel gene ibal in the major histocompatibility complex class III region encoding an EF hand protein expressed in a monocytic
                                                                                                                                                                                                                                                                                                      InterPro; IPR002490; V_ATPase_sub_a.
Pfam; PF01496; V_ATPase_sub_a; 1.
Hydrolase; Hydrogen ion transport; Transmembrane; Complete proteome.
SEQUENCE 690 AA; 75223 WW; 30D7785EFF388EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Utans U., Arceci R.J., Yamashita Y., Russell M.E.;
"Cloning and characterization of allograft inflammatory factor-1:
novel macrophage factor identified in rat cardiac allografts with
                                                                                                                    CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Allograft inflammatory factor-1 (ALF-1) (Ionized calcium-binding adapter molecule 1) (Microglia response factor) (MRF-1).
AIF OR IBAI OR MRF1.
                                                               radiodurans R1.";
Science 286:1571-1577(1999).
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                    "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                           Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AA
                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 70; DB 29.9%; Pred. No. 25; Live 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Invest. 95:2954-2962(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-LEWIS; TISSUE-Heart;
MEDLINE-95286865; PubMed-7769138;
                                                                                                          GRADIENT ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P55009; P70491;
01-0CT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                 EMBL; AE001926; AAF10273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chronic rejection
                                                                                                                                     H(+)(Out)
                                                                                                                                                                                                                                                                                                DR0695;
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Best Local S
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                                                                                                                                                                                                                                                                               EXPRESSION PEAKS AT DAY 7.

-! INDUCTION: BY INTERFERON GAMMA.

-! SIMILARITY: SOME, TO EF-HAND CALCIUM BINDING PROTEINS.

-! SIMILARITY: STRONG, TO BALLOON ANGIOPLASTY RESPONSIVE TRANSCRIPT 1.
81 GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAALGK-----ILAEEQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 SLKRMLEKLGVPKTHLELKKLIREVSSGSEETF-SYSDFLRMMLGRRSAILRMILMYEEK 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AFG----RELLLDGINRP-----SGDGDVH-----IAPTDPEGLSDVSIRLQV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AFGLLKAQQEERLDGINKHFLDDPKYSSDEDLQSKLEAFKTKYMEFDLNGNGDIDI---M 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANCESTRAL CALCIUM SITE.
MSQSKDLQG -> MKPEEISR (IN
76EA1DAC977A71DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Oscillatoriales; Phormidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EF-HAND (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 69.5; DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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MEDLINE-97009001; Pubmed-8856106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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Pfam; PF00036; efhand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U17919; AAA80105.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB000818; BAA19189.1;
HSSP; P02593; 1AK8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 AA; 16827
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105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 33; Conserv
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Hexokinase 1 (EC 2.7.1.1).
HXK1 OR SPAC24H6.04.
                                                                                                                                                                                                                                                                                              hexokinases
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                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBURIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING
CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN.
-:- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE (PROBABLE).
-:- SIMILARITY: BELONGS TO THE CYTOCHROWE C FAMILY.

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Wagner M.J., Packer J.C.L., Howe C.J., Bendall D.S.; "Some characteristics of cytochrome f in the cyanobacterium Phormidium laminosum: its sequence and charge properties in the reaction with
                                                                                                                                                                                                                                         cyanobacterium Phormidium laminosum.";
Biochemistry 38:9590-9599(1999).
-!- FUNCTION: TRANSLOCATES PROTONS ACROSS THE THYLAKOID MEMBRANE AND TRANSFERS ELECTRONS FROM PHOTOSYSTEM II TO PHOTOSYSTEM II. IT RECEIVES ELECTRONS FROM THE RIESKE IRON-SULFUR PROTEIN AND PASSES THEM TO PLASTOCYANIN; THIS FUNCTION IS VERY SIMILAR TO THAT OF MITOCHONDRIAL CYTOCHROME C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 RIPEEMKEEVGPSYLFQPYADDKQNIVLVGPLPGDQYEEIVFPVLSPNPATNKSVAFGKY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 LLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTD---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 SIHLGANRGRG----QIYPTGEK-----SNNAVYNASAAGVITAIAKADDGSA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KIPVELRYETR-----DPYA-----VRMTFHLPGDA------PV------TWAFGRE 46
                                                                                                                                                         MEDLINE=99352179; PubMed=10423236;
Carrell C.J., Schlarb B.G., Bendall D.S., Howe C.J., Cramer W.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 338;
                                                                                                                                                                                                  Smith J.L.; shift soluble domain of cytochrome f from the "Structure" of the soluble domain of cytochrome f from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01333; Apocytochrome_F; 1.
PRINTS; PR00610; CYTOCHROMEF.
PROSITE; PS00190; CYTOCHROME_C; 1.
Electron transport; Heme; Photosynthesis; Photosystem I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APOCYTOCHROME F.
IRON (HEME AXIAL LIGAND).
HEME (COVALENT).
HEME (COVALENT).
IRON (HEME AXIAL LICAND).
#; BD3D52036181FB50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 ------KSVPLGQEQTLGDFEDSLEAALGKILAEEQNAG 135
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                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.90 ANGSTROMS) OF 46-295
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Last sequence update)
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); Mismatches
                                                                                       Biochim. Biophys. Acta 1276:246-252(1996).
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SIGNAL 1 45
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InterPro; IPR000345; CytC_heme_bind.
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22.3%; Final
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66 H
70 I
36069 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y09612; CAA70824.1; -.
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32,
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Best Local Similarity
Matches 37; Conserv
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46
69
70
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                                                                    plastocyanin.
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01-NOV-1995
15-JUL-1998
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Q09756;
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HXK1_SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: HAS LOW AFFINITY FOR GLUCOSE AND SOME OF ITS ANALOGS.
-!- CATALYTIC ACTIVITY: ATP + D-haxose = ADP + D-haxose 6-phosphate.
-!- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
-!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96140736; PubMed-8549830;
Petit T., Blazquez M.A., Gancedo C.;
"Schizosaccharomyces pombe possesses an unusual and a conventional
hexokinase: blochemical and molecular characterization of both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ELSFKIPVELRYETRDPYAVRMTFHL---PGDAPV--TWAFGRELLLDGINRPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 EEQFTIPTELLHRVTDRFVSELYKGLTTNPGDVPMVPTWIIGTP---DGNEHGSYLALDL
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BINDING 115 115 ATP (BY SIMILARITY).
DOMAIN 154 180 GLUCOSE-BINDING (POTENTIAL).
SEQUENCE 484 AA; 53597 WW; 16550F19E6BBB0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches . 52;
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16-OCT-1996 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Hypochetical 65.8 kDa protein Rv2917.
RV2917 OR MT2985 OR MTCY338.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barrell B.G., Rajandream M.A., Walsh S.V.;
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ProDom; PD001109; Hexokinase; 1.
PROSITE; PS00378; HEXOKINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001312; Hexokinase.
Pfam; PF00349; hexokinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X92894; CAA63487.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEBS Lett. 378:185-189(1996)
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Best Local Similarity 26.29
Matches 33; Conservative
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HSSP; P19367; 1HKC.
                                                                                                                                                                                                             Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=4896;
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Job time: 946 sec

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                                                                                                                                                                                                                                                           Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bardon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Davies K., Bardon D., Chillingworth T., Connor R., Davies R., Devlin K., Krogh A., McLean J., Moule S., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Shelton S., Squares S., Squares R., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 VRTEARKTLVVFDEIHHGGDAK-TWGDAIREAFGDATRRLALTGTPFRSDDSPIPFVSYQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEGLSDVSIRLQV----GADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSLEAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.0%; Score 69.5; DB 1; Length 602; Best Local Similarity 30.5%; Pred. No. 24; Matches 40; Conservative 11; Mismatches 57; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 LRYETRDPYAVRMTFHLPGDAPVTW-----AFG---RELLLDGINRPSGDGDVHIAPTD 67
                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: STRONG, TO M.LEPRAE ML1624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ALC.

11GR; MT2985; -.

A TUBCCULIST; RV2917; -.

R InterPro; IPR001410; DEAD.

DR SMART; SM00382; AAA; 1.

DR SMART; SM00487; DEXDC: 1.

W Hypotherical protein; Complete proteome.

W Hypotherical protein; Complete proteome.

TOTAL STORY ST
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EMBL; AE007120; AAK47311.1; -.
                                                                                                                                                                                                                                            MEDLINE=98295987; PubMed=9634230;
Mycobacterium tuberculosis
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                                                                                                                                                                      SEQUENCE FROM N.A.
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Search completed: July 18, 2002, 14:31:57

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99BLC7
99RDC04
99RAG7
99RAG7
99L742
99L718
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99L71922
99RE2
 (without alignments)
166.638 Million cell updates/sec
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692
1 MSFLVSEELSFKIPVELRYE......FEDSLEAALGKILAEEQNAG 135
                                                                                       July 18, 2002, 14:30:57; Search time 140.15 Seconds
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            4.5
Compugen Ltd.
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            GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

09blc6 cellana gra 09blc7 aplysia kur 09k0c4 neisseria m 09rkd0 streptomyce 09aag7 caulobacter 09e175 escherichia 09i742 pseudomonas 091218 streptomyce 093h9 streptomyce 09by5 caenorhabdi 09ub29 caenorhabdi 09ub28 caenorhabdi 09af19 streptomyce 09sr03 arabidopsis 034788 bacillus su 09k452 streptomyce 099k7 mus musculu 099k10 porcine tes P6465 escherichia 099f19 porcine tes 099f19 porcine tes P6465 escherichia

ALIGNMENTS

Q9rwe6 deinococcus Q99fi5 porcine tes

RESULT 1	QYEYBS ID OPPORS. PRELIMINARY; PRT; 145 AA.	01-MAR-2001 (TrEMBLrel. 16,	DI 01-MAK-2001 (TrEMBLEEL. 10, Last sequence upwate) DI 01-OCT-2001 (TrEMBLEEL. 18, Last annotation update)	SSGA.	OS Streptoverticillium netropsis (Streptoverticillium flavopersicus).		RP SEQUENCE FROM N.A.	RA van Wezel G.P., Rousseau C., Kraal B.; RT "Cloning and sequencing of the Streptomyces netropsis ssqA gene.";				Query Match 100.0%; Score 692; DB 2; Length 145; Best Local Similarity 100.0%; Pred. No. 8.3e-62;	ative (Qy 1 MSFLVSEELSFKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGD 60	Dh 11. MERI VERRI CRIVI BUYEN DARBURDAN ANTHAN ECRETITA CHINELLE III	٠	Qy 61: VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120		Db 71 VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 130	1	OY 121 EALGRIAGEONG 135	Dh 131 EARLGETTAEFONAG 145	1	<u> </u>
	o: Sp_manmal:* 7: sp_mhc:* 8: sp_oraanelle:*		10: Sp_rodent:*	12: sp_virus:*	14: sp_unclassIfled:*	 17: sp_archeap:*	Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Ouerv	Score Match Length DB ID Description	692 100.0 145 2 09F9B5 09F9b5 streptovert	87.6 136 2 P95753	79.2 136 2 09x9u2 09x9u2	544 78 6 135 2 09F9B7 09F9B7 8treptomyce	35.5 159 2 Ogt.268	34.2 142 2 09S2F7 . 09s2f7	156 2 Q9FC07 . Q9fc07	23.0 138 2 Q9X7M8	2 Q9X7R1	13.0 126 2 Q9KKC9	2 Q9ACIZ	11.6 514 16 09UVC9	11.4 341 16 Q9CKD1 Q9C	76.5 11.1 313 17 Q9HSS8 Q9hss8 halobacteri
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Result No.

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Streptomycineae; Streptomycetaceae; Streptomyces
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122 DEALDRILAEEQSAG 136
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                                                                               STRAIN=A3(2);
Seeger K., Harris D.;
Submitted (JUL-1999)
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James K.D., Parkhill
Submitted (JUL-1999)
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105; Conserva
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    Actinomycetales;
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                             STRAIN-B2682;
Shinichi K., Ensign J.;
"Cloning and characterization of a gene involved in sporulation and
cell division of Streptomyces griseus.";
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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"Cloning and characterization of a gene involved in regulation of
"sporulation and cell division of Streptomyces griseus.";
Nippon Hosenkin Gakkaishi 9:136-151(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=B2682;
Kawamoto S., Ensign J.C.;
"Isolation of mutants of Streptomyces griseus that sporulate in nutrient rich media.";
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Pred. No. 3.2e-53;
7; Mismatches 12; Indels
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Best Local Similarity 85.99
Matches 116; Conservative
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                                                                                                                                                                Streptomyces griseus.
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SEQUENCE FROM N.A.
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Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J., Klashl H., Hopwood D.A.;

"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL, AL096823; CA846664.1;

SEQUENCE 136 AA; 14920 MW; 4B67CIFIEOBECC88 CRC64;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
NCBI_TaxID=121022;
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the EMBL/GenBank/DDBJ databases
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
van Wezel G.P., Rousseau C., Kraal B.;
van Wezel G.P., Rousseau C., Kraal B.;
"Cloning and sequencing of the Streptomyces albus ssgA gene.";
"Cloning and sequencing of the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF195771; AAG28482.1; .
SEQUENCE 135 AA; 14735 MW; OFCBF4BDBZBA201B CRC64;
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121 DDALNRSLAEEQSAG 135
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Seeger K.J., Harris D
Submitted (JAN-2000)
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EMBL, AL096852; CAB51005.1; ... SEQUENCE 142 AA, 15364 MW; 857862390AA51CCB CRC64;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL137778; CAB70943.1;
EMBL, AL137778; CAB70943.1;
EMBLOBIOLE 159 AA; 17472 MW; BA41013F940D7315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61: VHIAPTDPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLGDFEDSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                              33 LRLVVSSESSLPVPAGLRYDTADPYAVHATFHTGAEETVEWVFARDLLAEGLHRPTGTGD 92
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                            Query Match 35.5%; Score 246; DB 2; Best Local Similarity 43.1%; Pred. No. 5.1e-17; Matches; 56; Conservative 15; Mismatches 55
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RESULT Q9FC07

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STRAIN=A3(2);
MEDLINE-97000351; PubMed=8843436;
Redenbach M., Klesser H.M., Denapaite D., Eichner A., Cullum J.,
Klasshi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 RTVLEFHAPEGTAVIHVR------SGELRRFLQAAGELVPVGLEHLQLDLDHD 129
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MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kisser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood DA.;
"A set of ordered cosmids and a detailed genetic and physical map
A Streptomyces coellicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049863; CAB42928.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 138;
                                                                                                                                                       Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Indels
                                     STRAIN=A3(2);
Oliver K., Harris D.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                     F531BA295144ABA5 CRC64;
                                                                                                                                                                                                                                                                                                                            the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049587; CAB40672.1; -.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                     138 AA; 15261 MW;
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SC5H1.03.
Streptomyces coellcolor.
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Submitted (MAY-1999)
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77 VRVWPSKTEGRSVVLVALSSPDGDALLEAPTPQVSAWLERTLRAVPPGTEGAQLGIDDGL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Saunders D.C., Harris D.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL391041; CACOL575.1. -
SEQUENCE 156 AA; 17188 MW; 7181972EEFF33FBO CRC64;
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Last annotation update)
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
PUTATIVE REGULATOR.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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Best Local Similarity
Matches 48; Conserv
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                                     121 EAALGK 126
                                                                          137 AELLAR 142
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Scheer M.P., van der Maarel S., Kuebart S., Schulz A., Wirth J., Schweiger S., Ropers H.-H., Nothwang H.G.; "DXS6673E Encodes a Predominantly Nuclear Protein, and Its Mouse Ortholog DXHXS6673E Is Alternatively Spliced in a Developmental and Tissue-Specific Manner.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEGLSDVSIRLQVGA 82
                                                                                                    Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.orgi:TaxID=1902;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Redenbach M., Ikeda K., Yamasaki M., Kinashi H.;
Cloning and physical mapping of the EcoRI fragments of the giant
linear plasmid SCP1.".
J. Bacteriol. 180:2796-2799(1998).
Bacteriol. 180:2796-2799(1998).
InterPro; IPRO10687, PTP. GTP. A.
SEQUENCE 537 AA; 58705 MW; 638B8F89EB02D821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 81; DB 2; Length 537;
Pred. No. 8.8;
5; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    Brown S.P., Murphy L.D., Harris D.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
PUTATIVE ATP/GTP-BINDING PROTEIN.
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Last sequence update)
Last annotation update)
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EMBL; AF156605; AF37800.1; -
MGD; MGI:1927231; Zfp261.
SEQUENCE 1370 AA; 152878 MW:
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36.0%;
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Best Local Similarity 36.0
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                   STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2)
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Q9JLM4
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9
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EMBL; ALJ32674; CAB59654.1; -.
Hypothetical protein.
SEQUENCE 126 AA; 13742 MW; D54A8574D28B4D69 CRC64;
                                                                                                                                                                                                                       71 LSDVSIRLQVGAD-----RALFRAGAPPLVAFLDRTDKSVPLGQEQT-LGDFEDSLE 121
                                                                                           Gaps
                                                                                                                         11 FKIPVELRYETRDPYAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDPEG 70
                                                                                                                                                31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 IPVELRYETR-DPYAVRMTFHLPG-----DAPVTWAFGRELLLDGINRPSGDGDVHIAPT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 126;
                                                       Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRVQAVVEFHSPQGCSVVQFE----NKALIR-----FLRRT 116
15741 MW; E24AA52C00AF40F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ------DPEGLSDVSIRLQVGADRALFRAGAPPLVAFLDRT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 13.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 103.5; DB 2; 33.3%; Pred. No. 0.0074; tive 10; Mismatches 29;
                                                   19.1%; Score 132.5; DB 2; 30.6%; Pred. No. 1.1e-05; Live 21; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                      126 AA
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 33.3%;
Conservative 1
                                               Query Match
Best Local Similarity 30.69
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                          140 A 140
                                                                                                                                                                                                                                                                        122 A 122
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537 AA

PRT;

PRELIMINARY;

RESULT 12 Q9ACY2 ID Q9ACY2

82

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Gaps

26;

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Search completed: July 18, 2002, 14:30:58
Job time: 947 sec
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                                                                                         Q9CKD1
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ZA91/ SEROROUP A / SEROTYPE 4A;
MEDLINE-2022556; PubMed-10761919;
MEDLINE-2022556; PubMed-10761919;
Rales S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamilin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spraft B.G., Barrell B.G.;
meningitidis 22491.
                                                                                                    72 SDVSIRLQVGADRALFRAGAPPLVAFLDRTDKSVPLGQEQTLG--DFEDSLEAALG---- 125
                                                                                                                   20 LAGDLPVDMEFGEDLLESQTAPSRGWAPPGPSPSSGALDLLDTPSG-----LEKDPGGV 73
                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90; Gaps
                                                    ------LDGINRPSGDGDVHIAPTDPEGL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ELRYETRDPYA------VRMTFHLP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 GDA------PVTWAF-GRELLL--DGI-----NRPSGDGDVHIAPTDP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GLSDVSIRLQVGAD------RALFRAGAPPLVAFL 98
   Length 1370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 514;
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                            Indels
                                                                                                                                                                                                                                                               01-07T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE AMIDOPHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00443; GATĀSE_TYPE_II; UNKNOWN_1.
PROSITE; PS00103; PUR_PRR_TRANSFER; 1.
COMDLete Protecome; Glycosyltransferase; Transferase.
SEQUENCE 514 AA; 56010 WW; 57188EF89EA6E9E4 CRC64;
                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
EMB.; ALL62754; CAB84172.1; -185P: P00496; 1ECB.
   DB 11;
30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 80; DB 16; 23.0%; Pred. No. 10; live 24; Mismatches 53;
                                                                                                                                                                                                                                             514 AA
 11.7%; Score 81; DB 26.9%; Pred. No. 30; ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000583; GATase_2.
InterPro; IPR000836; Pribosyltran.
InterPro; IPR002375; Pur_pyr_pr_transf.
                                                    33 LPGDAPVTWAFGRELL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00310; GATase_2; 1.
Pfam; PF00156; Pribosyltran; 1.
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSFLVSEELSFKIPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 404:502-506(2000)
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                     123 EVMPPDPGAG 132
                                                                                                                                                    126 KILAEEQNAG 135
Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C44.UNW;
                                                                                                                                                                                                                                                                                                                   PURF OR NMA0892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 E--
                                                                                                                                                                                                                                         09JVC9;
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404 EVRYPNVYGIDMPTREELIANGRSAAEIAAEIGADGIVFQDLGDLEAVVKALNPKIESF- 462
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24) (PORPHOBILINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 YAVRMTFHLPGDAPVTWAFGRELLLDGINRPSGDGDVHIAPTDP----EGLSDVSIRLQV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S. A. 98:3460-3465(2001).
-i- CATALYTIC ACTIVITY: 2 5-AMINOLEVULINATE = PORPHOBILINOGEN + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%; Score 79; DB 16; Length 341; 29.9%; Pred. No. 7.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro: IPR001731; D_ala_dehydratase.
Pfam; PF00490; ALAb; I.
PR00144; DALDHYDRTASE.
ProDom; PD002304; D_ala_dehydrtse; 1.
PR0STITE; PS001069; D_ALA_DEHYDRATASE; 1.
Complete proteome; Lyase; Porphyrin blosynthesis.
EQUENCE 341 AA; 38389 MW; E28FA4503960A587 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                          253 GADMYWVKPGMPYLDLVYRVKTHFGVPTFAYQVSGEY 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GADRALFRAGAPPL-VAFLDRTDKSVPLGQEQTLGDF 116
                                                                                                                                                                                                                   341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-PM70;
MEDLINE-21145866; Pubmed-11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            SYNTHASE) (ALADH).
HEMB OR PM1692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                         Q9CKD1;
                                                                                                                                                                                                                Q9CKĎ1
                                                                                                                                                                    RESULT 15
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